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<b>(21) International Application Number:</b> PCT/US97/20313 <b>(22) International Filing Date:</b> 5 November 1997 (05.11.97)  <b>(30) Priority Data:</b> 60/030,455                      6 November 1996 (06.11.96)                      US  <b>(71) Applicant (for all designated States except US):</b> WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH [US/US]; Nine Cambridge Center, Cambridge, MA 02142 (US).  <b>(72) Inventors; and</b> <b>(75) Inventors/Applicants (for US only):</b> LANDER, Eric, S. [US/US]; 151 Bishop Allen Drive, Cambridge, MA 02138 (US). WANG, David [CN/US]; Apartment 314, 276 Mass- achusetts Avenue, Arlington, MA 02173 (US). HUDSON, Thomas [CA/US]; 361 Metcalfe Avenue, Westmount, Quebec H3Z 2J2 (CA).  <b>(74) Agents:</b> GRANAHAN, Patricia et al.; Hamilton, Brook, Smith & Reynolds, Two Militia Drive, Lexington, MA 02173 (US).		<b>(81) Designated States:</b> JP, US, European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE).  <b>Published</b> <i>Without international search report and to be republished upon receipt of that report.</i>
<b>(54) Title:</b> BIALLELIC MARKERS  <b>(57) Abstract</b>  The invention provides nucleic acid segments of the human genome including polymorphic sites. Allele-specific primers and probes hybridizing to regions flanking these sites are also provided. The nucleic acids, primers and probes are used in applications such as forensics, paternity testing, medicine and genetic analysis.		

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## BIALLELIC MARKERS

## RELATED APPLICATIONS

This application claims priority to U.S. provisional application Serial No. 60/030,455, filed November 6, 1996, the entire teachings of which are incorporated herein by reference.

## BACKGROUND OF THE INVENTION

The genomes of all organisms undergo spontaneous mutation in the course of their continuing evolution, generating variant forms of progenitor sequences (Gusella, *Ann. Rev. Biochem.* 55, 831-854 (1986)). The variant form may confer an evolutionary advantage or disadvantage relative to a progenitor form or may be neutral. In some instances, a variant form confers a lethal disadvantage and is not transmitted to subsequent generations of the organism. In other instances, a variant form confers an evolutionary advantage to the species and is eventually incorporated into the DNA of many or most members of the species and effectively becomes the progenitor form. In many instances, both progenitor and variant form(s) survive and co-exist in a species population. The coexistence of multiple forms of a sequence gives rise to polymorphisms.

Several different types of polymorphism have been reported. A restriction fragment length polymorphism (RFLP) is a variation in DNA sequence that alters the length of a restriction fragment (Botstein et al., *Am. J. Hum. Genet.* 32, 314-331 (1980)). The restriction fragment length polymorphism may create or delete a restriction site, thus changing the length of the restriction fragment.

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RFLPs have been widely used in human and animal genetic analyses (see WO 90/13668; W090/11369; Donis-Keller, *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 85-99 (1989)). When a heritable trait can be linked to a particular RFLP, the presence of the RFLP in an individual can be used to predict the likelihood that the animal will also exhibit the trait.

Other polymorphisms take the form of short tandem repeats (STRs) that include tandem di-, tri- and tetra-nucleotide repeated motifs. These tandem repeats are also referred to as variable number tandem repeat (VNTR) polymorphisms. VNTRs have been used in identity and paternity analysis (US 5,075,217; Armour et al., *FEBS Lett.* 307, 113-115 (1992); Horn et al., WO 91/14003; Jeffreys, EP 370,719), and in a large number of genetic mapping studies.

Other polymorphisms take the form of single nucleotide variations between individuals of the same species. Such polymorphisms are far more frequent than RFLPs, STRs and VNTRs. Some single nucleotide polymorphisms occur in protein-coding sequences, in which case, one of the polymorphic forms may give rise to the expression of a defective or other variant protein and, potentially, a genetic disease. Examples of genes, in which polymorphisms within coding sequences give rise to genetic disease include  $\beta$ -globin (sickle cell anemia) and CFTR (cystic fibrosis). Other single nucleotide polymorphisms occur in noncoding regions. Some of these polymorphisms may also result in defective protein expression (e.g., as a result of defective splicing). Other single nucleotide polymorphisms have no phenotypic effects.

Single nucleotide polymorphisms can be used in the same manner as RFLPs and VNTRs, but offer several advantages. Single nucleotide polymorphisms occur with greater



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frequency and are spaced more uniformly throughout the genome than other forms of polymorphism. The greater frequency and uniformity of single nucleotide polymorphisms means that there is a greater probability that such a

5 polymorphism will be found in close proximity to a genetic locus of interest than would be the case for other polymorphisms. The different forms of characterized single nucleotide polymorphisms are often easier to distinguish than other types of polymorphism (e.g., by use of assays

10 employing allele-specific hybridization probes or primers).

Only a small percentage of the total repository of polymorphisms in humans and other organisms has been identified. The limited number of polymorphisms identified to date is due to the large amount of work required for

15 their detection by conventional methods. For example, a conventional approach to identifying polymorphisms might be to sequence the same stretch of DNA in a population of individuals by dideoxy sequencing. In this type of approach, the amount of work increases in proportion to

20 both the length of sequence and the number of individuals in a population and becomes impractical for large stretches of DNA or large numbers of persons.

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## SUMMARY OF THE INVENTION

The invention provides nucleic acid sequences comprising nucleic acid segments of from about 10 to about 200 bases as shown in the Table, column 7, including a polymorphic site. Complements of these segments are also included. The segments can be DNA or RNA, and can be double- or single-stranded. Segments can be, for example, 10-20, 10-50 or 10-100 bases long. Preferred segments include a biallelic polymorphic site. The base occupying the polymorphic site in the segments can be the reference (Table, column 3) or an alternative base (Table, column 4).

The invention further provides allele-specific oligonucleotides that hybridize to a segment of a fragment shown in the Table, column 7, or its complement. These oligonucleotides can be probes or primers. Also provided are isolated nucleic acids comprising a sequence shown in the Table, column 7, or the complement thereto, in which the polymorphic site within the sequence is occupied by a base other than the reference base shown in the Table, column 3.

The invention further provides a method of analyzing a nucleic acid from an individual. The method determines which base is present at any one of the polymorphic sites shown in the Table. Optionally, a set of bases occupying a set of the polymorphic sites shown in the Table is determined. This type of analysis can be performed on a number of individuals, who are tested for the presence of a disease phenotype. The presence or absence of disease phenotype is then correlated with a base or set of bases present at the polymorphic sites in the individuals tested.

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## DETAILED DESCRIPTION OF THE INVENTION

## DEFINITIONS

- An oligonucleotide can be DNA or RNA, and single- or double-stranded. Oligonucleotides can be naturally occurring or synthetic, but are typically prepared by synthetic means. The oligonucleotides of the present invention can comprise all of an oligonucleotide sequence presented in column 7 of the Table or a segment of such an oligonucleotide which includes a polymorphic site.
- Oligonucleotides can be all of a nucleic acid segment as represented in column 7 of the Table; a nucleic acid sequence which comprises a nucleic acid segment represented in column 7 of the Table and additional nucleic acids (present at either or both ends of a nucleic acid segment of column 7); or a portion (fragment) of a nucleic acid segment represented in column 7 of the Table which includes a polymorphic site. Preferred oligonucleotides of the invention include segments of DNA, or their complements, which include any one of the polymorphic sites shown in the Table. The segments can be between 5 and 250 bases, and, in specific embodiments, are between 5-10, 5-20, 10-20, 10-50, 20-50 or 10-100 bases. The polymorphic site can occur within any position of the segment. The segments can be from any of the allelic forms of DNA shown in the Table.
- Hybridization probes are oligonucleotides which bind in a base-specific manner to a complementary strand of nucleic acid. Such probes include peptide nucleic acids, as described in Nielsen et al., *Science* 254, 1497-1500 (1991).
- As used herein, the term primer refers to a single-stranded oligonucleotide which acts as a point of initiation of template-directed DNA synthesis under appropriate conditions (e.g., in the presence of four different nucleoside triphosphates and an agent for

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polymerization, such as, DNA or RNA polymerase or reverse transcriptase) in an appropriate buffer and at a suitable temperature. The appropriate length of a primer depends on the intended use of the primer, but typically ranges from 15 to 30 nucleotides. Short primer molecules generally require cooler temperatures to form sufficiently stable hybrid complexes with the template. A primer need not reflect the exact sequence of the template, but must be sufficiently complementary to hybridize with a template.

10 The term primer site refers to the area of the target DNA to which a primer hybridizes. The term primer pair refers to a set of primers including a 5' (upstream) primer that hybridizes with the 5' end of the DNA sequence to be amplified and a 3' (downstream) primer that hybridizes with 15 the complement of the 3' end of the sequence to be amplified.

As used herein, linkage describes the tendency of genes, alleles, loci or genetic markers to be inherited together as a result of their location on the same 20 chromosome. It can be measured by percent recombination between the two genes, alleles, loci or genetic markers.

As used herein, polymorphism refers to the occurrence of two or more genetically determined alternative sequences or alleles in a population. A polymorphic marker or site 25 is the locus at which divergence occurs. Preferred markers have at least two alleles, each occurring at frequency of greater than 1%, and more preferably greater than 10% or 20% of a selected population. A polymorphic locus may be as small as one base pair. Polymorphic markers include 30 restriction fragment length polymorphisms, variable number of tandem repeats (VNTR's), hypervariable regions, minisatellites, dinucleotide repeats, trinucleotide repeats, tetranucleotide repeats, simple sequence repeats,

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and insertion elements such as Alu. The first identified allelic form is arbitrarily designated as the reference form and other allelic forms are designated as alternative or variant alleles. The allelic form occurring most frequently in a selected population is sometimes referred to as the wildtype form. Diploid organisms may be homozygous or heterozygous for allelic forms. A diallelic or biallelic polymorphism has two forms. A triallelic polymorphism has three forms.

10 A single nucleotide polymorphism occurs at a polymorphic site occupied by a single nucleotide, which is the site of variation between allelic sequences. The site is usually preceded by and followed by highly conserved sequences of the allele (e.g., sequences that vary in less than 1/100 or 1/1000 members of the populations).

A single nucleotide polymorphism usually arises due to substitution of one nucleotide for another at the polymorphic site. A transition is the replacement of one purine by another purine or one pyrimidine by another pyrimidine. A transversion is the replacement of a purine by a pyrimidine or vice versa. Single nucleotide polymorphisms can also arise from a deletion of a nucleotide or an insertion of a nucleotide relative to a reference allele. Typically the polymorphic site is occupied by a base other than the reference base. For example, where the reference allele contains the base "T" at the polymorphic site, the altered allele can contain a "C", "G" or "A" at the polymorphic site.

Hybridizations are usually performed under stringent conditions, for example, at a salt concentration of no more than 1 M and a temperature of at least 25°C. For example, conditions of 5X SSPE (750 mM NaCl, 50 mM NaPhosphate, 5 mM EDTA, pH 7.4) and a temperature of 25-30°C, or equivalent

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conditions, are suitable for allele-specific probe hybridizations. Equivalent conditions can be determined by varying one or more of the parameters given as an example, as known in the art, while maintaining a similar degree of identity or similarity between the target nucleotide sequence and the primer or probe used.

The term "isolated" is used herein to indicate that the material in question exists in a physical milieu distinct from that in which it occurs in nature. For example, an isolated nucleic acid of the invention may be substantially isolated with respect to the complex cellular milieu in which it naturally occurs. In some instances, the isolated material will form part of a composition (for example, a crude extract containing other substances), buffer system or reagent mix. In other circumstance, the material may be purified to essential homogeneity, for example as determined by PAGE or column chromatography such as HPLC. Preferably, an isolated nucleic acid comprises at least about 50, 80 or 90 percent (on a molar basis) of all macromolecular species present.

#### I. Novel Polymorphisms of the Invention

The novel polymorphisms of the invention are listed in the Table. The first column of the Table lists the names assigned to the fragments in which the polymorphisms occur. The fragments are all human genomic fragments. The sequence of one allelic form of each of the fragments (arbitrarily referred to as the prototypical or reference form) has been previously published. These sequences are listed at <http://www-genome.wi.mit.edu/> (all STS's (sequence tag sites)); <http://shgc.stanford.edu> (Stanford STS's); and <http://ww.tigr.org/> (TIGR STS's). The Web sites also list primers for amplification of the fragments,

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and the genomic location of fragments. Some fragments are expressed sequence tags, and some are random genomic fragments. All information in the websites concerning the fragments listed in the Table is incorporated by reference  
5 in its entirety for all purposes.

The second column lists the position in the fragment in which a polymorphic site has been found. Positions are numbered consecutively with the first base of the fragment sequence as listed in one of the above databases being  
10 assigned the number one. The third column lists the base occupying the polymorphic site in the sequence in the data base. This base is arbitrarily designated the reference or prototypical form, but it is not necessarily the most frequently occurring form. The fourth column in the Table  
15 lists the alternative base(s) at the polymorphic site. The fifth column of the Table lists a 5' (upstream or forward) primer that hybridizes with the 5' end of the DNA sequence to be amplified. The sixth column of the Table lists a 3' (downstream or reverse) primer that hybridizes with the  
20 complement of the 3' end of the sequence to be amplified. The seventh column of the Table lists a number of bases of sequence on either side of the polymorphic site in each fragment. The indicated sequences can be either DNA or RNA. In the latter, the T's shown in the Table are  
25 replaced by U's. The base occupying the polymorphic site is indicated in EUPAC-IUB ambiguity code.

## II. Analysis of Polymorphisms

### A. Preparation of Samples

Polymorphisms are detected in a target nucleic acid  
30 from an individual being analyzed. For assay of genomic DNA, virtually any biological sample (other than pure red blood cells) is suitable. For example, convenient tissue

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samples include whole blood, semen, saliva, tears, urine, fecal material, sweat, buccal, skin and hair. For assay of cDNA or mRNA, the tissue sample must be obtained from an organ in which the target nucleic acid is expressed. For  
5 example, if the target nucleic acid is a cytochrome P450, the liver is a suitable source.

Many of the methods described below require amplification of DNA from target samples. This can be accomplished by e.g., PCR. See generally *PCR Technology: Principles and Applications for DNA Amplification* (ed. H.A. Erlich, Freeman Press, NY, NY, 1992); *PCR Protocols: A Guide to Methods and Applications* (eds. Innis, et al., Academic Press, San Diego, CA, 1990); Mattila et al., *Nucleic Acids Res.* 19, 4967 (1991); Eckert et al., *PCR Methods and Applications* 1, 17 (1991); PCR (eds. McPherson et al., IRL Press, Oxford); and U.S. Patent 4,683,202.  
10  
15

Other suitable amplification methods include the ligase chain reaction (LCR) (see Wu and Wallace, *Genomics* 4, 560 (1989), Landegren et al., *Science* 241, 1077 (1988),  
20 transcription amplification (Kwoh et al., *Proc. Natl. Acad. Sci. USA* 86, 1173 (1989)), and self-sustained sequence replication (Guatelli et al., *Proc. Nat. Acad. Sci. USA*, 87, 1874 (1990)) and nucleic acid based sequence amplification (NASBA). The latter two amplification  
25 methods involve isothermal reactions based on isothermal transcription, which produce both single stranded RNA (ssRNA) and double stranded DNA (dsDNA) as the amplification products in a ratio of about 30 or 100 to 1, respectively.

#### 30 B. Detection of Polymorphisms in Target DNA

There are two distinct types of analysis of target DNA for detecting polymorphisms. The first type of analysis,



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sometimes referred to as de novo characterization, is carried out to identify polymorphic sites not previously characterized (i.e., to identify new polymorphisms). This analysis compares target sequences in different individuals to identify points of variation, i.e., polymorphic sites. By analyzing groups of individuals representing the greatest ethnic diversity among humans and greatest breed and species variety in plants and animals, patterns characteristic of the most common alleles/haplotypes of the locus can be identified, and the frequencies of such alleles/haplotypes in the population can be determined. Additional allelic frequencies can be determined for subpopulations characterized by criteria such as geography, race, or gender. The de novo identification of polymorphisms of the invention is described in the Examples section. The second type of analysis determines which form(s) of a characterized (known) polymorphism are present in individuals under test. There are a variety of suitable procedures, which are discussed in turn.

#### 1. Allele-Specific Probes

The design and use of allele-specific probes for analyzing polymorphisms is described by e.g., Saiki et al., *Nature* 324, 163-166 (1986); Dattagupta, EP 235,726, Saiki, WO 89/11548. Allele-specific probes can be designed that hybridize to a segment of target DNA from one individual but do not hybridize to the corresponding segment from another individual due to the presence of different polymorphic forms in the respective segments from the two individuals. Hybridization conditions should be sufficiently stringent that there is a significant difference in hybridization intensity between alleles, and preferably an essentially binary response, whereby a probe

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hybridizes to only one of the alleles. Some probes are designed to hybridize to a segment of target DNA such that the polymorphic site aligns with a central position (e.g., in a 15-mer at the 7 position; in a 16-mer, at either the 8 or 9 position) of the probe. This design of probe achieves good discrimination in hybridization between different allelic forms.

Allele-specific probes are often used in pairs, one member of a pair showing a perfect match to a reference form of a target sequence and the other member showing a perfect match to a variant form. Several pairs of probes can then be immobilized on the same support for simultaneous analysis of multiple polymorphisms within the same target sequence.

## 2. Tiling Arrays

The polymorphisms can also be identified by hybridization to nucleic acid arrays, some examples of which are described in WO 95/11995. One form of such arrays is described in the Examples section in connection with de novo identification of polymorphisms. The same array or a different array can be used for analysis of characterized polymorphisms. WO 95/11995 also describes subarrays that are optimized for detection of a variant form of a precharacterized polymorphism. Such a subarray contains probes designed to be complementary to a second reference sequence, which is an allelic variant of the first reference sequence. The second group of probes is designed by the same principles as described in the Examples, except that the probes exhibit complementarity to the second reference sequence. The inclusion of a second group (or further groups) can be particularly useful for analyzing short subsequences of the primary reference

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sequence in which multiple mutations are expected to occur within a short distance commensurate with the length of the probes (e.g., two or more mutations within 9 to 21 bases).

### 3. Allele-Specific Primers

5       An allele-specific primer hybridizes to a site on target DNA overlapping a polymorphism and only primes amplification of an allelic form to which the primer exhibits perfect complementarity. See Gibbs, *Nucleic Acid Res.* 17, 2427-2448 (1989). This primer is used in  
10       conjunction with a second primer which hybridizes at a distal site. Amplification proceeds from the two-primers, resulting in a detectable product which indicates the particular allelic form is present. A control is usually performed with a second pair of primers, one of which shows  
15       a single base mismatch at the polymorphic site and the other of which exhibits perfect complementarity to a distal site. The single-base mismatch prevents amplification and no detectable product is formed. The method works best when the mismatch is included in the 3'-most position of  
20       the oligonucleotide aligned with the polymorphism because this position is most destabilizing to elongation from the primer (see, e.g., WO 93/22456).

### 4. Direct-Sequencing

      The direct analysis of the sequence of polymorphisms of  
25       the present invention can be accomplished using either the dideoxy chain termination method or the Maxam Gilbert method (see Sambrook et al., *Molecular Cloning, A Laboratory Manual* (2nd Ed., CSHP, New York 1989); Zyskind et al., *Recombinant DNA Laboratory Manual*, (Acad. Press,  
30       1988)).

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## 5. Denaturing Gradient Gel Electrophoresis

Amplification products generated using the polymerase chain reaction can be analyzed by the use of denaturing gradient gel electrophoresis. Different alleles can be identified based on the different sequence-dependent melting properties and electrophoretic migration of DNA in solution. Erlich, ed., *PCR Technology, Principles and Applications for DNA Amplification*, (W.H. Freeman and Co, New York, 1992), Chapter 7.

## 10 6. Single-Strand Conformation Polymorphism Analysis

Alleles of target sequences can be differentiated using single-strand conformation polymorphism analysis, which identifies base differences by alteration in electrophoretic migration of single stranded PCR products, as described in Orita et al., *Proc. Nat. Acad. Sci.* 86, 2766-2770 (1989). Amplified PCR products can be generated as described above, and heated or otherwise denatured, to form single stranded amplification products. Single-stranded nucleic acids may refold or form secondary structures which are partially dependent on the base sequence. The different electrophoretic mobilities of single-stranded amplification products can be related to base-sequence differences between alleles of target sequences.

## 25 III. Methods of Use

After determining polymorphic form(s) present in an individual at one or more polymorphic sites, this information can be used in a number of methods.

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## A. Forensics

Determination of which polymorphic forms occupy a set of polymorphic sites in an individual identifies a set of polymorphic forms that distinguishes the individual. See  
5 generally National Research Council, *The Evaluation of Forensic DNA Evidence* (Eds. Pollard et al., National Academy Press, DC, 1996). The more sites that are analyzed, the lower the probability that the set of polymorphic forms in one individual is the same as that in  
10 an unrelated individual. Preferably, if multiple sites are analyzed, the sites are unlinked. Thus, polymorphisms of the invention are often used in conjunction with ~ polymorphisms in distal genes. Preferred polymorphisms for use in forensics are biallelic because the population  
15 frequencies of two polymorphic forms can usually be determined with greater accuracy than those of multiple polymorphic forms at multi-allelic loci.

The capacity to identify a distinguishing or unique set of forensic markers in an individual is useful for forensic  
20 analysis. For example, one can determine whether a blood sample from a suspect matches a blood or other tissue sample from a crime scene by determining whether the set of polymorphic forms occupying selected polymorphic sites is the same in the suspect and the sample. If the set of  
25 polymorphic markers does not match between a suspect and a sample, it can be concluded (barring experimental error) that the suspect was not the source of the sample. If the set of markers does match, one can conclude that the DNA from the suspect is consistent with that found at the crime  
30 scene. If frequencies of the polymorphic forms at the loci tested have been determined (e.g., by analysis of a suitable population of individuals), one can perform a statistical analysis to determine the probability that a

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match of suspect and crime scene sample would occur by chance.

$p(ID)$  is the probability that two random individuals have the same polymorphic or allelic form at a given polymorphic site. In biallelic loci, four genotypes are possible: AA, AB, BA, and BB. If alleles A and B occur in a haploid genome of the organism with frequencies  $x$  and  $y$ , the probability of each genotype in a diploid organism is (see WO 95/12607):

- 10 Homozygote:  $p(AA) = x^2$   
 Homozygote:  $p(BB) = y^2 = (1-x)^2$   
 Single Heterozygote:  $p(AB) = p(BA) = xy = x(1-x)$   
 Both Heterozygotes:  $p(AB+BA) = 2xy = 2x(1-x)$

The probability of identity at one locus (i.e., the probability that two individuals, picked at random from a population will have identical polymorphic forms at a given locus) is given by the equation:

$$p(ID) = (x^2)^2 + (2xy)^2 + (y^2)^2.$$

These calculations can be extended for any number of polymorphic forms at a given locus. For example, the probability of identity  $p(ID)$  for a 3-allele system where the alleles have the frequencies in the population of  $x$ ,  $y$  and  $z$ , respectively, is equal to the sum of the squares of the genotype frequencies:

25 
$$p(ID) = x^4 + (2xy)^2 + (2yz)^2 + (2xz)^2 + z^4 + y^4$$

In a locus of  $n$  alleles, the appropriate binomial expansion is used to calculate  $p(ID)$  and  $p(exc)$ .

The cumulative probability of identity ( $\text{cum } p(ID)$ ) for each of multiple unlinked loci is determined by multiplying the probabilities provided by each locus.

30 
$$\text{cum } p(ID) = p(ID1)p(ID2)p(ID3) \dots p(IDn)$$

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The cumulative probability of non-identity for  $n$  loci (i.e. the probability that two random individuals will be different at 1 or more loci) is given by the equation:

$$\text{cum } p(\text{nonID}) = 1 - \text{cum } p(\text{ID}).$$

- 5        If several polymorphic loci are tested, the cumulative probability of non-identity for random individuals becomes very high (e.g., one billion to one). Such probabilities can be taken into account together with other evidence in determining the guilt or innocence of the suspect.

10        B. Paternity Testing

The object of paternity testing is usually to determine whether a male is the father of a child. In most cases, the mother of the child is known and thus, the mother's contribution to the child's genotype can be traced.

- 15        Paternity testing investigates whether the part of the child's genotype not attributable to the mother is consistent with that of the putative father. Paternity testing can be performed by analyzing sets of polymorphisms in the putative father and the child.

- 20        If the set of polymorphisms in the child attributable to the father does not match the set of polymorphisms of the putative father, it can be concluded, barring experimental error, that the putative father is not the real father. If the set of polymorphisms in the child  
25        attributable to the father does match the set of polymorphisms of the putative father, a statistical calculation can be performed to determine the probability of coincidental match.

- 30        The probability of parentage exclusion (representing the probability that a random male will have a polymorphic form at a given polymorphic site that makes him

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incompatible as the father) is given by the equation (see WO 95/12607):

$$p(\text{exc}) = xy(1-xy)$$

where x and y are the population frequencies of alleles A  
5 and B of a biallelic polymorphic site.

(At a triallelic site  $p(\text{exc}) = xy(1-xy) + yz(1-yz) + xz(1-xz) + 3xyz(1-xyz)$ ), where x, y and z are the  
respective population frequencies of alleles A, B and C).

The probability of non-exclusion is

10  $p(\text{non-exc}) = 1 - p(\text{exc})$

The cumulative probability of non-exclusion  
(representing the value obtained when n loci are used) is  
thus:

$$\text{cum } p(\text{non-exc}) = p(\text{non-exc1})p(\text{non-exc2})p(\text{non-exc3}) \dots$$

15  $p(\text{non-excn})$

The cumulative probability of exclusion for n loci  
(representing the probability that a random male will be  
excluded)

$$\text{cum } p(\text{exc}) = 1 - \text{cum } p(\text{non-exc}).$$

20 If several polymorphic loci are included in the  
analysis, the cumulative probability of exclusion of a  
random male is very high. This probability can be taken  
into account in assessing the liability of a putative  
father whose polymorphic marker set matches the child's  
25 polymorphic marker set attributable to his/her father.

### C. Correlation of Polymorphisms with Phenotypic Traits

The polymorphisms of the invention may contribute to  
the phenotype of an organism in different ways. Some  
polymorphisms occur within a protein coding sequence and  
30 contribute to phenotype by affecting protein structure.  
The effect may be neutral, beneficial or detrimental, or  
both beneficial and detrimental, depending on the



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circumstances. For example, a heterozygous sickle cell mutation confers resistance to malaria, but a homozygous sickle cell mutation is usually lethal. Other polymorphisms occur in noncoding regions but may exert phenotypic effects indirectly via influence on replication, transcription, and translation. A single polymorphism may affect more than one phenotypic trait. Likewise, a single phenotypic trait may be affected by polymorphisms in different genes. Further, some polymorphisms predispose an individual to a distinct mutation that is causally related to a certain phenotype.

Phenotypic traits include diseases that have known but hitherto unmapped genetic components (e.g., agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary hemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and acute intermittent porphyria). Phenotypic traits also include symptoms of, or susceptibility to, multifactorial diseases of which a component is or may be genetic, such as autoimmune diseases, inflammation, cancer, diseases of the nervous system, and infection by pathogenic microorganisms. Some examples of autoimmune diseases include rheumatoid arthritis, multiple sclerosis, diabetes (insulin-dependent and non-independent), systemic lupus erythematosus and Graves disease. Some examples of cancers include cancers of the bladder, brain, breast, colon, esophagus, kidney, leukemia, liver, lung, oral cavity, ovary, pancreas, prostate, skin, stomach and uterus. Phenotypic traits also include characteristics such as longevity, appearance

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(e.g., baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments.

Correlation is performed for a population of  
5 individuals who have been tested for the presence or  
absence of a phenotypic trait of interest and for  
polymorphic markers sets. To perform such analysis, the  
presence or absence of a set of polymorphisms (i.e. a  
polymorphic set) is determined for a set of the  
10 individuals, some of whom exhibit a particular trait, and  
some of which exhibit lack of the trait. The alleles of  
each polymorphism of the set are then reviewed to determine  
whether the presence or absence of a particular allele is  
associated with the trait of interest. Correlation can be  
15 performed by standard statistical methods such as a  $\chi^2$ -  
squared test and statistically significant correlations  
between polymorphic form(s) and phenotypic characteristics  
are noted. For example, it might be found that the  
presence of allele A1 at polymorphism A correlates with  
20 heart disease. As a further example, it might be found  
that the combined presence of allele A1 at polymorphism A  
and allele B1 at polymorphism B correlates with increased  
milk production of a farm animal.

Such correlations can be exploited in several ways. In  
25 the case of a strong correlation between a set of one or  
more polymorphic forms and a disease for which treatment is  
available, detection of the polymorphic form set in a human  
or animal patient may justify immediate administration of  
treatment, or at least the institution of regular  
30 monitoring of the patient. Detection of a polymorphic form  
correlated with serious disease in a couple contemplating a  
family may also be valuable to the couple in their  
reproductive decisions. For example, the female partner

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might elect to undergo in vitro fertilization to avoid the possibility of transmitting such a polymorphism from her husband to her offspring. In the case of a weaker, but still statistically significant correlation between a

5 polymorphic set and human disease, immediate therapeutic intervention or monitoring may not be justified. Nevertheless, the patient can be motivated to begin simple life-style changes (e.g., diet, exercise) that can be accomplished at little cost to the patient but confer

10 potential benefits in reducing the risk of conditions to which the patient may have increased susceptibility by virtue of variant alleles. Identification of a polymorphic set in a patient correlated with enhanced receptiveness to one of several treatment regimes for a disease indicates

15 that this treatment regime should be followed.

For animals and plants, correlations between characteristics and phenotype are useful for breeding for desired characteristics. For example, Beitz et al., US 5,292,639 discuss use of bovine mitochondrial polymorphisms

20 in a breeding program to improve milk production in cows. To evaluate the effect of mtDNA D-loop sequence polymorphism on milk production, each cow was assigned a value of 1 if variant or 0 if wildtype with respect to a prototypical mitochondrial DNA sequence at each of 17

25 locations considered. Each production trait was analyzed individually with the following animal model:

$$Y_{ijkpn} = \mu + YS_i + P_j + X_k + \beta_1 + \dots \beta_{17} + PE_n + a_n + e_p$$

where  $Y_{ijkpn}$  is the milk, fat, fat percentage, SNF, SNF percentage, energy concentration, or lactation energy

30 record;  $\mu$  is an overall mean;  $YS_i$  is the effect common to all cows calving in year-season;  $X_k$  is the effect common to cows in either the high or average selection line;  $\beta_1$  to  $\beta_{17}$  are the binomial regressions of production record on mtDNA

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D-loop sequence polymorphisms;  $PE_n$  is permanent environmental effect common to all records of cow  $n$ ;  $a_n$  is effect of animal  $n$  and is composed of the additive genetic contribution of sire and dam breeding values and a  
5 Mendelian sampling effect; and  $e_p$  is a random residual. It was found that eleven of seventeen polymorphisms tested influenced at least one production trait. Bovines having the best polymorphic forms for milk production at these eleven loci are used as parents for breeding the next  
10 generation of the herd.

#### D. Genetic Mapping of Phenotypic Traits

The previous section concerns identifying correlations between phenotypic traits and polymorphisms that directly or indirectly contribute to those traits. The present  
15 section describes identification of a physical linkage between a genetic locus associated with a trait of interest and polymorphic markers that are not associated with the trait, but are in physical proximity with the genetic locus responsible for the trait and co-segregate with it. Such  
20 analysis is useful for mapping a genetic locus associated with a phenotypic trait to a chromosomal position, and thereby cloning gene(s) responsible for the trait. See Lander et al., *Proc. Natl. Acad. Sci. (USA)* 83, 7353-7357 (1986); Lander et al., *Proc. Natl. Acad. Sci. (USA)* 84,  
25 2363-2367 (1987); Donis-Keller et al., *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 185-199 (1989)). Genes localized by linkage can be cloned by a process known as directional cloning. See Wainwright, *Med. J. Australia* 159, 170-174 (1993); Collins, *Nature Genetics* 1, 3-6  
30 (1992).

Linkage studies are typically performed on members of a family. Available members of the family are characterized

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for the presence or absence of a phenotypic trait and for a set of polymorphic markers. The distribution of polymorphic markers in an informative meiosis is then analyzed to determine which polymorphic markers co-

5 segregate with a phenotypic trait. See, e.g., Kerem et al., *Science* 245, 1073-1080 (1989); Monaco et al., *Nature* 316, 842 (1985); Yamoka et al., *Neurology* 40, 222-226 (1990); Rossiter et al., *FASEB Journal* 5, 21-27 (1991).

Linkage is analyzed by calculation of LOD (log of the  
10 odds) values. A lod value is the relative likelihood of obtaining observed segregation data for a marker and a genetic locus when the two are located at a recombination fraction  $\theta$ , versus the situation in which the two are not linked, and thus segregating independently (Thompson &  
15 Thompson, *Genetics in Medicine* (5th ed, W.B. Saunders Company, Philadelphia, 1991); Strachan, "Mapping the human genome" in *The Human Genome* (BIOS Scientific Publishers Ltd, Oxford), Chapter 4). A series of likelihood ratios are calculated at various recombination fractions ( $\theta$ ),  
20 ranging from  $\theta = 0.0$  (coincident loci) to  $\theta = 0.50$  (unlinked). Thus, the likelihood at a given value of  $\theta$  is: probability of data if loci linked at  $\theta$  to probability of data if loci unlinked. The computed likelihoods are usually expressed as the  $\log_{10}$  of this ratio (i.e., a lod  
25 score). For example, a lod score of 3 indicates 1000:1 odds against an apparent observed linkage being a coincidence. The use of logarithms allows data collected from different families to be combined by simple addition. Computer programs are available for the calculation of lod  
30 scores for differing values of  $\theta$  (e.g., LIPED, MLINK (Lathrop, *Proc. Nat. Acad. Sci. (USA)* 81, 3443-3446 (1984)). For any particular lod score, a recombination fraction may be determined from mathematical tables. See

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Smith et al., *Mathematical tables for research workers in human genetics* (Churchill, London, 1961); Smith, *Ann. Hum. Genet.* 32, 127-150 (1968). The value of  $\theta$  at which the lod score is the highest is considered to be the best estimate of the recombination fraction.

Positive lod score values suggest that the two loci are linked, whereas negative values suggest that linkage is less likely (at that value of  $\theta$ ) than the possibility that the two loci are unlinked. By convention, a combined lod score of +3 or greater (equivalent to greater than 1000:1 odds in favor of linkage) is considered definitive evidence that two loci are linked. Similarly, by convention, a negative lod score of -2 or less is taken as definitive evidence against linkage of the two loci being compared. Negative linkage data are useful in excluding a chromosome or a segment thereof from consideration. The search focuses on the remaining non-excluded chromosomal locations.

#### IV. Modified Polypeptides and Gene Sequences

The invention further provides variant forms of nucleic acids and corresponding proteins. The nucleic acids comprise one of the sequences described in the Table, column 8, in which the polymorphic position is occupied by one of the alternative bases for that position. Some nucleic acids encode full-length variant forms of proteins. Similarly, variant proteins have the prototypical amino acid sequences encoded by nucleic acid sequences shown in the Table, column 8, (read so as to be in-frame with the full-length coding sequence of which it is a component) except at an amino acid encoded by a codon including one of the polymorphic positions shown in the Table. That position is occupied by the amino acid coded by the

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corresponding codon in any of the alternative forms shown in the Table.

Variant genes can be expressed in an expression vector in which a variant gene is operably linked to a native or  
5 other promoter. Usually, the promoter is a eukaryotic promoter for expression in a mammalian cell. The transcription regulation sequences typically include a heterologous promoter and optionally an enhancer which is recognized by the host. The selection of an appropriate  
10 promoter, for example trp, lac, phage promoters, glycolytic enzyme promoters and tRNA promoters, depends on the host selected. Commercially available expression vectors can be used. Vectors can include host-recognized replication systems, amplifiable genes, selectable markers, host  
15 sequences useful for insertion into the host genome, and the like.

The means of introducing the expression construct into a host cell varies depending upon the particular construction and the target host. Suitable means include  
20 fusion, conjugation, transfection, transduction, electroporation or injection, as described in Sambrook, *supra*. A wide variety of host cells can be employed for expression of the variant gene, both prokaryotic and eukaryotic. Suitable host cells include bacteria such as  
25 *E. coli*, yeast, filamentous fungi, insect cells, mammalian cells, typically immortalized, e.g., mouse, CHO, human and monkey cell lines and derivatives thereof. Preferred host cells are able to process the variant gene product to produce an appropriate mature polypeptide. Processing  
30 includes glycosylation, ubiquitination, disulfide bond formation, general post-translational modification, and the like.

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The protein may be isolated by conventional means of protein biochemistry and purification to obtain a substantially pure product, i.e., 80, 95 or 99% free of cell component contaminants, as described in Jacoby, 5 *Methods in Enzymology* Volume 104, Academic Press, New York (1984); Scopes, *Protein Purification, Principles and Practice*, 2nd Edition, Springer-Verlag, New York (1987); and Deutscher (ed), *Guide to Protein Purification, Methods in Enzymology*, Vol. 182 (1990). If the protein is 10 secreted, it can be isolated from the supernatant in which the host cell is grown. If not secreted, the protein can be isolated from a lysate of the host cells.

The invention further provides transgenic nonhuman animals capable of expressing an exogenous variant gene 15 and/or having one or both alleles of an endogenous variant gene inactivated. Expression of an exogenous variant gene is usually achieved by operably linking the gene to a promoter and optionally an enhancer, and microinjecting the construct into a zygote. See Hogan et al., "Manipulating 20 the Mouse Embryo, A Laboratory Manual," Cold Spring Harbor Laboratory. Inactivation of endogenous variant genes can be achieved by forming a transgene in which a cloned variant gene is inactivated by insertion of a positive selection marker. See Capecchi, *Science* 244, 1288-1292 25 (1989). The transgene is then introduced into an embryonic stem cell, where it undergoes homologous recombination with an endogenous variant gene. Mice and other rodents are preferred animals. Such animals provide useful drug screening systems.

30 In addition to substantially full-length polypeptides expressed by variant genes, the present invention includes biologically active fragments of the polypeptides, or analogs thereof, including organic molecules which simulate



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the interactions of the peptides. Biologically active fragments include any portion of the full-length polypeptide which confers a biological function on the variant gene product, including ligand binding, and  
5 antibody binding. Ligand binding includes binding by nucleic acids, proteins or polypeptides, small biologically active molecules, or large cellular structures.

Polyclonal and/or monoclonal antibodies that specifically bind to variant gene products but not to  
10 corresponding prototypical gene products are also provided. Antibodies can be made by injecting mice or other animals with the variant gene product or synthetic peptide-fragments thereof. Monoclonal antibodies are screened as are described, for example, in Harlow & Lane, *Antibodies, A*  
15 *Laboratory Manual*, Cold Spring Harbor Press, New York (1988); Goding, *Monoclonal antibodies, Principles and Practice* (2d ed.) Academic Press, New York (1986). Monoclonal antibodies are tested for specific immunoreactivity with a variant gene product and lack of  
20 immunoreactivity to the corresponding prototypical gene product. These antibodies are useful in diagnostic assays for detection of the variant form, or as an active ingredient in a pharmaceutical composition.

#### V. Kits

25 The invention further provides kits comprising at least one allele-specific oligonucleotide as described above. Often, the kits contain one or more pairs of allele-specific oligonucleotides hybridizing to different forms of a polymorphism. In some kits, the allele-specific  
30 oligonucleotides are provided immobilized to a substrate. For example, the same substrate can comprise allele-specific oligonucleotide probes for detecting at least 10,

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100 or all of the polymorphisms shown in the Table. Optional additional components of the kit include, for example, restriction enzymes, reverse-transcriptase or polymerase, the substrate nucleoside triphosphates, means  
5 used to label (for example, an avidin-enzyme conjugate and enzyme substrate and chromogen if the label is biotin), and the appropriate buffers for reverse transcription, PCR, or hybridization reactions. Usually, the kit also contains instructions for carrying out the methods.

10 The following Examples are offered for the purpose of illustrating the present invention and are not to be construed to limit the scope of this invention. The teachings of all references cited herein are hereby incorporated herein by reference.

#### 15 EXAMPLES

The polymorphisms shown in the Table were identified by resequencing of target sequences from three to ten unrelated individuals of diverse ethnic and geographic backgrounds by hybridization to probes immobilized to  
20 microfabricated arrays or conventional sequencing. The strategy and principles for design and use of such arrays are generally described in WO 95/11995. The strategy provides arrays of probes for analysis of target sequences showing a high degree of sequence identity to the reference  
25 sequences of the fragments shown in the Table, column 1.

The reference sequences were sequence-tagged sites (STSs) developed in the course of the Human Genome Project (see, e.g., *Science* 270, 1945-1954 (1995); *Nature* 380, 152-154 (1996)). Most STS's ranged from 100 bp to 300 bp in size.

30 A typical probe array used in this analysis has two groups of four sets of probes that respectively tile both strands of a reference sequence. A first probe set

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comprises a plurality of probes exhibiting perfect complementarily with one of the reference sequences. Each probe in the first probe set has an interrogation position that corresponds to a nucleotide in the reference sequence.

5 That is, the interrogation position is aligned with the corresponding nucleotide in the reference sequence, when the probe and reference sequence are aligned to maximize complementarily between the two. For each probe in the first set, there are three corresponding probes from three

10 additional probe sets. Thus, there are four probes corresponding to each nucleotide in the reference sequence. The probes from the three additional probe sets are identical to the corresponding probe from the first probe set except at the interrogation position, which occurs in

15 the same position in each of the four corresponding probes from the four probe sets, and is occupied by a different nucleotide in the four probe sets. In the present analysis, probes were 25 nucleotides long. Arrays tiled for multiple different references sequences were included

20 on the same substrate.

Multiple target sequences from an individual were amplified from human genomic DNA using primers for the fragments indicated in the listed Web sites. The amplified target sequences were fluorescently labelled during or

25 after PCR. The labelled target sequences were hybridized with a substrate bearing immobilized arrays of probes. The amount of label bound to probes was measured. Analysis of the pattern of label revealed the nature and position of differences between the target and reference sequence. For

30 example, comparison of the intensities of four corresponding probes reveals the identity of a corresponding nucleotide in the target sequences aligned with the interrogation position of the probes. The

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corresponding nucleotide is the complement of the nucleotide occupying the interrogation position of the probe showing the highest intensity (see WO 95/11995). The existence of a polymorphism is also manifested by

5 differences in normalized hybridization intensities of probes flanking the polymorphism when the probes hybridized to corresponding targets from different individuals. For example, relative loss of hybridization intensity in a "footprint" of probes flanking a polymorphism signals a

10 difference between the target and reference (i.e., a polymorphism) (see EP 717,113). Additionally, hybridization intensities for corresponding targets from different individuals can be classified into groups or clusters suggested by the data, not defined *a priori*, such

15 that isolates in a give cluster tend to be similar and isolates in different clusters tend to be dissimilar. Hybridizations to samples from different individuals were performed separately. The Table summarizes the data obtained for target sequences in comparison with a

20 reference sequence for the individuals tested.

From the foregoing, it is apparent that the invention includes a number of general uses that can be expressed concisely as follows. The invention provides for the use of any of the nucleic acid segments described above in the

25 diagnosis or monitoring of diseases, such as cancer, inflammation, heart disease, diseases of the CNS, and susceptibility to infection by microorganisms. The invention further provides for the use of any of the nucleic acid segments in the manufacture of a medicament

30 for the treatment or prophylaxis of such diseases. The invention further provides for the use of any of the DNA segments as a pharmaceutical.

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All publications and patent applications cited above are incorporated by reference in their entirety for all purposes to the same extent as if each individual publication or patent application were specifically and  
5 individually indicated to be so incorporated by reference.

1	2	3	4	5	6	7
						TGTGAACCTCCACTTGAAGCCAAAGAAAGAACTCACACTTAAACACATGCCAGTTGGGAAGGTCT
						GAAAACTCAGTGCATAATAGGAACACTTGAGACTAATGAAGAGAGAGTTGAGACCAATCTTTATTT
						GTACTGGCCAAATACTGAATAAACAGTTGAAGGAAAGACATTGGAAAAGCTTTTGAGGATAATGT
WI-7070	226	CT	---		---	TACTAGACTTTATGCCATGGTGTCTTTC/TJAGTTTAATGCTGTGTCTCTGTCTG
						AAGCCATTGACGTAACTCTCAGAGGTTATTTGCATGGATTGACTCCTGGGACAAAAGGAC/GC/JAA
						AAACACTCTTCTGTGGATATCTGTGCAGATAGATGACCCAAAGATCAGATGCTACCCAGATGTGTTTT
						GATAATACATAAGCCCTAGGATTTAGATACAATCTTGAAGAAACTGAGACAGATAATTTCTGAATT
WI-10744	61	GC	---		---	AAATGAGGTAAAGTTTCAGGCACCTCA
						GGGCAAAATACCAGCAAAAAGTCAAAATACCAGCATCAAAGTCAGGTGCAAGGAGGTAGAACAA
						TTACAGTAACATATGCAATCTTTTGTATATTAGTATTATCTGCCCAATGCCTAGAATA/C/TJAGTG
						GGTCCCTAATAGTTATTAGTTCTTTTCTCCTCTTCTCTCATCTCTGAAATTTATTTTATACITTA
WI-9975	126	CT	---		---	GGGATTAGTTACCACCAAAAATGTATGTATCAATTTGATTTACTGTAA
						GCTAGGTTTGTCTGTCTGCTCTCACTAGACTTGAGATGACTTGATTACAGTAATCCCTATGT
						GATGTAACATAGCTAGACCTTCCCTCTCCGCAATCCAGCTCCAGGTTTCAGAAAAGTATGCCACAC
						TCAACCTTCTCTCCAGTTCACTCTGTATTAAATTTCTTCCCATATTAATTCAAAGGGAGTGGACAGGT
WI-8010	247	GT	---		---	CCCTGGCTGAAAAGAAATAAAGAGATCCCCAAAGTGGTGGG/GTJCTT
						GCCCGGCTATCTTTTAAATTTAACTTGATCTTTGGTGTCTCTCCATCTCTAGGATTCGCCCTTATAAT
						CTTTGTCTGTCTGTG/CJATTACCTGATTCTACTTTTGATACACAAGGCTGATGGCTCACAATGT
						AGTAGTGCCTAATCTCAGGTCTCTTTGAAATTTTCTCTGCTATTGAGGACATTTCCACTTTCTACTTA
WI-5222b	85	GC	---		---	TCTCGACTCTATAACAACCTCCAAACAGAA
						GCCCGGCTATCTTTTAAATTTAACTTGATCTTTGGTGTCTCTCCATCTG/CJGATTCTGCTTAT
						AATCTTTGTCTGTCTGTAGATTACCTGATTCTACTTTTGATACACAAGGCTGATGGCTCACAATGT
						AGTAGTGCCAAATCTTCAGGTCTCTTTGAAATTTTCTCTGCTATTGAGGACATTTCCACTTTCTACTTA
WI-5222	52	GC	---		---	TCTCGACTCTATAACAACCTCCAAACAGAA
						TATGCACCTCCACAAAAGCGATATAATTTAAAAGTTTTTTCATTAGAAATAAATGTATAAAAATAA
						ATATGTTATTATAGGCATTTATTAATACTATAGTCTCTCTTGAAAGGAACACCCCAACCAATACCT
						ATAAAGTACATGTAAATTTATAGTAACATATTTACTATATACATATGGAATAATCATATTCACACA
WI-8007	242	CA	---		---	GAAGAGCTGAACAGACATTCACCGGATACGACTGTGGAC/CJAJAGCTGCTG
						TCAGTTGCAAAAATTGCTGCCATAAACATGCTTTGCTTATCTCTGTGCATATGTATGTTTGTAG
						TCTATATTCACACATATGAGTGAAATTTCTG/TGGGGCATGGGAATACATCTTTATGAGACATTGA
						ACTGCTCACCACATCATAGTATCCATTTAAACAGACCAACAATGTATAAGAAATCCCTTTGTTTAC
WI-9823	97	CT	---		---	ATGCTTTCCAATCTGATTTGTATGACTATTGTATGCACAGTTGGATCACC

[illegible]

WI-10826	132	A C ---	---	TCTATTGCAATTCACAGTAGCCCCATGAAGTAGGTATACCGCCTCTATTTAAACATGAGAAGAT GGAGGCCTTTCCAAATGGACTAAGTAATGTGTCTCAGGTTTCTTAATAGCAAGACCTGCAIAC JCCCTGGCTTCTGACTCCAAAGCTTATCCCTTCTCATGCTGTGCTGTAGCCAGGACCCCATGCGCA GAAAGCCAGCCTCTCCATCCCCAC
TIGR- A004S25	145	G A ---	---	AGATCTGCCATTAGTATTATTCCTTTGAAGATACITTTGGAGATTCATTTCTTGAGTGGCACTGCAT GCTCATTAGTGAAGAACTTTGGGGTATAGAAATGGAATGGAGAGTTTCAACAGAGCTTTGCTGAAAC TGACTTTGG[G/A]CTCCAGACTTCACTGTCTTAGGCATTGAAACCATCACCTGGTTTGCACTTCTC ATGACTGAGGTTAACTTAAATGACTGAGGTTAACTTAAAC
WI-1021	24	A T ---	---	AAACACAGAAATCATCAAAGCACIATATCTGTGTTTGAGATAAATGATAGTCTGAGTCACCTATG TAAGAAGTAACTCTGAATAGTAGGATAGTATTATCATTTCTGTATAGATTCACCTCTCAGCAAT TGGTCTGTTTCACTTATGGAACCTCTCCGTACTGTATTTTCACTTCTATGGAACTCCCCATACTGT AATTGGACAGTTTGGTTCCAC
WI-4687	121	G T ---	---	TAGTATGTCACCTGCCATGGTAAGGACTTTGATCACTAGGAAATAAGAACACTTTGAATGGTCTTGTC TTTCAATAAAAGAGTGACATGATTGAACATGTGTTTAGATAAAGGGCCTTT[G/T]GCAGGAGTGT TTAGGATGAAGAGAGAGAGATTAAAGGAAGATCAGGAAGAAAGTAGCAATGGGAATGAAATAG GAGGCCCTGAGATCCACTGGATAATCTAAAAACCAAGAGAAAGAACTTGAT
WI-4719b	107	T G ---	---	TTCAATTCCTTCCAAATCCTTAGGAAATTTACATTATGGGCTAGTGTCTTGGGTGTAGCGGATT ATGCTGACGCCATGGGTGTTCAATAGTGACTTGAGAGTT[G/A]CTGTAGAGGCTACACAGAAATCT CTGTGAGGGGCATGTAATTGTATTCAATCAACAATCTGCTATGCTTCTCAGATTGCAGAAAAATCAC TGCTCAAAATCCCCACTTGCAACTTATCCTTAAGACATTTTCACAGGA
WI-4719	70	G A ---	---	TTCAATTCCTTCCAAATCCTTAGGAAATTTACATTATGGGCTAGTGTCTTGGGTGTAGCGGATT AT[G/A]CTGACGCCATGGGTGTTCAATAGTGACTTGAGAGTTACTGTAGAGGCTACACAGAAATCT CTGTGAGGGGCATGTAATTGTATTCAATCAACAATCTGCTATGCTTCTCAGATTGCAGAAAAATCAC TGCTCAAAATCCCCACTTGCAACTTATCCTTAAGACATTTTCACAGGA
WI-9484b	216	G C ---	---	TCAACACGCTTTTATTGCCACTTCTGGCTCCCTCGTCCCAGCAAGATTCTACCTCTTACCCGTAGG AATACTGAGTCCGATGCAGGGGAATGGGTGGGGTGTACCACCTCTCCTCTGCACACTGCCAAGT TAAAGAAACCCCTGCTTCTGGAGAGGGAGGGCCAGAGAGGGAATTCAGGGCATGTATGGCTC AGTCCCACTTCT[G/C]ACTGCAGAGTATAGGGACCAAGGTTCCAACTTT
WI-9484	178	G A ---	---	TCAACACGCTTTTATTGCCACTTCTGGCTCCCTCGTCCCAGCAAGATTCTACCTCTTACCCGTAGG AATACTGAGTCCGATGCAGGGGAATGGGTGGGGTGTACCACCTCTCCTCTGCACACTGCCAAGT TAAAGAAACCCCTGCTTCTGGAGAGGGAGGGCCAGACAGG[G/A]AGGAATTCAGGGCATGTATG GCTCAGTCCCACTTCTGACTGCAGAGTATAGGGACCAAGGTTCCAACTTT





WI-931c	191 C A ---	---	GACCAGGGCACCAGAAAGCCACGGGAAGCCACAGCCACTAGCCCTGAACCTTGCACACCCCTGGAGTT TCTCTCCCTCCCTATCCCTACCAACACCTTCCAGTGCATTATCTGCTGTGTCAAAATGATCCTCT GTTGCTGCACTGTCATTACTGTTGATGGATTATAATTATTGTCCTCAAAAAGCC[C/A]CGAGCCTGG TACAGAAAAGGCATGGGAAAGATGTGTCAGA
WI-931b	81 A G ---	---	GACCAGGGCACCAGAAAGCCACGGGAAGCCACAGCCACTAGCCCTGAACCTTGCACACCCCTGGAGTT TCTCTCCCTCCCTA/GJTCCCTCACCAACACCTTCCAGTGCATTATCTGCTGTGTCAAAATGATCCT TCTGTTGCTGCACTGTCATTACTGTTGATGGATTATAATTATTGTCCTCAAAAAGCCCTGGAGCCTGG TACAGAAAAGGCATGGGAAAGATGTGTCAGA
WI-931	31 A G ---	---	GACCAGGGCACCAGAAAGCCACGGGAAGCCAC/A/GJCCACTAGCCCTGAACCTTGCACACCCCTGGA GTTCTCTCCCTCCCTATCCCTCACCAACACCTTCCAGTGCATTATCTGCTGTGTCAAAATGATCCT TCTGTTGCTGCACTGTCATTACTGTTGATGGATTATAATTATTGTCCTCAAAAAGCCCTGGAGCCTGG TACAGAAAAGGCATGGGAAAGATGTGTCAGA
WI-10870b	91 C T ---	---	GGATGACTTACCCAATAGCAGGGTGGGTACATTCATGGGTAAACACCCCTGGACTGGGATGGCAGA GACATCCACCTTAGCAAGTGGGG[C/T]ACCTACTTAGAGCAGTGGAGTACCCTGAGTACGACCCCC TTAGCAGCAGAAATTACAAGAAATCTTGGGACCTGTACTCTGATACAAAATAAGGACATGGGTCAGC CTGAGCCACTCTTAAACCATGAACCATCACCAITTTAAACGTTGCCCCCCC
WI-10870	103 G A ---	---	GGATGACTTACCCAATAGCAGGGTGGGTACATTCATGGGTAAACACCCCTGGACTGGGATGGCAGA GACATCCACCTTAGCAAGTGGGGACCTACTTAGA/GJACGTGGAGTACCCTGAGTACGACCCCC TTAGCAGCAGAAATTACAAGAAATCTTGGGACCTGTACTCTGATACAAAATAAGGACATGGGTCAGC CTGAGCCACTCTTAAACCATGAACCATCACCAITTTAAACGTTGCCCCCCC
WI-7719b	281 T C ---	---	AGTTTATCTTCCAGATGACCAGCAGTAGACAAATGGGATCTAGCAGAGTCTTAGGTAAAAGTCTT GGGAAATATTTGGCATTGGTCTGGCCAAAGTCTACAATGTCCCAATATCAAGGACAACCCCTAGC TTCTTAGTGAAGACAATGTACAGTTATCCATTAGATCAAGACTACACGGTCTATGAGCAATAATGTG ATTTCTGGACATTGCCCATGTATAATCCTCACTGATGATTTCAAGCTAAAGCAA
WI-7719	163 A G ---	---	AGTTTATCTTCCAGATGACCAGCAGTAGACAAATGGGATCTAGCAGAGTCTTAGGTAAAAGTCTT GGGAAATATTTGGCATTGGTCTGGCCAAAGTCTACAATGTCCCAATATCAAGGACAACCCCTAGC TTCTTAGTGAAGACAATGTACAGTTATCC[C/G]TTAGATCAAGACTACACGGTCTATGAGCAATAAT GTGATTCTGGACATTGCCCATGTATAATCCTCACTGATGATTTCAAGCTAAA
WI-10396	72 C A ---	---	GCCTTGGAGTATATCTAAACTGTGGCCCTCCACTTTCATTTTCTTGAACATTGCTATCAACTGGGAA GAGT[C/A]TGACTTTATGCCCAGTTTCCCTCTCAGATTTTATGACGGTTGTTTCTTTTGTTA TGCCATTGAGGGATTGATGTTTCTTAAACTATGAAGTACTTGGCTGTCTCTCCATTGCTGTTTCAGG TTAACAGCCACCATTTGTAAACACTTTGT

WI-10673	94 C G ---				TCCCTTTATGACCCCAAGAGATATTTATTAAACACCAATTAAGTAGCAGGCCATGGCTCATGGGACC CACCCCGGTGGCACTCATGGAGGGG[C/G]TGCAAGTTGGAACATATGCAAGTGTCTCCGGCCACACA TCCTGCTGGGCCCTACCTGCCCAATTCAATCCTGCCAATAAATCCTGCTCTATTGTTTCATCCTG GAGAAITGAAGGAGGTCAAGTTGTTTGTCATGATTGTCAGAGAACCT
WI-7842	57 T C ---				CACAGCCATGCCCTTGAGGAGCCGCCACCAAGATGCTGAATCCCCTATCCCATTCGT[C/G]GTATGAG TCCCATTTGCCCTTGCAATTAGCATTCGTCTCCCCCAAAAGAAATGTCATGAAGCTTTCTTTCCCT ACACACTGTGAGTCTCTGAATGAAGCTGAAGGCTTAGTACCAGAGCTAGTTTTTCAGCTGCTCAGAAT TCATCTGAAGAGAGACTTAAGATGAAGCAAAATGATTCAGCTCCCTTATA
WI-7721	145 A C ---				CTGCCATCACGCCACTGGAGTCCACACTTTGAATTTGGGCAGCTACCACGGGTCTGCCATGCTCTGG AGGAGCAAGGGGGCACATCCCACCCACAGCTGTACCCAGCCGGGAGGTGCGAGCCCTTCCTCCOC TGCTCTGC[A/C]TCTGACTCTCTTTTGAGGTCCCTGTATGTCTACCTCTGACTTCTGTGGTCCCTCTG TGCTGCTCTCATCCATTCCTTACTGGGGCCTGGGGCTCTAGCCCCAA
WI-4767b	173 C A ---				TTTCCAGTCTGTTTTATCCTTTTCATTGTCAAAAGATGCTCTTAGACTGAAATTCATAAAGAGTTCTCT CAGGCTGGGTAACTCTAGATCTCTATATCCATTGAGTGTGAGTTGGAGAGGGTATGTTT CTTGCCCTTGAGAAATCCTAGAAGCACAGGGATGACA[C/A]AAATCACTAAGGAATTCACACTAAGA CTCCTCTAACCCAGAGATTTTAACCT
WI-4767	50 A G ---				TTTCCAGTCTGTTTTATCCTTTTCATTGTCAAAAGATGCTCTTAGACTGA[A/G]ATTCATAAAGAGTT CCTCAGGCTGGGTAATCCTAGATCTCTCTATATCCATTGAGTGTGAGTTGGAGAGGGTATG TTTCTTGCCCTTGAGAAATCCTAGAAGCACAGGGATGACACAAATCACTAAGGAATTCACACTAAGAC TCCTCTAACCCAGAGATTTTAACCT
WI-7718f	222 C T ---				ATTGCACTGAAGTTTTGAAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGATAGATG ACTTTGCAGATGGAAGAGGTGAAATGAAGAAGGAAGCTGTGTTGAAACAGAAAAATAAGTCAAA AGGAACAAAAATTACAAAGAA[C/T]CATGCAGGAAGGAAACTATGTATTAAAT
WI-7718e	60 T C ---				ATTGCACTGAAGTTTTGAAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGAT[C/G]CAA GGATTACAGAACTGATGCCAAGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTGAAATGAAGAAGGAAGCTGTGTTGAAACAGAAAAATAAGTC AAAAGGAACAAAAATTACAAAGAACCCATGCAGGAAGGAAAACTATGTATTAAAT
WI-7718d	31 G A ---				ATTGCACTGAAGTTTTGAAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAA GGATTACAGAACTGATGCCAAGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTGAAATGAAGAAGGAAGCTGTGTTGAAACAGAAAAATAAGTC AAAAGGAACAAAAATTACAAAGAACCCATGCAGGAAGGAAAACTATGTATTAAAT

WI-7718c	91 C G ---				ATTGCACTGAAGTTTTGAAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGGCGJTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTGAAATGAAGAAGGAGCTGTGTTGAAACAGAAAAATAAGTC AAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTAAT
WI-7718b	248 A G ---				ATTGCACTGAAGTTTTGAAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGATAGTG ACTTTCAGATGGAAGAGGTGAAATGAAGAAGGAGCTGTGTTGAAACAGAAAAATAAGTCAAA AGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTAAT
WI-7718a	42 A T ---	C			ATTGCACTGAAGTTTTGAAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGTC AAGGATTACAGAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGAT AGATGACTTTGCAGATGGAAGAGGTGAAATGAAGAAGGAGCTGTGTTGAAACAGAAAAATAAG TCAAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAAACTATGTATTAAT
WI-7227d	99 G C ---				AGGGAATTGTGCTCCTGGAGGAAGCCAGGCATCATTAACAAGCCAGTAGGTCACTGGCTTC CGTGGACCAATTCATCTTTAGACAAAGCTTTA[G/C]AGAAATGGACTCAGGGAAGAGACTCACATGC TTTGGTTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCCAGAAAGGAGCTGAGCTAAACA GTGTTATTATGGGAAAGGAAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7227c	291 G A ---				AGGGAATTGTGCTCCTGGAGGAAGCCAGGCATCATTAACAAGCCAGTAGGTCACTGGCTTC CGTGGACCAATTCATCTTTAGACAAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGCTTT GGTTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCCAGAAAGGAGCTGAGCTAAACAGTG TTATTATGGGAAAGGAAATGGCATTGCTGCTTTCAACCAGCGACTAATGCAAT
WI-7227b	93 G T ---				AGGGAATTGTGCTCCTGGAGGAAGCCAGGCATCATTAACAAGCCAGTAGGTCACTGGCTTC CGTGGACCAATTCATCTTTAGACAAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTTGGTTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCCAGAAAGGAGCTGAGCTAAACA GTGTTATTATGGGAAAGGAAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7227a	24 A G ---				AGGGAATTGTGCTCCTGGAGGAAGCCAGGCATCATTAACAAGCCAGTAGGTCACTGGCTTC TTCCGTGGACCAATTCATCTTTAGACAAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTTGGTTAGTATCTGTGTTCCGGTGGGTGTAATAGGGGATTAGCCCCAGAAAGGAGCTGAGCTAAACA GTGTTATTATGGGAAAGGAAATGGCATTGCTGCTTTCAACCAGCGACTAATG
WI-7310b	234 A C ---				CCACAAATGCCTCTCCACGATGTCAGGACTCCTGCTGCTGCTGGAGGTGGGAGACAAGAACCTCCG AAGAGGAAGCAAGAAAGCCGTACTGCTATGTTGATGCTTCATCGAACAACTGATCGGAAAACT TGAATCTGTTACTGAAATGAGGAGAGAAAGGACATGTGCTATTGAACCTGAGCCAAACACACTGTAAT ATCCACAGACTCCCTCCCTGCCCCCATCCCA[AG/C]ATGATCTTGAGATTTC

WI-7310a	64 T A ---	---	---	CCACAATGCCTCTCCACGATGTCAAGGACTCCTGTCTGTCTGGAGGTGGAGACAAAGGAACCTTAA JCCGAAGAGGAAGCAAGAAAGCCGTACTGTCTATGTTGTGATCCTTCATCGAACAAACTGATGCGAA AACTTGAATCTGTACTGAAATGAGGAGAGAGGACATGTGCTATTGAAGTGAAGCAAAACACACTGT AAATATCCACAGACTCCCTCCCTGCCCATCCCAATGATCTTGAGATTTC
WI-7878b	162 A G ---	---	---	CCAGCAACACCTACACCTTTGTCACCTGCCCTGGACTCCTATGATGGCCTGTC/GTGGTTGATAATCA GATCATGCCAAGACGGCCTCCTGATAATCGTCTGGCATGATTGCAATGGAGGGCAAATGCGTCC CTGAGGAGAAAACTCTGGAGGAGCTG/G/GTGTGATGAAGGTGTATGTTGGAGGGAGCACAGTGT CTGTGGGAGGCCAGGAAGCTGCTACCCCAAGATTGTTGGCAGGAAAACTA
WI-7878a	51 C G ---	---	---	CCAGCAACACCTACACCTTTGTCACCTGCCCTGGACTCCTATGATGGCCTGTC/GTGGTTGATAATCA TCAGATCATGCCAAGACGGCCTCCTGATAATCGTCTGGCATGATTGCAATGGAGGGCAAATGCG GTCCCTGAGGAGAAAACTCTGGAGGAGCTGATGTGATGAAGGTGTATGTTGGAGGGAGCACAGTG TCTGTGGGAGGCCAGGAAGCTGCTACCCCAAGATTGTTGGCAGGAAAACTA
WI-7381c	213 C T ---	---	---	CTCCACATTCCACAGGCCCTTGAGCAGAAATTTCTGAGACTGAAGGAAATCCCTTTCTTTCTACC AGCCCTGCAAGTTTCTCATGGACGCTCGGAGGAGCAGGCTGCAGGTTTCTGCCTATGGTGAGATC AGATGTGGCCAAAGGAAGGAGCTCTGTTTCCAGAGAAATTTGCACAAAGTTCCCTCTGTACAGAGACA AAACGGCCTC/GTGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-7381b	54 C G ---	---	---	CTCCACATTCCACAGGCCCTTGAGCAGAAATTTCTGAGACTGAAGGAAATCCCTC/GCTTTCTTTCT ACCAGCCTGCAAGTTTCTCATGGACGCTCGGAGGAGCAGGCTGCAGGTTTCTGCCTATGGTGAG ATCAGATGTGGCCAAAGGAAGGAGCTCTGTTTCCAGAGAAATTTGCACAAAGTTCCCTCTGTACAGAG ACAAAAGGCCCTCCGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-7381a	53 C G ---	---	---	CTCCACATTCCACAGGCCCTTGAGCAGAAATTTCTGAGACTGAAGGAAATCCCTC/GCTTTCTTTCT ACCAGCCTGCAAGTTTCTCATGGACGCTCGGAGGAGCAGGCTGCAGGTTTCTGCCTATGGTGAG ATCAGATGTGGCCAAAGGAAGGAGCTCTGTTTCCAGAGAAATTTGCACAAAGTTCCCTCTGTACAGAG ACAAAAGGCCCTCCGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-1017b	93 G A ---	---	---	AAATTGCTCTATTCCGACCCTCATATTAAATAAGAGCAATGAGAGCGGAAATTTGAACCTCTCTC AGGTACTGACTGTGGACCAGACAA/G/GATGTAGATTGTACATTCAATCCTGAAACAAACCTG CCAGGCAAGTCTCTTCCCATTTACAATAAGGAGACAAAAATTAGGAGATTAAATAACTCATCAC TGTTTCAAAATAAGGAGTGTGTGAGGTTTGTCCC
WI-1017a	92 G A ---	---	---	AAATTGCTCTATTCCGACCCTCATATTAAATAAGAGCAATGAGAGCGGAAATTTGAACCTCTCTC AGGTACTGACTGTGGACCAGACAA/G/GATGTAGATTGTACATTCAATCCTGAAACAAACCTG CCAGGCAAGTCTCTTCCCATTTACAATAAGGAGACAAAAATTAGGAGATTAAATAACTCATCAC TGTTTCAAAATAAGGAGTGTGTGAGGTTTGTCCC



WI-1126a	97	T C	---			CTCTATTTCTGCGGCACTGCTTTCTTTGGGGGCAAACTCCAGTATCACTGATACATAATAAAAA CCCTGTAGTCTGCTTGCATTTTCAAGATTC/CAATATATATCCAGATGTTTTTCCAGCAAGAAA ATTTTATTTCTCAAGATATAAAAAATAATATTTAAATTCAGTTTCCCTCAAAAGGAATATGAAATTT GTTAAATGCAAAATCCAGCTGTAACCTTTTGGACTTGTCTTTTATTTCTT
WI-11183c	124	C T	---			TAGTGCTAAATTTTGGAAAAGTTTGTGCTGATTTTAAAAATCTTTTAAAACTTGAAAAATTTAGAGTAC ATATAAATAAAATAAGACCAGATAGGTATTAATCAGATGATTTTTTGGCCCTTGTCACATAACATTT TTTATGACATACAAATGACCAAAATGATGTTTTTATGAAGTGTAGGATAGAGTTTTTAAATATTGGT ATGGTGCTAGAGTTAGTAATGGAA
WI-11183b	192	T C	---			TAGTGCTAAATTTTGGAAAAGTTTGTGCTGATTTTAAAAATCTTTTAAAACTTGAAAAATTTAGAGTAC ATATAAATAAAATAAGACCAGATAGGTATTAATCAGATGATTTTTTGGCCCTTGTCACATAACATTT ATGACATACAAATGACCAAAATGATGTTTTTATGAAGTGTAGGATAGAGTTTTTAAATATTGGT ATGGTGCTAGAGTTAGTAATGGAA
WI-11183a	118	C T	---			TAGTGCTAAATTTTGGAAAAGTTTGTGCTGATTTTAAAAATCTTTTAAAACTTGAAAAATTTAGAGTAC ATATAAATAAAATAAGACCAGATAGGTATTAATCAGATGATTTTTTGGCCCTTGTCACATAACATTT TTTATGACATACAAATGACCAAAATGATGTTTTTATGAAGTGTAGGATAGAGTTTTTAAATATTGGT ATGGTGCTAGAGTTAGTAATGGAA
WI-10770b	174	G A	---			GCTTGGTTTGTCTTAGTCTTATTGTCTCAGTCTGAGTTCTCCCTTCTGCTGCGCCCTTTTGTATTCA CCCATACCTCTATGCCCTGCTCAGACCATTTCTCTATCTGGAGCGCTCTCCCTTGACTTTCTCTG TTCACCAACCTTCTTTTATCTTCAGGACACTCA/GAJTTCACATGCCACTCTCGTGACACTGTCTCT TTCACATCTTTCTGTGTCCTTTTCCC
WI-10770a	49	G T	---			GCTTGGTTTGTCTTAGTCTTATTGTCTCAGTCTGAGTTCTCCCTTCTG/CTCCCTGGCCCTTTTGTATT TCACCCATACCTCTATGCCCTGCTCAGACCATTTCTCTATCTGGAGCGCTCTCCCTTGACTTTCTC CTGTTACCAACCTTCTTTTATCTTCAGGACACTCAGTTTCACATGCCACTCTCGTGACACTGTCTCT TTCACATCTTTCTGTGTCCTTTTCCC
WI-9667b	82	C T	---			GATGACAACTTCTGCTGTGACCCCTTAGTCTGCTCATGACACTTTTCAATCTCTGCTGTATCATGG TTATCACTGGACA/C/JAGCCACCTCCCCAGCAGGCTTAGAACTCCATGAGTAAGGAGCCCTGTCTA ATGTGCCGTTTCTCCTTATGGTATTACACACAGTCATAGGCATGGTAGTCAACTAATGGATCTTGGCT GTTTAAACCTTTTCTGTACCCAGTACCTAAGTCCAAACTTGCATTCT
WI-9667a	68	G C	---			GATGACAACTTCTGCTGTGACCCCTTAGTCTGCTCATGACACTTTTCAATCTCTGCTGTATCATG G/CJTATCACTGGACACAGCCACCTCCOCAGCAGGCTTAGAACTCCATGAGTAAGGAGCCCTGTCTA ATGTGCCGTTTCTCCTTATGGTATTACACACAGTCATAGGCATGGTAGTCAACTAATGGATCTTGGCT GTTTAAACCTTTTCTGTACCCAGTACCTAAGTCCAAACTTGCATTCT

WI-10400d	189 A G ---			ACATTTATTAGCAAAATCAGCAAAATAATAATAGAAAGTAATTGCAATTCAGACATCTGCTG GTTAACTGTTATAAGATGGTTAGCACACATGTAGCACCTTACTAACACAATATTTTATTCTAAATTT TCCTCCCTTACCTTACTCTCCCAACCCAAATAACGTAAGTACCTATGTCAGJTGCCATGTAG TTTTTGGTTCATTTACTTGCAAAATATTCAAAGGCGTTAATGCATTATG
WI-10400c	166 A C ---			ACATTTATTAGCAAAATCAGCAAAATAATAATAGAAAGTAATTGCAATTCAGACATCTGCTG GTTAACTGTTATAAGATGGTTAGCACACATGTAGCACCTTACTAACACAATATTTTATTCTAAATTT TCCTCCCTTACCTTACTCTCCCAACCCAAATAACGTAAGTACCTATGTCATGCCATGTAG TTTTTGGTTCATTTACTTGCAAAATATTCAAAGGCGTTAATGCATTATG
WI-10400b	165 A G ---			ACATTTATTAGCAAAATCAGCAAAATAATAATAGAAAGTAATTGCAATTCAGACATCTGCTG GTTAACTGTTATAAGATGGTTAGCACACATGTAGCACCTTACTAACACAATATTTTATTCTAAATTT TCCTCCCTTACCTTACTCTCCCAACCCAAATAACGTAAGTACCTATGTCATGCCATGTAG TTTTTGGTTCATTTACTTGCAAAATATTCAAAGGCGTTAATGCATTATG
WI-10400a	46 T C ---			ACATTTATTAGCAAAATCAGCAAAATAATAATAGAAAGTAATTGCAATTCAGACATCT GCTGGTTAACTGTTATAAGATGGTTAGCACACATGTAGCACCTTACTAACACAATATTTTATTCTA ATTTTCTTCCCTTACCTTACTCTCCCAACCCAAATAACGTAAGTACCTATGTCATGCCATGT AGTTTTTGGTTCATTTACTTGCAAAATATTCAAAGGCGTTAATGCATTATG
WI-10809b	78 C T ---			AAAGGGCTACAACTAAGGCCAAACCATGAACGGTATAAGGAGGGTAATGCAAGGGGAGACCC CACCTCTACCA/C/TTTAGAAAGGGCATTTCAGCACATTCATGAGGCTTCATATCTGTTAG CAACAAATGGAATGTATTAGCCCAAGGCAGGTATGGACCAAAAGTGCCAGTGATGAGGCCACA GTGAATATCCACCTAACGACCTTCTTGGATGATGTACACATGACATAGGCTTAA
WI-10809a	33 C T ---			AAAGGGCTACAACTAAGGCCAAACCATGAACGGTATAAGGAGGGTAATGCAAGGGGAGAGA CCCCACCTCTACCACTTAGAAAGGGCATTTCAGCACATTCATGAGGCTTCATATCTGTTAGC AAACAAATGGAATGTATTAGCCCAAGGCAGGTATGGACCAAAAGTGCCAGTGATGAGGCCACAG TGAATATCCACCTAACGACCTTCTTGGATGATGTACACATGACATAGGCTTAA
WI-7038c	266 T C ---			CGAGCTTGGGATAAAGCAAGGGGACCTTGGCGCTCTCAGCTTCCCTGCCACATCCAGCTTGTGTCC CAATGAATACTAGATGCTGGGCTGTCTCCTCCCTCCAGGATGCTGGCCCCCAGCCCTGGCCAGAC AAGAAGACTGTCAGGAAGGGTCGGAGTCTGTAAACACAGATACAGTTTGGCTTTTTCACATTGAT CATTTTATATGAATAAAAGATCCTGCAATTTATGGTGTAGTCTGAGTCC
WI-7038b	140 A C ---			CGAGCTTGGGATAAAGCAAGGGGACCTTGGCGCTCTCAGCTTCCCTGCCACATCCAGCTTGTGTCC CAATGAATACTAGATGCTGGGCTGTCTCCTCCCTCCAGGATGCTGGCCCCCAGCCCTGGCCAGAC AAGA/CJGACTGTCAGGAAGGGTCGGAGTCTGTAAACACAGATACAGTTTGGCTTTTTCACATT GATCATTTTATATGAATAAAAGATCCTGCAATTTATGGTGTAGTCTGTA



WI-7038a	31 G A ---	---	CGAGCTTGGGATAAAGCAAGGGGACCTTGGC[G/A]CTCTCAGCTTCCCTGCCACATCCAGCTTGTG TCCCAATGAAATACTGAGATGCTGGGCTGTCTCTCCCTCCAGGAATGCTGGGCCCCCAGCCTGGCCA GACAAAGAGACTGTCAGGAAGGTCGGAGTCTGTAAACACGACATACAGTTGGCTTTTTCACATT GATCATTTTATATGAAATAAAAGATCCCTGCATTATGGTGTAGTTCTGA
WI-3429b	64 G T ---	---	ATACGCTTCTGTCTGTCCACAGTGGAAACAGCACCCAGGTGGCCAGGGTCCGAGTCCACACA[G/T] CCCTCAGCCCCCTCAGCTTTGCATGTGTCATCGGTGACTCAGCACAGAGTTTCCAACTCATGTGA CAAAATACAGATTCCAGTCTCTCTCTGGATTGGATCTAGCAAGACAGACGGTCTCTAGAA TCCTGACTGTTAACAGCACTCCAGGCAATCTTAAGACCAAGCACGGAGC
WI-3429a	62 C T ---	---	ATACGCTTCTGTCTGTCCACAGTGGAAACAGCACCCAGGTGGCCAGGGTCCGAGTCCACAC[CT]AG CCCTCAGCCCCCTCAGCTTTGCATGTGTCATCGGTGACTCAGCACAGAGTTTCCAACTCATGTGA CAAAATACAGATTCCAGTCTCTCTCTGGATTGGATCTAGCAAGACAGACGGTCTCTAGAA TCCTGACTGTTAACAGCACTCCAGGCAATCTTAAGACCAAGCACGGAGC
WI-6786c	151 G A ---	---	ATTTAGGACAGTGAAAAAAGGGATTATAAATAAAATCTATGCCATCCAGGAGGTATGTGCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCTTTGGCGAAAGGATAAAGAGTGAGTGACGGTGACCT GTAGCCCCATTCTTCT[G/A]TGGGATAAGGTGCCATTGTTCTTGGAGGGTGAAATGCCACATTC TTTTGGCAGGGGACACTCCTTCTGGGTGCTCTATTGCTCAGTTTCATCATT
WI-6786b	111 A T ---	---	ATTTAGGACAGTGAAAAAAGGGATTATAAATAAAATCTATGCCATCCAGGAGGTATGTGCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCTTTGGCGAAAGGAT[TA]AAGAGTGAGTGACGGTGA CCTGTAGCCCCATTCTTCTGTGGGATAAGGTGCCATTGTTCTTGGAGGGTGAAATGCCACATTC TTTTGGCAGGGGACACTCCTTCTGGGTGCTCTATTGCTCAGTTTCATCATT
WI-6786a	106 A T ---	---	ATTTAGGACAGTGAAAAAAGGGATTATAAATAAAATCTATGCCATCCAGGAGGTATGTGCAGT GTCCAGAACATCCTAGATGAAGTGGCTTCTTTGGCGAA[TA]GGATAAAGAGTGAGTGACGGTGA CCTGTAGCCCCATTCTTCTGTGGGATAAGGTGCCATTGTTCTTGGAGGGTGAAATGCCACATTC TTTTGGCAGGGGACACTCCTTCTGGGTGCTCTATTGCTCAGTTTCATCATT
WI-6711b	226 G T ---	---	GGCTATTTGTAATGCTTGGTTATTGACTCCAAAATTGAATAAGTATTGGGAAGAATCCCTCACCT ACTTCCAAATCCCTTACATATCAATTTACACAAAGCCCTTAACTTCACTTCCAACTCTGAAT TTCATATACCTCCATTATTAAATCAATACATCATTCAGAGAGAAAGACAAACGGTGCCAACTGGGTT TGGTTGGTGGCTGCACACCCACA[G/T]TGGCAACTAAGTGTATCTCTAAA
WI-6711a	36 T C ---	---	GGCTATTTGTAATGCTTGGTTATTGACTCCAAA[TA]TGAATAAGTATTGGGAAGAATCCCTC ACCTACTTCCAAATCCCTTACATATCAATTTACACAAAGCCCTTAACTTCACTTCCAACTCACTCT GAATTTTCATATACCTCCATTATTAAATCAATACATCATTCAGAGAGAAAGACAAACGGTGCCAACTG GGTTTGGTTGGTGGCTGCACACCCACAGTGGCAACTAAGTGTATCTCTAAA

WI-10613b	172 A C ---	---	---	ATGTATGCCAAAATCATAACCCCTGCATTCTAGAAACATACAGTGTAAATAGAAATTTTGAGCCATA TGGTGAAAAATTTAGAAGTATTATCTCTATATGTATATACAGTTTAAACATCAATGAATGTGATTT TTTGTCAACTTTTGACAAGGCCAGGCAATTTATTGAC/GCCCTAGGAGGTTACTATAATTTAGA AAGGCTCTACCTCCACTCTATAATTTAAGTCTCGGACTTAGGATGTAG
WI-10613a	44 G A ---	---	---	ATTGTATGCCAAAATCATAACCCCTGCATTCTAGAAACATACAGTGTAAATAGAAATTTTGAGCC ATATGGTGAAAAATTTAGAAGTATTATCTCTATATGTATATACAGTTTAAACATCAATGAATGTG ATTTTGTCAACTTTTGACAAGGCCAGGCAATTTATTGAGCCCTAGGAGGTTACTATAATTTAG AAAGGCTCTACCTCCACTCTATAATTTAAGTCTCGGACTTAGGATGTAG
WI-7587c	133 A T ---	---	---	GCTCTAGTGGGAAACCTCAGGTAGTCCCGAAGATCTGTGCTTCCAAACAAGTGACTACCCCTTGAAGC ACATCCCTTCTGGATCTGAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCTGAGGAAA(A/ TJGGAATGAACCACTCCCTGCCATTCCTTATAAGAAATATCCAAAGACCAGGCAATTTTGCCCTCT TTCCACATGCCCCCATATGTCTGAGCCAAACTGCACCTGGGGGCTGCCCTC
WI-7587b	81 G A ---	---	---	GCTCTAGTGGGAAACCTCAGGTAGTCCCGAAGATCTGTGCTTCCAAACAAGTGACTACCCCTTGAAGC ACATCCCTTCTGGATCTGAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCTGAGGAAA AGGAATGAACCACTCCCTGCCATTCCTTATAAGAAATATCCAAAGACCAGGCAATTTTGCCCTCTT TCCACATGCCCCCATATGTCTGAGCCAAACTGCACCTGGGGGCTGCCCTC
WI-7587a	28 C T ---	---	---	GCTCTAGTGGGAAACCTCAGGTAGTCCCGTGAAGATCTGTGCTTCCAAACAAGTGACTACCCCTTGA AGCAGATCCCTTCTGGATCTGAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCTGAGGAAA AGGAATGAACCACTCCCTGCCATTCCTTATAAGAAATATCCAAAGACCAGGCAATTTTGCCCTCTT TCCACATGCCCCCATATGTCTGAGCCAAACTGCACCTGGGGGCTGCCCTC
WI-10681b	103 T A ---	---	---	ATGACTCAGGTGACAAAAGAGCATGTCCTAGACCCCATTGACTTAGGCAAACTCAATCAGCCAAACC ACAGAAAAGCTAAAGACATCCTTTTAAAAAGCC(T/A)AAGACAGCCATTTTAACTAATTCCG TAGTTTATGATTTTCTCAAAATTTCCACACACACAGAAAGAACTTCAAGGTTAGGTTCTAATGTTA CCATTGCTAACACTATTGCTTTGGAGAGGAGGTGACGCTCTGTAAAG
WI-10681a	41 A T ---	---	---	ATGACTCAGGTGACAAAAGAGCATGTCCTAGACCCCATTG(TA)CTTAGGCAAACTCAATCAGCCA ACCACAGAAAAGCTAAAGACATCCTTTTAAAAAGCC(TA)AAGACAGCCATTTTAACTAATTCCG TAGTTTATGATTTTCTCAAAATTTCCACACACACAGAAAGAACTTCAAGGTTAGGTTCTAATGTTA CCATTGCTAACACTATTGCTTTGGAGAGGAGGTGACGCTCTGTAAAG
WI-7222c	126 G T ---	---	---	GCCTCTCCTCAACTGTCTGGACCCCAAGGCTAGGAAAGGCTGCTTGAGATGACTGTGGTCCCCCTT AGACTCCCTAAGCCGAGTGAGCTCAGGTGTCACCTGTTCTCAAGTTGGGGGATGGG(G/T)AATAA AGGAGGGGGAATCCCTTGAACAAGAAGAACTGGGGATAGTTATATTTCCACCTGCCCTTGAAGCTT TAAGACAGTGAATTTTGTGTAAGTTGTATTTCAAAGACTCGAATTCATTTT

WI-7222b	255 G A ---	---	---	GCCTCTCCTCAACTGTCTGGACCCAAAGGCTAGGAAAGGGCTGCTTGAGATGACTGTGGTCCCCCCTT AGACTCCCTAAGCCGAGTGAGCTCAGGTGTCAACCCTGTTCTCAAGTTGGGGATGGGAATAAAGG AGGGGAATTCCCTTGAACAAGAAGAACTGGGATAGTTATATTCACCTGCCCTTGAAGCTTTAA GACAGTGATTTTGTGAAGGTTGATTTCAAGAACTCGAATTCATTTCTCA
WI-7222a	126 G T ---	---	---	GCCTCTCCTCAACTGTCTGGACCCAAAGGCTAGGAAAGGGCTGCTTGAGATGACTGTGGTCCCCCCTT AGACTCCCTAAGCCGAGTGAGCTCAGGTGTCAACCCTGTTCTCAAGTTGGGGATGGGIG/JAATAA AGGAGGGGAATTCCCTTGAACAAGAAGAACTGGGATAGTTATATTCACCTGCCCTTGAAGCTT TAAGACAGTGATTTTGTGAAGGTTGATTTCAAGAACTCGAATTCATTTT
WI-8054d	41 C A ---	---	---	AAAGATGACACTTAGAACTGGATCACTTGGCCCTTCTCTTCTATCTCTCCAGTTCAAAATG CTTGATCTTTTAATAGCCAGCATCTCTTAGATCTGCAGTTGGGCTCAAGCACTCAAGCCTTAGCA CAATCTCTTTGTAGTTTAGCCTTTTCCGGAAATCGGCTTAGTTGCCACCATAGCCACTCTGCT TCCTGTCTAATACGCCGCTTCCCTGGGCGTACAGAGAACTCCTTGCCCTT
WI-8054c	237 G T ---	---	---	AAAGATGACACTTAGAACTGGATCACTTGGCCCTTCTCTTCTATCTCTCCAGTTCAAAATGCTT GCATCTTTAATAGCCAGCATCTCTTAGATCTGCAGTTGGGCTCAAGCACTCAAGCCTTAGCAAA TCTCTTTGTAGTTTAGCCTTTTCCGGAAATCGGCTTAGTTGCCACCATAGCCACTCTGCTTCC TGTCTAATACGCCGCTTCCCTGGGCGTACAGAG/JAATCCTTGCCCTT
WI-8054b	148 T C ---	---	---	AAAGATGACACTTAGAACTGGATCACTTGGCCCTTCTCTTCTATCTCTCCAGTTCAAAATGCTT GCATCTTTAATAGCCAGCATCTCTTAGATCTGCAGTTGGGCTCAAGCACTCAAGCCTTAGCAAA TCTCTTTGTAGT/JCTTTAGCCTTTTCCGGAAATCGGCTTAGTTGCCACCATAGCCACTCTGCT TCCTGTCTAATACGCCGCTTCCCTGGGCGTACAGAGAACTCCTTGCCCTT
WI-8054a	131 C G ---	---	---	AAAGATGACACTTAGAACTGGATCACTTGGCCCTTCTCTTCTATCTCTCCAGTTCAAAATGCTT GCATCTTTAATAGCCAGCATCTCTTAGATCTGCAGTTGGGCTCAAGCACTCAAGCCTTAGC/JA CAATCTCTTTGTAGTTTAGCCTTTTCCGGAAATCGGCTTAGTTGCCACCATAGCCACTCTGCT TCCTGTCTAATACGCCGCTTCCCTGGGCGTACAGAGAACTCCTTGCCCTT
WI-10854b	152 G T ---	---	---	TTCCACAAAACCTTCCCTGGGCGGGTGACTAAGATGAGAAAGTGGGAGAACTGGATGTTAATAA ATGTTTATATTTACTTTAAAGCGAAGTTGAACACGAAAGCAGATAGTTAACGCTGGTAAGTTTAT ACGGTGTGCGAGGCAACA/G/JGAGAGGTACGGGAATAGTTCTACTTCTTGTTTTTATTCTGTG TTTTAGACACAGGGTCTGCTGTGTG
WI-10854a	102 C T ---	---	---	TTCCACAAAACCTTCCCTGGGCGGGTGACTAAGATGAGAAAGTGGGAGAACTGGATGTTAATAA ATGTTTATATTTACTTTAAAGCGAAGTTGAACACGAAAGTGAACGCTGGTAAGTTTAT TATACGGTGTGCGAGGCAACAGGGAGAGGTACGGGAATAGTTCTACTTCTTGTTTTTATTCTGTG TTTTAGACACAGGGTCTGCTGTGTG

WI-9826b	127	G A ---	---	---	AATTTATATGTGAAGGTTAGCAAATATGCCACAGGGCCCATCTAGCCATGCCATATTTTGTG TGCTGATGGCTGTTGGTGTTCGACGCGAGTTGAGCCATTGTGACAGAGGCTGTTATGAGCCTT CAAAGCCAAAAAATAATTTACTCTCTGGCCTTGACGGGAAAGTTTGTCTGATTCTAGATATTTAAA GGCAGAGAAGATCAGAAAGTGTGAA
WI-9826	125	A T ---	---	---	AATTTATATGTGAAGGTTAGCAAATATGCCACAGGGCCCATCTAGCCATGCCATATTTTGTG TGCTGATGGCTGTTGGTGTTCGACGCGAGTTGAGCCATTGTGACAGAGGCTGTTA/TJGGCCTTC AAAGCCAAAAAATAATTTACTCTCTGGCCTTGACGGGAAAGTTTGTCTGATTCTAGATATTTAAAG GCAGAGAAGATCAGAAAGTGTGAA
WI-15986	60	T G GTGGGTTTT	TTGTTTGTGT	TGACATTATAT AAACGTAAAA GAAAATGT	CGGACACGTGATATACAAATACAGATCGTATGGGTTGTTGTGTGGGTTTTTTTTT/GJTTAC ATTTCTTTTACGTTTATATAATGTCAGCATTTCAA
WI-8655	29	A G AG	AACTGCAAAT AGGAACCAG	CCACCTGGGG TCCC	TTCAAGTAAGTCAAATAGGAAACCAGAGAG/GJGGAGCCCCAGGTGGGACAAATCATGGCTACCCC TCCCCAACAGAACAGGGGGAGGAGGTGGCCCCCTACACCCCTTTAT
WI-8170b	259	G A ---	---	---	GCACCTCTCTCTGAGCAACAGGTACACTTTTTTCTCTAACATTGATCTATAACACACAGAACCG TGTTTTAATAGCTGCTGATAAATGAACCTATTTTAAAGTACTCTACCAAGATGCTGTGGTAAGGTTAG CATTTGGTGAGAGATTACAAAGTTAAGATCATGTGCCATCAAAGTGCAATCCTATCAATCAGAA ATAAAGGTAAGGGCCCTCAAATGAATCTACGGAAAAACATAACACAAGA
WI-8170a	204	T A ---	---	---	GCACCTCTCTCTGAGCAACAGGTACACTTTTTTCTCTAACATTGATCTATAACACACAGAACCG TGTTTTAATAGCTGCTGATAAATGAACCTATTTTAAAGTACTCTACCAAGATGCTGTGGTAAGGTTAG CATTTGGTGAGAGATTACAAAGTTAAGATCATGTGCCATCAAAGTGCAATCCTATCAATCAGAA AT/AJAAAGGTAAGGGCCCTCAAATGAATCTACGGAAAAACATAACACAC
WI-8172	136	C G GACA	CCTTATTAAA ATTGTTTCTT	GAAGAGAAAT GTAATACCTGT AAAGGTAC	CAGGATTCCTTAAGTCATCTCCAACTACTCCAGGTACATGGTGAAGAGTCACCTGTTAAACACGAA ATCTAACCATTAACAAGCTTTTAAATCCTTCGGTAACCTCCCTTTATTAAATTTGTTTTCTTGACAT A/C/GIAGTACCTTTACAGGTATTACATTTCTCTCACCGTTTACA
WI-8183	56	G A TGC	TGAAATAAAA ACAAATTCGT	TGTGTTGAAAT CAACCTGC	AGCAGGGTTTGAATTTGATCCCTTATTTTACATGAAATAAAAAACAATTTCTGTTCG/GA/GCAGGTT TGATTTCAACACAGTTGAATCTGTAAAAACCAAGCTCGTTTCTGATGCAGGACAAATATCCCAAT ATTTAAACCTGCAAGCACCATGC
WI-14149	83	C T ---	---	---	GCTTTATTGGGATTGCAAGCGTTACAAGGTTAAAGACAAAACCCCAAGCATGGGATTTGCCGGAAT ATTAGCGTTAAAGGAG/C/TTGAGTTGAGTCAACACACCGG
WI-8712	44	G A G	CACAGGGAAG AGGTAGTGA	CAGGAAGCCTG ACCATCTC	TCAACAATGACACTGTGTAAACAGCACAGGGAAGAGGTAGTGGAG/GA/GAGATGGTCAGGCTTCCTG TTCCCTAACAGCAGAGCCCCAGCAACCTAGAAAGCGCTCACCTAGCCTCTTAAT

WI-8827	22	C T	TCCTGGGAG ACTATGG	GCATTAGGAT TTTAGTGTTC C	GGTGTCCCTGGGAGACTATGG[C]/TAGTGAACACTAAATCCTAATCGCCATGCAATGGGAATTATT CCGACTATTACTTTCITTAGTCCCTTCTTAICCAACCCAGTCTTCT
WI-8833	51	A T	TCCTCCATGCC ATTCTCTG	CCTCACACATT ATAGGGCA	CTCCGGCCTCTTAAAGCTCTCTGTAGACTGTCTCTTCCATGCCATTCTCTG[A]/TJGCCCTATAATGT GTGAGGGTATTACAATAGTCCCTATTCAAACTGCCTTGTATATAAAAGGTCAGCTATGT
WI-8377	63	A G	---	---	ATTTTATGCCATGTTGTTAAAGTTCAITTTTTCAGTACATGGGTAAACACCCAGGCCCTTTTCCC[A]/GJT TATATCCAGGTATGCTACAAGTTCTTTTAACTCTTATCAGAAGTTATTATTACTGTTTCTTAGAGAG GCTACCAGGCTAAAATTCACITTAGTTGGTTTGTCTAATGTCCTCATTAITTTATCTGAAGCTCGTG
WI-8850	21	A G	GGGACTTAAC CTTTGGCT	CAACAGCCA GGCAGG	GAGGACTTAACCTTTGGCCT[A]/GJCTGCCCTGGCTGTTTGGCTCTGCGCTTGTCTGTTTGGTTTCTT TCTCTTCTACTGGTCTTCTTGTCTTTTGGCAGCCACTATGCTGCTGT
WI-8853	79	C T	CCGGGCATTG AGGATA	AGTCTTCCCTGA GCTTCCAT	ACTTTTCTGAGCTGAGCAACCTCATCATCTTCTAGCTTCTGGTTGATAACGCTGGTTAATCCCCGGG CAITGAGGATA[C]/TATGGAAGGCTCAGGAAGACTTTCATTCTCAA
WI-8865b	52	A G	---	---	AGGGTGAAGTGAATCACAGGCACAGACTGAGGAAGACAGTCAATGGTGGTGAACAGTCAATGCT TCGGACTTACCAAGGAGAGTCGAGCTTTCATATAAA
WI-8865a	42	T C	CACAGACTGA GGAAGACAGT CA	GGTAAGTCCGA AGCATGTTG	AGGGTGAAGTGAATCACAGGCACAGACTGAGGAAGACAGTCA[T]/CJGGTCGAACAAACAACATGCT TCGGACTTACCAAGGAGAGTCGAGCTTTCATATAAA
WI-8895	32	A C	---	---	GTGCCACAAACCTGGACACCACCAACAGAAAT[A]/CJCTCCCGTCTTTGAAATTTCCATTGAAGACA CAATGGGGTAAATTATACCGGATGCTCCCAATCGCTCTTC
WI-8456	93	G C	---	---	CCTTTAAAGTCACAGTCAACTCGACTGTGGAGTGAATATTTGTGAAATATAATAAAACTCTTTTCC AAGGTCCCATGCTTGGATGTCACA[G]/JTATGTCAAGTTAATAAACAATTTCTAAGTGTCTCACTC TCAACTTCTGTGTTATCTTGGCATGGTCCAGTAACAGTTCACACGGCAGACCAAGTTGTGTAGCAC TGGCATAGACGAGGGCTTCTCAAACCTCCGCTCGCTCAGTCACCCAC
WI-8496b	157	A G	---	---	TTTCATCATCAAAAGTTTCTTTCCATAGAAGATGGTAATGTTGTATCATGTCATATCTATGGAAA ATTCATATCTCAAGTAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA AAGACACAATGCTGCCAATGCA[A]/GJTATATATAGAAATAATACGACGCTGTTAGAAAAAGTCT GTGGCCAAGTGGGATAAAACAGTAGCAGTGCAC
WI-8496	41	G A	---	---	TTTCATCATCAAAAGTTTCTTTCCATAGAAGATGGTAATGTTGTATCATGTCATATCTATGG AAAATTCATATCTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG GTCAAAGACACAATGCTGCCAATGCAATTAGTATATAGAAATAATACGACGCTGTTAGAAAAAGTC TGTGGCCAAGTGGGATAAAACAGTAGCAGTGCAC
WI-14153	28	A' G	GTGAGGAAG GCCAGC	AACGGCAGGA GGGA	CTGCAGGTCTATGTGCAGGAAGGCCAGC[A]/GTCCCTCTCCCTGCTGTCACCCACATCCACAGAGCA GCCCTAGTGCCAGGTGCAGCCACTGOCACOCACGGCAGGGAACAGGACCCATGCTGC

WI-12108	40	C T A T A	TGAAAAGGG TTAAACTCAA	TTGACCTGGTA TAATGAAAGT ATTC	TCATGATTACTTTCTGGAAAAGGGTTAAACTCAAAATATC[CT]GAAATACITTTTCAATTATACCAGGT CAAGAAAAATGCCACAGCCAGAAAAATTTATTTAA
WI-5989	29	G A C A C A G G C A	CCACAAAGGT CACAGGCA	GGGTATAACAG AACCGTATGTA CG	CAGGCAACGTCCACAAAGGTCACAGGCA[GA]CGTACATACGGTCTGTTATACCCCATATATTAC CCCTTCATGTCCTAAAGAGACATTTCTCTTAGAGATTTTCATTTAGTGATCTTTAAAAAAAAT CTTGTTAACTTGCCTCATCTTTTCTGGGAGGACACC
WI-12201	61	C T C T G C A T G	CCCACTGATCA CCTGCATG	CCGACCACATA CCTGGC	ATAGCTTTTAGCCTTTTCTCGAGTGTATGTCCCAAGCCCACTGATCACCTGCATG[CT]GCCA GGTATGGTGGGGTGTGATGGACGTGGGTTGCAGCCCTCCACTGCTCGATAAAAGGC
WI-12018	31	A T T C T G A C T T	GGCAGCCAGC TCTGACTT	GGAGATGAC AGAAACAGAG AG	TTTTATCTGTCCAGGCCAGCTCTGACTT[AT]CTCTCTGTTTCTGTCTCTCTCCCCACATACCA ACTTCTCACCATGATGATTATACCAATAATACAGTTCTTATATGAGGGGCTCTGGAAAAATTAGAC AGTGAAGCAITGTCAG
WI-14162	57	A G C C T C	TGGCCTGCTG CCTC	AGGGATCAA GAGAAAAGGC	TTTTGCTTTGTTTAAATGATCCGAATGCTTGAGAGAAACCCCTGGCTCGCTC[GA]GJGCCTTTT CTCTTTGATCCCTGAGTTGCTGAGATTAAAGATGAGGTCCCAATGAGAGCTACCAAGATGTAGTCG AGCGG
WI-15407	92	A G T T	CATGCCCTTA AGGATTAAGT	TCCTTTCTCTTT TGGTAGTGG	AGCATGTAAGGAGCAGTTTTTATTGATTGGTATATTACAGGTTTCTAACCCAGCTGAAAAATTCAAATA CATGCCCTTTAAGGATTAAGTTTAA[GA]GCCACACTACCAAAAGAGAAAAAGATTTATATGATCACAT ATAAGCAATGGAATCAGCA
WI-12319	109	T C A A T T	GTTGAGTATTT GTTCTGCTCAT	GGGAAGGCTG GTACATATTGG	TCTGATGTCATTTATTGGCACAAAAATTTCTGTATACAACATGGTGTCTAGACATGGCTACACTTTA TACTTTGIGCATTTAGTTGAGTATTGTCGCTCATAATTT[CT]CCAATATGTACCAGACCTTCCC
WI-12326	25	G A C A	GACAGACTC AAAAGCAATT	AGGTTTGA TATGTATTAAG TACTTTGT	CTGACAGACTTCAAAGCAATTCAC[GA]CTTCCAGAAATACAAAGTACTTAATACATAATTTTCAAAG CTGTTTGCAATTTCAAACAAAGTTAGCGTTTGTAAATCAAATTTGATAACCCGACTAAAAAT
WI-12361	63	C T	---	---	TTAAATCCACACTGAAGATCTGGAGTATGGGGGGATATAGGAATTTTCAGCATATGATTTAT[CT] TGAACATAATTTACAAAAGTGGAAACAGTTGGAAGGTACTTATAGGTAGACCTGAGGGTCTGTTACC
WI-11305	87	C T A T C A C A C C A	CAGACACAGC ATCACCCA	GACCTCCCGT GGGC	ATACTGGTTTAAATCCATGTCAAATGTAGTTTACAAAGGAAAGGACAAGTACCTTTTGTATAGAATAT ACAGACACAGCATCACACCA[CT]AGGGCCCCACGGGAGGTCTGGGAGACGACACTTTTCCCTGGG AAAGG
WI-11321	67	A G T T T T	GGGAGGAAAA TCCAATAAAT	CATTGGGAAT AGCTAAACCTT	ATTTTATATGAAGGTTTCTGGTGAATCTTTTAAAGCAGGAGGAAAAATCCAATAAATTTTTTAA[ A/G]AAGGTTTAGCTATTCCCAATGCTATTTAATAACAATGAGGTAGGACGTTAAGTCTTATCAGA CTGTGACTGGAGCCCCG
WI-11324	40	C G T G T G C C C A	GGATAAATCA TGTCGCCA	ATCAAGCTTTG GGGCTCT	AGCATACTGCATCTCCTTTATGGATAAATCATGTGCCCCA[CT]GAGAGCCCCAAAGCTTGATGACAT TCTGTAAAGTTACACAAATGTATCTGAAGAAGTTATCTGTTCTGTC

WI-11352a	69	T C G	AGCAGGCAC ATAGTGGAAA	GACCTCTCGTA GGACACTTAGC	TGACACATGGTTCTGTTTCCAGAAGGAGAGAGAGTCATCTACATAAGCACAGCACATAGTGGAA AGTTCGCTAAGTGTCTACGAGAGGTCAGATCATATCCATAGAAAAACAGCTCTCTTTTACTTGCA CACTTA
WI-11371	84	C T G	CAGCTTGGAG ATTCTGATTCA	GCCCGGCTGGA GCAC	TTAGCCCATGCTGTCAATTGCAATCACCTGTGAACCTATGAAACTATACCTGCCAGGCTCAGCTT GGAGATTCTGATTGAGTCGTCGTCTCAGCGGGCTGGACATCCATGTTTGGGAAGAGTTGCGCGGGT GATTCGATGCGTATAT
WI-11385	75	T C G	ACAGAAGACT TTCATATTCTT	GATTCATTCT AGTCATGGTCA	CTTAAAGCATTATAGTTTGGCCTGATGGTGGACACAGAAGACTTTCATATCTTGTGTTTTTAAAGTC TCTTCAGTCGAGGAAAAAGCTACAGATTTAAAAATATGACCATGACTAGATAAGATCAGC
WI-11388	88	C A A G T T C	TGTTTGAAT ACACGTAAC	TGCCCTGTATC CAAGTTAAAT	TCATGTGCCAGTAGCTCAGTTGGTTAGAGTGTGGAGCTCATAAAAAATTAAGAATGAATGTTT AAATTACACGTAACTAAGTTCGTCATATAATTTAACTGGATACAGGCAATGTTATGCTAAT
WI-11392	55	T G A T A A A T A C	GGTTATGTGTT CTTGAACCTTA	GTACATTACG TGTTTTGTAA	TTCTATCATTCCTTAAAAATGGCAGGTTATGTGTTCTTGAACCTTAAATAACAGTTCGCTTTTACA AAACACGTGAATGACTCTTCTGTCAGAAGGGGAACACTGAGTCTCCGCTAGATCCATTAACTGT CATACTCCTTCCCCAGA
WI-11396	52	A T T	TTTTGTTTTG AAATGGTGT	AGCTTATTTTC ATATTCACCCA	AAAGAATAAGATGGCATTGTTTCAGTTAATTTGTTTTGAAATGGTGTGTTTATGATGGGTGAATA TGAATAAAGCTTACCTCATCCCACTCTAAAAGGTAGTTGGTGAATTTTGAACCGTTGTCAAT
WI-11441	100	C A C A G C	TCCCCACCAAC TGAGAAGCCA	TGCCAGGGCCT TATTTG	CTGTGAGTCTTCCCAACTAAACCGTGAGTCCAGTATGCTGGCAGCACGCTGCTGTTCTTGGTG TATCCCACTTACTGAAATCCCCACCAACCAGC/C/A/CAAAATAAGGCCCTGGCACAAAGTAAGCTCTCC ATTTTGTAGAATGAAT
WI-11466	26	C T T T A T T T T G C A	TGAGAAGCCA	GTTTATTGTTA TAAAAATGAC	ACTTTGAGAAGCCATTATTTTGCAGTC/CTTTCAGTCCAAAAAAGTCAACATTTTCAGAAATTTT TATATAAGTTGTAGGTCAATTTTATAACAATAAACTTCTATTATCTATTATCTCTCAGATACATTT CATGTATCTCTG
WI-13364	35	A G	---	---	TTTTCTTTTGTGCTCTTTTTTTAGTAGAAGC/A/GJGGAACAGTTGTCAATACTACCTTCTGTGTTGG TCCCTGTTAGACAACATACCTTTCTTTGAAATGTAAAAATGTCA
WI-11276	41	A G A G C A G A C	GGCAGCCAGG AGCAGAC	TGTAAGTGGGA GGGGTG	AGGCAACACTGCTTTATTAGCGCGGCGAGGCCAGGAGCAGAC/A/GJACCCGGCTCCTCAGTACACATT CCCCACCCCTGCTGCTGGTCTGCCCACTCAGGGCTGGGCTGGGAGGGGCGGTAGGCTGGAA
WI-12210	76	A G A	ACTGGGAAA CAACTATTGC	TGCTAGTTTGC ATATGTTTTCC	ATTGGAAACAACCTTAATAATTTGCATCTCTACATATAGAAAGCTGCTTTGAATACTGGGAAAAACAA CTATTGCAAT/A/GJGGAACAACATATGCAAACTAGCATCATTTGCTCTAGA
WI-14186b	88	A G	---	---	AATGGTCTGGTTTTATTGAGAAGCTGTGGTCAATTTGATGGAAAGACACATACGGTACAAAAATTACA GGTGGTTTATGTTTCAATACATG/A/GJACAAATCATTAGAGTCTTTACAAGTCATTAGAGTCTTTGGAT TTT

WI-14186a	52	C T A	GGTCATTGGAT GGAAAGACAC	AACFAAACCA CCTGTAATTTT GTAACC	AATGGTCTGGTTTATTGAGAAAGCTGTTGGTCATTGATGGAAAGACACATA[C/T]GGTACAAAATT ACAGGTGGTTAGTTTCATTACATGATACAAATCATTAGAGTCTTTACAAGTCATTAGAGTCTTTGGAT TTT
WI-12234	66	A G	GAGAACACTT GTGGGCTT	GGACCTATCAG TCCATGTTTGA	ATTTTTTTTGGCTATAGGTCAGTGGTTCTAAACTTGAGCTTGCAAGAGAACACTTGTGGGGCTT[A/ G]TTCAACATGGACTGATAGGTCCACCCAGATTCTAACTGGTAGGTCTGGGGTG
WI-12345	37	C A	GTGGCAGGAA AAAGAGGAA	TTGACAGGGG TTCAGG	GGAACAGACCTGATCCACGTGGCAGGAAAGAGGAA[C/A]CCTGAACCCCTCTGCAAGTATTCTCT TTCTGACCAGCTGGGCTTGGCACTTTGTGAGATTGCAAAA
WI-13416	71	C A	AAATTTTGG AAGTTTTTCAG	AGTGTATTATAG TTCAATGAATA ATTCAA	GAAAGGCTGTAATTTTATTTCAAATTTTGGAGTTTTTCAGAAAAAAATAAAATGACAAGAACA CATA[C/A]AAATATTGAAATTATTCATTGAACATAAACACTTAGCAGAGGAAGGACTTTTGAT
WI-12310	46	G A	TTATTCCCAAG TATAATTTTA AAAAGC	TGTTTAAATAT GTTTGGTCT AAA	TTTGAAAGATGCTGAATTTATCCCAAGTATAATTTTAAAAAGCT[G/A]TTAGGACCCAAACATA TTTAAACATCTCTTACACATACAGAAATTCAGTTTACAAATATCCAGAAGGCATTTTCTTAAAGCAG T
WI-12086	72	C T	CCGGGAAAC TTGGATT	GGAGTCTCGG GTCTGG	GAACCGAGCTTTATTGGAGCAAGAGTGTGGACACTGTTTACAACAAAACGTTTCCGGGAAAACCTTG GATT[C/T]CCAAAGACCCGAAGACTCCTCCAAGTTCTCACTGTTAGTAAGGTCAATTTGGGGCAGA ACAGGAACATGCCTTAGCT
WI-11549	102	T G	GGCATAAAGT TCATAATATTC TTTTATG	GGAAAGTCTGT ACAAATCCCC	ATGTCTCACAGGTGTAATTTTGTAAAGAGTTTGTCTATCTAAATTTTCATATTTATTGGCATAAAGT TCATAATATCTTTTATGATCTTTTAAATATCTG[T/G]GGGGATTGTACAGACTTTCCCTC
WI-11585	79	T C	TGGGTTTGCA AAACAAAA	CCATGCTTCAG TGATACCTCC	TTAGAAGGAAGAAATAAAACACGGTAATGGGAAATTCAGTTGAGGTTAGGAAGGAGCTGGGT TGCAAAAACAAA[T/C]GGAAGTATCAGTGAAGCATGGCCTAGAAGTCCAAGAGCAGGGGTAGAGT TT
WI-11604	68	G C	---	---	TTAGTTGGTTTCCCTGAACTTTATGCTGTTTATTTTAAACCAATAGGATGTTCCAGTTACCAGCATTT G/C]AGAAGTGGGACTTTCCATGAAAAATAATTAGAGCTAAGGAATTTCTGACGCTCACCAATTTTTC TTTGTACTCTGCAGTT
WI-11614c	108	C A	---	---	CAAAATCAAAAATTGAGGAGGCAAGAACAGAGAGTAAAAATCCAGAAAGACTGCTGTGAGGCAT GTTCCACCCCTGGACTTGCCAACTTTCACTGTGAAACTGCAACATATTAAGTATTCGTGAGCTAC GGACTTCGT
WI-11614a	60	A G	CCAGAAGACT CAGCTGCTTG	AGGGTGGGAAC ATGCC	CAAAATCAAAAATTGAGGAGGCAAGAACAGAGTAAAAATCCAGAAAGACTCAGCTGCTG[A/G]GG CATGTTCCACCCCTGGACTTGCCAACTTTCACTGTGAAACTGCAACATATTAAGTATTCGTGAGCTAC GGACTTCGT
WI-11626b	83	T C	---	---	TTGATTTTACTAAGGTCTTCCACTGGAACATGAAGGTAGGGATAAGTGTACAGGATAATATACTCAG ATATTTTAAAAATAAA[T/C]TACTTAATAAAGAAATTAGCCATACCACATTTGTTCCATTTTGCTAC AAGAACAATTTGGCAATGA



WI-11626a	39	G A G	TCCACTGGAA CATGAAGGTA	GTGGTATGGCT AATTTCTTATT ATTAAGT	TTGATTTTACTAAGGTCTCCACTGGAACATGAAGTAG[G/A]GATAAGTGTACAGGATAATATACT CAGATAATTTTAAATAAAATTTACTTAATAATAAGAAATTAGCCATACCACATTGTTCCATTTGCTAC AAGAACAATTTGGCAATGA
WI-11627	23	T C A	CCTTCTTCG CATGTCCTC	CATTTGCAACC CATCTCAAG	ACCCCTTTCCTTCCATTGTCCCTC[T/C]CTTGAGATGGGTGCAAAATGGGAAGTAAAAAGCAAAAAGGG AGATGAGAAATACTGATGCCCTTTTGTCTGGCTTACTTCCATTCGATGCAAGTCCATCCATG
WI-11636	61	A G T C T	GGACTTAAAA AGATCTGCTTA	AGAACTTGCT AAATATTTTAT	TCAGAAATGTTGCAAGCAAAATACTATTTGTAAAGGTGGACTTAAAGATCTGCTTATCC[T/A]GJTA TATCCACATACTCTAGTGTACATAAAATATTTAGCAAGTTCTGTGACAGGTGCTCAGTAAACAC TTTGACTCCTTTTTTGGTA
WI-11637	119	C G T	ATTGCTCATCT TACTCTGACCA	GACCCAGCAA AAAGAATGAT T	GTACCATTCTTATGGTGCAAAATAGCAAACTGTGAGTAAACGAGGGCAGCTGAATAAATTTACAG TATACAATATTAGAGAAATATTATGTTGCAATTGCTCATCTACTCAGAGTTCACACTCATATTTTCATATTTT TTTGCTGGGTCCAGGACC
WI-11654	37	G C T G	GCCAAAAGAC TATTCAGCAA	GGCTCTCCAG GACAGTTT	AGTAGAACATCAGTGCCTGCAAAAGACTATTCAGCAAACTG[G/C]AAACTGTCTGGGAGAGCCACTCCAG AGCTATTTCTAAGACTTCTGTGGTGTTCATCTACTCAGAGTTCACACTCATATTTTCATATTTT ATTTTGGGTGTTGGGT
WI-11656	28	G A A	ATTGATTTAG AAGGAAGTC	CAAGGCTTTGT CCTCAAGTAAA	ACCTGATTGATTTTAGAAGGAAGTCAA[G/A]CTTTACTTGAGGACAAAAGCCTTGCCGTCAGTTGTTT AAATGTCTGAAACAATCAGATTCCAGGCTGGAT
WI-11680	55	T C ---		---	ACAGATACTTTTCCACGCAACATTTCTGAAATGAAAGCTTTGATTCTCCCTTTT[T/C]TTGCATAAAA GGCTGGGAAGGTGGTTTGGCCAGACCGTACATCTTTT
WI-11696	47	T C A G G G A C A G	TTATCACAGC AGGGGACAG	GGCATTAGAGA AGCCAACCTT	GTCCAAGAACAAAGATACTTTGACATCTTTATCACAGCAGGGGACAG[T/C]AAGGTTGGCTTCTCTA ATGCCACCACCTCTTGTTTTCAGAACTTTCCACTTCGCC
WI-11702	69	C T C A G C A G	GAATAATACT GAAATAACCA	AGAACAACTT AAGCAAATTAT	TTACATGTGGTCAATGGTGACATACTTTCAATAATTAATAATCGAATAAATACTGAAATAACACACAGC AG[C/T]TTTCAGTATAATTGCTTAAGTTGTTCTAGAAAACACTGCTAATTTTGTGTTTCTGCAGA
WI-11706	60	C T T C T C T C T	TGGCTGGAATT TTCTCTTCT	ATCACCAAAG AACAAATCCA	TGCTGATTATCGCTTCTACCATCTGGCTGGAATTTTCTCTTCTTGTAATAATTTTGC[T/J]GGCTG GAATTTGTTCTTTGGTGATTGTCCCTTGCTGCT
WI-11709	105	T A T T C A G T T T G C	AGAAGCTTGC ATTCAGTTGC	TCATTTCTCT AATTTACGGG A	AATATCATCACTCATATCAGGCATGTTTATAAAAATGAGAGATTATGCTCTTTTGGCATACTTCATC TTCTTCAGGACACAGAGAGAGCTTGTCTCAGTTTGC[T/A]GTCCCGTAAAATAGAAGAAATGAAT GGCCAGATGGATGGAAAA
WI-11710	103	C A C A G T C T T C A	GCACCTAGCCT CAGTCTTCA	GTGTGGAGGAG GGAGGAG	TTATTACCATCAACCTGTCCCCAGCTTTCAGCACACAGCCACACTCTAGACACGCTTCAC TCCAGTCCATTCTGGCACCTAGCCTCAGTCTTCAC[C/A]CTCTCCCTCCTCCACACACTCCTTC



WI-11909	78	A G	TTTGTGGG TGGTCAAG	CTCTCTGAG ATTTCTGAAT AG	GCAGTTCTCTGAAAGACAAATGGATTGTGGAGCATACTGAAGACTATTCCTAATGGCTATTGTGTG GGTGGTCAAGTATGCTATTAGAAATCTCAGAGGAGGACAAATGATAGTGCAGTGCAGCCAGCTCG GACTGGCTTGAAGATC
WI-11806	60	T G	CATGAAGAGT GGCAGTTCA	TCCTGTAAGC CAATTTTATAT ACTAATAA	AAAATACCATTTAGCATCAATGCCCAAGTTTGGCAGGCATGAAGAGTGGGCAGTTCA[T/G]GTT TTATTAGTATATAAATGGCTTTACAGGAAGCATTATGG
WI-11946	31	C A	---	---	CCCTAGTGAATACAACTTTGTCTGGAGAC[C/A]CCAGCTAGTCTAAGAAACTTCTCTAGGCTGAG CTCTCTGGGAATCTAAGATAAAGAACTGAGATCTCTGGGAAGAGGGAA
WI-11965	65	T G	TGAAGATCAG ATCTCTGGTT ATTT	CAGCTGTGGT AATGTTGAT	ACAAAATTCACAAAGTACAACTGCTTATTTCTGCTTGAAGATCAGATCTCTGGTTTATTTAA[T/ GIATCAACATTCACCACAGCTGAAGGAATTAACCTGAACCT
WI-11027	90	T A	TGCCCTACTAC GCTTTTAAAA A	TGAGGAAATGT GTTACAGTATT TTTTATT	ACCTATTTGAACTGCAGAAAGGCGAGGACAAACAAATCACTTCATAGATTTTCTGGGAAATAT TGCCCTACTACGCTTTTAAAAAT[T/A]AATAAAATCTGTAAACATTTCTCTCAATTCCTG ATACITTTCTTTTGATATTGCAATTTCTATGGCATACACAGAGGACCTCCTCAATGCCCTG
WI-11049	95	C T	---	---	TTCTGCTGAAGATCACAACAAATTTCAACCTCTGTGTTCAAAATAATTTAAGGATCTGTACCTTT GTGTTATTTCTGTTTCAACTAAGGA[C/T]AGACTTCAGAGGATAGCTTCCCTTGTAACTGTTTT AAACATCTTTTCAATTTGTAGGAAGGAACATTTCAAAAGCCCAA
WI-15488	69	C T	AAAAGGACAG CCAGATATCA AC	TTTCCATCTTA TTTCATTTCTG TAAC	CAACATTTATCAACATGGTAGGGAAAAAGTTCTCACTCTGCACATATAAAAGGACAGCCAGATATCA AC[T/G]TTACAGAAATGAAATAAGATGGAAAAATTTTAAACAAATTG
WI-13654	49	A G	AACAGTTAAT GAAACACATC CGT	GGCTGGTGAAA TGATGTCAT	TGCTCAATTTAATGTGATAATCTCCAACAGTTAATGAAACACATCCGT[A/G]GTATGACATCATTT CACCAGCCAGCTACTTCATGTGGCAGAAAAGGTAACTTTTCCCAATTTACAGACAAAACCCAGT
WI-11070b	135	C T	---	---	ATGAGACCTGCTTTGAACGTTAAACGTTTGGATAATGGAAGAGGAGCTAGGACAAATCTTGCTT TCAAGTAAATTTGACTGAGCAGAAAATCAGCCAGCTATCTTGGGTGCAGAGAGGTACTCCAAGTA C[T/G]TGGGGTTCTGATGACTTCCACGGTCACTGGGGATCCAAACAGAGGGAA
WI-11070a	110	G T	CAGAAAATCA GCCAGCTATCT T	TTGGAGTACCT CTCTGCACC	ATGAGACCTGCTTTGAACGTTAAACGTTTGGATAATGGAAGAGGAGCTAGGACAAATCTTGCTT TCAAGTAAATTTGACTGAGCAGAAAATCAGCCAGCTATCTTGGGTGCAGAGAGGTACTCCA GTACCGTGGGGTTCTGATGACTTCCACGGTCACTGGGGATCCAAACAGAGGGAA
WI-12020	121	T C	---	---	AATCTTTATATTTCCAGCTGTTGAGACAGTATTTTGGGGCTGATGTTACCTCTAGCGGCAAAACC AGAGCCAGCTATTAAGCAGCCAGAAAGCTACAGTAATGTAATACATGACCATTT[C]CTCTTTTAGC ACGTTCTTTGTTCTCTC

WI-11076b	142 G A ---				CATGGTTCTGCCAGCTTACAGGAAGCATGGTCTGGCATCGGCTTATCTCTTGGAGGCCCTCAGGAA ACTCTGAATTATGGCAGTAGGCAAGGGGAGCAGGCATGTACATACCCAGAGCAGGAGAGAGAG AAGAGAG[G/A]AAGTGCCACACATTTTAAATGATGAGTTCTCTCAAGGAACCTCACTCACTGTCTCAT G
WI-11076a	106 T C AGGCA	AAGGGGGAGC	TCCTGCTCTGG GTATGIGAC	GGTTATTCAAA AATTAGTATGG GACA	CATGGTTCTGCCAGCTTACAGGAAGCATGGTCTGGCATCGGCTTATCTCTTGGAGGCCCTCAGGAA ACTCTGAATTATGGCAGTAGGCAAGGGGAGCAGGCATGTACATACCCAGAGCAGGAGAGA GAGAAAGAGAGAGGAAGTGCCACACATTTTAAATGATGAGTTCTCTCAAGGAACCTCACTCACTGTCTCAT G
WI-14263	49 T C GGCATATTCA	CGCAGAAAAA	GGTTATTCAAA AATTAGTATGG GACA	GGTTATTCAAA AATTAGTATGG GACA	ACCTTTAAAGTTTCTCCCCACCTACTCCCGCAGAAAAAGGCATATTCAA[T/C]TGTCCTCACTAAATT TTTGAATAACCTAACTCTCCCTTTGTTTCTACTAAGAGAGGTTCTTTTGGCTACAAGTAACA AATTATTGCTGAAATTAGGAAGGAGCAT[T/C]TGAATGGGAAGGGGAGGTTAGAGAAGACAGAG ATTTAAAGAAAGCAAGTACCATTTTCCAAAGTATAAACTCGTA
WI-14267	28 T C ---				GATTTGTTTTATTCACTCTCGCTTTTTCATTTTGTCTTTTAAATAGAAC[A/G]CTTTGATTTTGTAGTA TATGACATCATCATCATGAATTTTCTCTTACTTTGTATTAGGCTCCACCTCAGTAGTTTGACAA AGGTAGATGAGTTCA
WI-15288	108 C G TTCCCTCTCTC	CATGAGAGGA	AAAAGCTTCTT TCCCTTGA	AAAAGCTTCTT TCCCTTGA	ACCTCTTTCTGATGACACTTGTAACCTGTAAAGGGTCTAGAGAGAAAGTAGTAGCTCCTACTTTGC TACAAATTCAGGATGCAGGGCATGAGAGGATCCCTCTCTC[G/T]CCAAAGGGAAGAAAGCTTTTGGC AATAAATGGAAGAGGAGTGAACAAAGTAATGAACAAACAGACAGACCCAGATCAGAGGGAAGAGATG GCTTTCCTGTTAATTCTGGAGCA[G/C]ATTCAAGCAGCAATATTTACTGAACACTTGCTATGTGCTG G
WI-13951b	88 G C ---	GGAGTGAACA AAGTAATGAA			AATAAATGGAAGAGGAGTGAACAAAGTAATGAACAAA[C/T]AGACCCAGATCAGAGGAAGAG ATGGCTTTCTTGTTAATTCTGGAGCAGATTCAAGCAGCAAAATATTTACTGAACACTTGCTATGTGCTG G
WI-13951a	39 C T CAAAA	AAAAAGGCTC TTGCCCAT	GGAGGGAGAG ACGGGAATA	GGAGGGAGAG ACGGGAATA	GAGACAAAAGGCTCTTGCCCAT[G/A]TATCCCGTCTCCCTCCTGACTGACCCAGTGTCTT ACAATGAACATCCCTCAGCCCCATGGCATGGTGCATCCCTCTCTCTTGGGATCTGTGAATATAACCA ACTGTCTTGTCATGGC
WI-13264	25 G A TTGCCAT	AGCAAAAGGA AGTTAAATAC	CATGAAAGGA CAAATTTGCAT C	CATGAAAGGA CAAATTTGCAT C	TTATTTGTCTATTAGCAAAAGGAAGTTAAATACTGATAGA[A/C]GATGCAAAATTTGTCTTTTCATGCA TTTGTGGAGCAAGTACTAACTTGTCTACTGTCTATTTCCCTCACAAGGAGTTGAGCCCCCTAGATGAG
WI-13960	39 A C TGATAGA	ATCTTATAACC AAGAAGCCTT	CTCTGGCTCAG ACTTGCTCT	CTCTGGCTCAG ACTTGCTCT	AACTCTTTATTGTTTAGCTAGCCCCAGTACTTTATGCTATTTAACCAGAAAGCCTTCAAG[C/T]AG AGCAAGTCTGAGCCAGAGGTTTATCACACTTTGTCTCAGGGTCCACCAGGAACCCAGGCTTTGGCT
WI-15843	62 C T CAG				

WI-13983	52 G A	TCTCTCCACT CCTTAAACCT	CAATACTCTCT TAGCCAGTGG	TTGTGTATCTGATTTCCGAAACATAGAAATCTCTCTCCACTCTCTTAACCTTG/AJCCACTGGGTAA GAGAGTATTGTACAGAAATATGCACACTACTGACTTAACAGAAATTAGAACAATCCAGGCACTCACTGAGA
WI-13850	51 A G T T	AATCTCAGGG TCACAGCTTTA	TGTTCCCTGAC AATGTTTGTA	CATGAATCTCAGGGTCACAGCTTTATTTATAGATTTTTTAACACAGCCATTA/GJTTACAAACATTGT CAGGGAACATTTACAAGAAATAAATAGATGGACTTGCAGGTGTAAAGATTACACTTCA
WI-15295	27 G C A	TGTCAGTTTGA ATGTATTCTCTG	TGAATAGTTGG CAAAGGAAAA	AGATGTCAGTTTGAATGTATTCCTGATG/CJTTTCCCTTTGCCAACTATTCATTATTGACCATCTTTTC CTCGTCAAGTGACCTGCCATCATCACAAGAAAGGCCCGAAATATGAGTGAGACTCA
WI-14284	55 C T ---	---	---	ATTTCAAAACAATCCAGAACAGGTTCTCACACTTTGAGCCTTTAGTGCAAAAACA/CJTTTATGCCAT GCGGGAATAAATGCTTATCCAGTGGAGCGCTCCCTGATGCATTGA
WI-14288	85 G C	CCGCTGCTATT CCAGAT	GGTCTCTTCC ACCAAATCTT	ATGACCAGACGAGAGCCCTGTCTATATGAAGACAACAGGTGGCCATACTTTGGGTGGAGGGATA CCGCTGCTATTCCAGATG/CJAGATTGGTGAAGGAGACCATGACAGATGACAACCGG
WI-13522	33 C T A C A A C	TGATGTAGTTA CCCCACTAAT	CATAATATTG AAGTCAGTGGT TCTC	TTTATTTTGATGTAGTTACCCCACTAATAACAAC/CJTGAGAACCACTGACTTCAAATATTATGAGAG AAATTTACTCCAGGGAATTTTGCAGAGAAGATAATA
WI-13529	42 T C T T A C C A	CACAAACATT TATTGAACAG	TCTATACATT CTCACTCTCTT GCTT	AAATATGATTCCATCCACAACATTTATTGAACAGTTACCA/CJAGCAAGAGAGTGAGAAAGTGT ATAGAGGTGATTTAAGAGTGGTCCCTGCTCCTCGAGGGGTTTATAGTCTAACAGGGGAACAACCTCTC A
WI-13859	84 G A ---	---	---	TTATTTGTCAGAAATTTCCAGAAATCAGAGTCTCTACTGGGCAAGTAGAAAAATAGAAAAAGTTTACTAC TTTGAAAAAGGAAACTATG/AJACAAACAAGTATATATTCAGGAAAGGGACTCCTAGAACTTGAGCA ACA
WI-13536	29 T C ---	---	---	TGAAAGGATACAGAAAAAATCAGCGAAGT/CJGAAAAGGTGGATAGCGTGGAGTAGAGGAGAAAT TAAGCACCGCTTCCAGTTGTCTCTCCAGTGCCATTACATGGAGTACACTTAATTTTCTCAGCA
WI-13373	52 G A ---	---	---	TTTATTTGTTGGTAGAAAAACAGGCTCTTTAACACTGAATAAACATCTCACG/AJAACCTGTCGCTC CTAGATTACAAAAAGTCAAAACCAATTTCCCTTTGACGCCGGCCCTTGAATCTGACATTTCAAGTCAC CGTAATAGAAACCAGAGCT
WI-13477b	61 A G ---	---	---	TTGGTTTTTAATACCTCTGTGGATAAAAGGACATGTTTTTTCATTAGCTTGTCTTCAAA/AJGAC AGAGAAATAAGATAAAATTAACCTTAAGAAATTAATAGAAAAATTAAGGGAACATGTACCAAGGTGG TTTTAGACTCTCCTCAGTT
WI-13477a	32 A G AAG	TTAATACCTCT TGTTGGATAA	GAAGACAAGC TAATGAAAAA CAATG	TTGGTTTTTAATACCTCTGTGGATAAAAGG/AJG/CATTTGTTTTTCATTAGCTTGTCTTCAAAAGAC AGAGAAATAAGATAAAATTAACCTTAAGAAAAATTAATAGAAAAATTAAGGGAACATGTACCAAGGTGG TTTTAGACTCTCCTCAGTT

WI-14297	86 A T G	AATGTTGGGT ACTTTTCCAA	TGTGCACATTC AGAAACATTTT	CTGACTTTATTAGCATGCAATGCAATTTATTCTGGCAATAAATTAATATGTCAGTTATAAAAAAT GTTGGGTACTTTTCCAAAG[A/T]AAATGTTTCTGAATGTGCACACTAGAATATATGCAGAAATCCTTTT AAACAGTCGACT
WI-12229	89 T G AAA	CATGTGCACA AAAAAGAGTAA	ACATGTGAATT GTCCCAAAAA	TCCATGTAAATATTCTCAACAGAGAACACTATCTTTAAATGAAGGATTTTACCATTAAAGAAATCAACA TGTGCACAAAAAGAGTAAAAAT[T/G]ACCAAAAAATTAAGATTTTGGGACAAATTCACATGTTT AAAAAT
WI-13582	43 C A AGACTGGGA	TGCAATCTAG	TCTGGCAGTT AGATTCCA	AAGGCTGCCCTTACTGGACCAATGCAATCTAGAGACTGGGA[C/A]TGGAAATCTAACTGGCGAGAG AAATCAAGACCGATGGTGAATCTGGGCAGCTTCAAAATTTCTGCCTCCTAAAAACATTTTCAC CCAAATTTTCATTATGGC
WI-13857	28 A G ...	...	...	TCTGAGTTGATAAAATGCTTTTCTGAAC[A/G]TACATTTTAGGTATCTGGCACAAATTAACCAATGT CTGCCCATTTTGTGTAGCTTTCATACAGTACAGATTTCATTTGATGTCGCTCCACATCTG
WI-15809	77 T G TGTAATGCC	TGTTTTCTGT TGTAATGCC	TAAGTAGCTA ATTCAATGTTT GTAAA	GTTTTAAGTTCAGAGATGTGAATGGTTTACAAATCTGAAGCTGAAGTTCAATCTTTGGTTTCTGTT GTAAATGCC[T/G]TTTACAAACATTGAATTAGTACCTTAAGTATTGAAGAGCTTCCATT
WI-15892	123 A T ...	...	...	TTAATCAGTCTGTGTCAGAAAGAAACAGGACTTGATCAAGCTTCCAGCCCTCACCACCTCTATCAGCA TAGCAATTTAAGGATCAGAGCTTTGTTTACATTTGTCTAAACCAAGAGAAGGA[A/T]GGAATCA ACTCCACAGATCAACATGT
WI-15801b	81 T G AA	CATACTCCACT CTAGCTGCAGT	AGAAGAGTGG ATGGGATGC	TCCTTTATTCCAAAGATGGGAAGC[G/A]CATTTTTCATTGGCTTGAATGAGAAAGCTTCATACTCCACT CTAGCTGCAGTAACTAGTCATCCCATCCACTCTCTCTCTTTTGTGACTGAAACTCTTCAAGAACT GCTGAATGTCCTCTCTC
WI-15801a	24 G A AATGGGAAGC	TTTATTCCAAG AATGGGAAGC	TCATTCAAGCC AATGAAAATG	GCTGTAATGAGACAGAACGCTACAATCTGTTCAACACTGGCTGGACACTGCAGTGAT[T/C]AGGG GCAGGTGGGGCAGGGTGGGGCTCTGAGCCGAGGACAAATGTCCATGGCAGAGCTTCCAGAA
WI-13763	59 T C GCAGTGAT	GGCTGGACACT GCAGTGAT	CCACACCTGC OCT	TTTTTTTTGTTGAGTGTGTTGTTCTCAATAAGAGCAGAGAAACCTT/AJAGACAAAAAGATGTT CTTACACACTGAGCTTTACACAGTCAACCAACATTGATATTTTGGCTTTTCCCGAGGGGCAAAAAA GAGTCTCCAGAAACCTC
WI-13578	48 T A AACC	TCAATAAAGA GCAGAAAGAA	CAGTGTGTAAG AACATCTTTT GTC	TCCAAAGAAAAAGAAAGAAACCAATCAGTGAGAAAACTCAAGAAATGGATGGCTGAGGGAG[G/A] GAACAGAGGAAGCGCACTGGGGCTGGGACTGAATATGGACAGTGGATGGTGGTCTCCTACTCTCTT GAGGTCCCT
WI-13789	62 G A AGGGAG	TGGATGGCTG	CAGTGGCTTC CTCTGTTT	...
WI-13594	66 G A AGC	TTTTTAACACA GATCACAAA	CCTTTGGCCA GTACTTTT	AATAACAAGTTTAAGTTTCAGCTGCAATGTTGGCAATGCAGGTTTTTAAACACAGATCACAAAAAGC[ G/A]TGCACAAAAAGTACTGGCGCAAGGACAAAAATGCTAAGAAATTAGGCCAAACAGCTGC

WI-15625	40 C T ---			GTCTCCCACTACTCCGCGAGAAAAGGCATATTCAA[C/T]GTCCCATACTAAATTTTGAATAA CCTAACTCTCCCTTGTCTCTACTAAGAGAGGTTCTTTTGGCTACAAGTAACA
WI-13367	84 C G A	CCACTGAA GACTCACCAG	TCCCACCCCA CCCT	GTCTCACTTCTGTCTAGGCTGTAAATTTTCAGTTTAACAAGTTTCTTATGTGATTTGTGGCCACACT GAAGACTCACCAAGAC[C/G]AGGGTGGGGTGGGAATACTTAATCAATATTTGTGGAATTTACCCGAT GAAATCCAGTTATTCCT
WI-13600	26 G T	TTAATGAGCC AAGCATCCAT	CATATTGAAA TTGTTACTAGA TGATGG	CTCACITTAATGAGCCAAGCATCCAT[G/T]CCATCATCTAGTAACAAATTTTCAATATGCACATTATAT TATACTGGAACAACAAGAAATACGGATTGTGTAGGGAAGAGCATAGAGGACCACCATCAGCAACCCTCT TGATTCCTTCTCTACCC
WI-13602	89 G T	TCCATTCTGGA GACAACACA	GCATACCTCAT GACAATATTTA ATATTAAT	GATAGGAAAAGAAAGAAATGAAGTCAATAGTCTTTAGCAAGCCCACTAGCTCAAGGAATAGACAGCCC CTTCCATTCTGGAGACAACACA[G/T]AAATCTATTAAATATTGTCATGAGGTATGCACCT GCCC
WI-13650	76 A T	AAAGATTCAC AATATTTCACT TTTAAAC	CAGGCTAGGAT ATGAAGAGTA GTTTT	GCATTAACATTTAAAAATCTGAGGGATATTGATGAGAACTATGATGAAGATTACAAATATTTTCAC TTTTAAAC[A/T]TAAAAACTACTCTTCATATCCTAGCCTGATGACTTAAAGTTACCGG
WI-14319	83 C T A	CAATCAAGG CACAAAGCTA	CCAAATCATCT ATATTGTTGCA TG	TGTTTTGATTGAAGAAACATCTCTAAAAATACCATCTGAGTGCAAGATAAAAAAGGAATAGCAATT CAAGGCACAAAGCTAAG[C/T]ACATGCAACAATATAGATGATTGGGGTGGGACAGTACAGAATT
WI-13528	80 A G AAAA	CAATACATTT GCATTTTCCTA	CATGATACCAC AGTTTCTCTG AA	ATTGGATACATGCTTTTAAAAATGGTAGCTTTTAACTGTAATCAATACATTTTGCATTTTCTTAAAA AAAGAAGACATTT[A/G]TTCAGAGAAAAGTGTGTATCATGCAGGAAAAGCAGAAAAAAT
WI-13909c	93 A T ---		---	ACTTAAACTGGCTTATCTTCACGGTAATCTATTCTGTATTTCCAGTGAAGTTTCATCTTCTCACACT CTCTTCAAACTCGAATATCTTTTTC[A/T]GAGATGTCTAGCTAGTACCCACTGCAACATCTCTCAA
WI-13909b	80 G A C	TTCTCACACT CTCTTCAAAC	GCAGTGGGTAC TAGCTAGACAT CTC	ACTTAAACTGGCTTATCTTCACGGTAATCTATTCTGTATTTCCAGTGAAGTTTCATCTTCTCACACT CTCTTCAAACTG[A/A]AATATCTTTTCAGAGATGTCTAGCTAGTACCCACTGCAACATCTCTCAA
WI-14323b	86 C A ---		---	TTTTATTGAATCCAAATGTAGCAAAATCATTAAACAAATTTATAAAAGGGACAGAAAAATTAAG AATCAACATCATCTCTGGAC[C/A]ATGGGAACCTTGAAAGGCATGGCAGTGGAGACCAGTAACATA
WI-14323a	78 T C ACATCA	ACAGAAAAAT TAAGAATCAA	GCCTTTTCAAG GTTCCCAT	TTTTATTGAATCCAAATGTAGCAAAATCATTAAACAAATTTATAAAAGGGACAGAAAAATTAAG AATCAACATCAT[C/T]CTGGACCATGGGAACCTTGAAAGGCATGGCAGTGGAGACCAGTAACATA
WI-15389b	104 G A AAA	AGATAATGAA ACATCTGCGA	GATGAGGTGAT TCCCACACTT	AAAATTGACAAATCAACTAGCTTGTCTTTTGTGTTTGGAGACTACCATTATTCAAATTTATTATGT AATACACTCATCCAGATAATGAACATCTGCGAAA[G/A]AGTGTGGGAATCACCTCATCTGTGC

WI-15389a	33 G A TC	AATCAACTAG CTTGCTTTTGG TC	TTTGAATAATG GTAGTCTTCCA AA	AAAATTGACAAATCAACTAGCTTGGCTTTTGTG[C/GA]TTTGAAGAGTACCATTATTCAAAATTTATT ATGTAATACACTCATCCAGATAATGAACATCTGCGAAAAGAGTGTGGAAATCACCTCATCTGTGCG TGTAATCTGCTTACAGTCCCTTTGCAAGACAGACATATGTTTTGCATAAAGATATAAATTTGCTTCAT TTTAACTAAATTTAGTGTTT[C/J]TTTAAATATATGAACITTTTGGTGAATTATGAACGTGACCAAAC C
WI-15747	88 T C AGTGTT		TAATTT	AAGAAAAGCACATACATTTCCAGAAATTTGGAAAAGTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTGCGATGAGTTCTCTCGTTAAGTGTGATATATCTTGGCTTGACCTGGAC[C/J]GGACACCTTTTACG GAGGGATCCGGACAAC
WI-13752b	117 C T ---		---	AAGAAAAGCACATACATTTCCAGAAATTTGGAAAAGTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTGCGATGAGTTCTCTCGTTAAGTGTGATATATCTTGGCTTGACCTGGACACCTTTTACG GAGGGATCCGGACAAC
WI-13752a	106 T C AGTGCTGA	CCCTCTCGTTA AGTGCTGA	CCCTCGTAA AGTGCTC	AAGAAAAGCACATACATTTCCAGAAATTTGGAAAAGTTCACTCTGCAGCAGCTGAATGGCAGATGGT CTCTGCGATGAGTTCTCTCGTTAAGTGTGATATATCTTGGCTTGACCTGGACACCTTTTACG GAGGGATCCGGACAAC
WI-14339	102 T G TTAC	CCCAATCAAA CAGTACATGA TTAC	TCCAGATTTCT GGAAACCG	AATCATTTAATGAATGTTCCAAACACACCCCTTCACTGGGTACAGGTAAATTTCACTGGGATGGAAG CAGATGAACCCACCCCAATCAACAGTACATGATTACT[G/CGGTTTCCAGAAATCTGGATAC TGGATGGATGGATGAGGCCACCTGTTTCAACAAAACACGTAAATGGAATTCATGCAGCTTTAGAT TTCTTTGGCCAGCTAGGAGCTTGTGTATGCTGCTGAACAAAACCTGA[C/J]GCTGTGCTTATCTTTC CTGATTCT
WI-13744	115 C T AAAACTGAA	TGGTGCTGAAC T AAAACTGAA	GC	CCTTTGACTATATTGTTTTTCCAAAAATAGGACTATGTGTAGAAGAGAGCCCCCGTACATACCTTAT [C/J]AACCATTTCATCCACCAATTTGTAAAAATCTCATCTTCTGGGTCTGGATACTCAAAAACAGAT
WI-14061	68 C T ---		---	TTACAGTTGGATTAACTACCACACTGAATATACTGAATTAACCTATTTCAACCTTTTCATCCATTTCAG C[A/C]AATTTAAAACTCTTGCCAACTATCATGAACCTTACGAAGAGGAGATAAGAGATCTGATC
WI-15719	69 A C CATTGAGC	ACCCTTTTCATC CATTGAGC	ATT	TAATCCATCAATCTAAAAATCACACATACTAGATCAACAGAAAGTACCACAGTATGCTTTATTTTGGCA GGTATTAAATGGTTCTCTAAATCGATACATCCAAAACCTT[C/J]AGTTAGCAGCAAGCATCAGTTCTTC
WI-13810	106 T C AACT	CTCTAAATCG ATACATCCAA AACT	GAACTGATGCT TGCTGCTAACT	TAATCCATCAATCTAAAAATCACACATACTAGATCAACAGAAAGTACCACAGTATGCTTTATTTTGGCA GGTATTAAATGGTTCTCTAAATCGATACATCCAAAACCTT[C/J]AGTTAGCAGCAAGCATCAGTTCTTC
WI-15736a	27 G T CACA	ATTTTATTCAC ATTAACATTG CACA	GTCTTTTGATA TGTTGGCTTAGT TTT	GGATTTTATTCACATTAACCTTGACACAGTGTAGCAAAAAAATCAAAACATAAAACTAAGCCACA TATCAAGAACAATATACATAGAGATTGAAATTTCTCAATAGCATTTGGAAGGTATTTCCATAAATA TCAAAACTGCACACTATAAAAGTGTCTTTAAATGACGACGAGGAGATGTGAAGACACAAAATGAAC AAGTGC[C/J]ATAGTGACACATAGCTGTCAACACACAGTG
WI-13785d	72 G A ---		---	TCAAAAGTGCACACTATAAAAGTGTCTTTAAATGACGACGAGGAGATGTGAAGAC[C/J]CAAAATG AACAAAGTGGTAGTGACACATAGCTGTCAACACACAGTG
WI-13785c	56 A C ---		---	



WI-13785b	40	C G ---	---	---	TCAAAGTGCACACTATAAAAGTGCTTTAAATGCAGCAG[C/G]AGGAGATGTGAAGACACACAAATG AACAAAGTGGTAGTGACACATAGCTGTCAACACACAGTG
WI-13785a	27	T C TGCTT	AAACTGCAC ACTATAAAG	TGTTGTGACAG CTATGTGTAC	TCAAAGTGCACACTATAAAAGTGCTTT[C/J]AAATGCAGCAGCAGGAGATGTGAAGACACACAAATG AACAAAGTGGTAGTGACACATAGCTGTCAACACACAGTG
WI-13793	88	C G ATAGG	GGATTTTACAT TCAGCCTAGAT	GGCAGGAGGA TTTGTACT	AGAAACCAAGTATATCATAGGCAAAATAAAAATAGTTTTTACCCCATTTGATACAAACATAAGGGATTT TACATTGAGCCTAGATATAGG[C/G]AGTAACAAATCCTCTGCCATAAAATCTATGACTTG
WI-13794	52	A G TTTCTTTCTC	TTCCTCACCCCT	AGATGGGCTC TTAACCTTGT	TAGTCTCCTACAAATCTTCAATCCATTTCTCTCACCCCTTTCTTTCTC[C/J]TACAAAGGTTAAGA GCCCATTTCTTCAACAAACAAAAACACATAGAGCAAT
WI-15729	35	A G GTGTAGACTGC	CTTTGAACCAT GGTCAGAGGC	CTCAGCTTCTT TCTAAAGTGCC	TCATTTAAGTGCACCTTTGAACCATGTGTAGACTGC[C/J]GGCCTTTAGAAAAGAGCTGAGACTGAA AAGTCTGTCTTGACTTCCAAAGGAAGGTAAGTCCCTGTTTGCAGCCCCGGGCTGCTCATTTGTTA
WI-13424	66	G A C	TGAGGTTTTTC ACCCTATTCTT	TTTTCTCCCC AGGTCTA	GTCCCTTGACAAAGTCTCCCAACTGGTTGGAGTTTCCCTTCTGAGGTTTTCACCCCTATTCTTC[G/A] JTAGACCCCTGGGAGAAAAACACATGTGTAAAGTGGCTCAGGACATGAGGCAGGCCGTTTCAACAAGAT GCTGGCTAAGCGGCTTC
WI-14065	29	T C AATT	TCTTATAAAA GGTCAGAGGC	CAAGCTGAATC TGGGATCTC	AACTGTCTTATAAAAGTGCAGAGGCAATTT[C/J]GAGATCCCAGATTCAGCTTGCTCATATAAAAAGAT TCAACTTCAAGTAGCACAAATTTCTGTCTGCTTTTAAICTTGAACATTTTGAAGCACGAA
WI-13446	22	G C TCACCTCAICA	GCCATGTTCTT	AAGGGAATCA AAATCAGAAG	TGCCATGTTCTTTCACTCATCA[C/J]CCTCTCTGATTTTGAATCCCTTTCTGCTCTGTAATTTTTTCTTC TTCCCTTTTAGGGCCTAGTCTGTTTAGAAATCTGTTTGTAGAGTAGTGAGCCCTTTTACTTTTTT CTGACTGCCCTAAT
WI-13725	56	A C TGGGTGCC	TGAGCACATA	CCTGCTGTCTC GGC	TCACACAAAGGCATTTGGAAATGTCACCTTACACATGGTGAGCACATATGGTGCC[C/J]GCCCGAG ACAGCAGGATAAGTTTCACAAAACTTGACCAGGCAGGTTAGAAAGCAAGGCATGGTTTCAGGATG
WI-15702d	107	T C ---		---	CAAATGTTTTATGAAGAGACTCCGAACAAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAAACTGTAAACCCTGTAAACAATACTAA[T/C/J]GGGTTCTTTGAACAAATAGTTT TGA
WI-15702c	101	T C ---		---	CAAATGTTTTATGAAGAGACTCCGAACAAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAAACTGTAAACCCTGTAAACAATACTAA[T/C/J]GGGTTCTTTGAACAAATAGTTT TGA
WI-15702b	90	C T ---		---	CAAATGTTTTATGAAGAGACTCCGAACAAAATAAAGGCTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAAACTGTAAACCCTGTAAACAATACTAA[T/C/J]GGGTTCTTTGAACAAATAGTTT TGA

WI-15702a	48 G C A A G	A C A A A A T A A A G C T T T C A A	C C T C A C C C C T T T A C C C C	C A A T G T T T A T G A A G A G A C T C C G A A C A A A A T A A A G G C T T T C A A A A A G [G/C] G G G T A A A G G G T G A G G A A A G C A T G T G A G A A A C T G T A C C C T G T A A C A A T A C T A T G G G T C T T T G A A C A A A T A G T T T T G A
WI-13831b	113 T C ---		---	T T T T T T T T A T G G A T G C A C T G T T A C A T G T T A T T A T T A G C G A A G G T G A C T T G G A A A G G A G A T T C A C A T A C T T C C A C T G T A T C C T C C G G T A A G T T T C C T T C T C T G T A G A T G T C C A T G T T A C A G T C A A C T A T A A A C A T G G C T C A
WI-13831a	56 G C ---		---	T T T T T T T T A T G G A T G C A C T G T T A C A T G T T A T T A T T A G C G A A G G T G A C T T G G A A A [G/C] G A G A T T C A C A T A C T C C A C T G T A T C C T C C G G T A A G T T T C C T T C T C T G T A G A T G T C C A T G T T A C A G T C A A C T A T A A A C A T G G C T C A
WI-13806	62 G A ---		---	T G A T T G A C T T A G A A A G A A G T C A T G T T G A A A T C A G A G A G A G G C C A A A A C T A G C C T C A G G T [G/A] C C C A T T A A G C A T G C T G T G A A T G C A A A G A A A A G C T T A A A A A A T T T T T A A G G G T G A C T C C A G T A A A C A T
WI-14372	86 A G ---		---	C A C A T T T T C A G C A A A C A A A T C G A G T G C A A C A C A G G T T A T T T C A C A T T A A T A T A A C T G G A T T T T T T G C A A A T A A A T A G G G A [A/G] T T C T C T T A A A T A A C C A T C T C C T C A C T T C A T G G C C A G T
WI-14373	95 A G ---		---	A G G C T G T T T T G A G G C T G A G G A C C C C A C A C A T G A C A C G T A A G A C T G T A C C A T G G T C A T G T G A T T A T G A C T A G A A C C C T G G A C G A A A C C A [A/G] C A C A T A T A C A A T C A T C T C C A C C T C C A A C G C C T T T A C T T T C A C A G C C T C T G C A
WI-14078	61 C T G C A A G A	A A G A A G T A A A T T A G G A A G A	T G T G T G A T G T C T C T T A C T G C	A G A A C C G A G A C T C A A A G A A C C A C A C A T G G T G T A T C A A A G A A G T A A A T A G G A A G A C A A G A [C/T] G C A G T A A G A G A C A T G C A C A C A A A T C G A A A C A A G G G C A T G G A G A A G G A C T T T A G A T G G T C A C G
WI-14083	47 C T A C A C T	A G A C T T G A G A G C T T A A A A C A	G C C T A C T G G A C C T C T A A A C T A C T G A	T T G C T A C A T A A C A C A T T A C T C C A G A C T T G A G A G C T T A A A C A C A C A C T [C/T] A T T T G T T A T T T C A C A G C T C A G T A G T T A G A G G T C C A G T A G G C T T G G C T G A G T T G T T G C T T A A G G T C T T A C A A G G C C A A
WI-14085	31 A G A A A A A	C A T T T A T T T C A T G T G T A A G A	C A G T C A T G T T C A C G T G C T A G T T	T G C A T T T A T T T C A T G T G T A A G A A A A A C [A/G] T A A C T A G C A C G T G A A C A C A T G A C T G C A T G G A T A C A C G G C T C A G C A C G A G G C T A A A G T C A G A A G T G A G T G A A A C A A A A T A G C A T G T T G A T T A A G T G A A A T A A C A G A A C A G G A G G C C T T T
WI-12169	121 G C T T G C T T	A A T A A A A C T T C C T A T T T T C T T	G G G T C T G A G G T G A A A G A A A A A	G T C A A A G G T T G G C A A A T T T A T T T C C A C T T A T C A A G A C T T A C A A A A T A T T T T G T T C A T T T C T A A A T T T T C A C C T T T A T G C T A A G T T A T A A A A T A A A A C T T C T A T T T C T T T G C T T [G/C] T T T T T T C T T T C A C C T C A G A A C C C C C T T A
WI-15705	50 A G A T C	G G A G G G A G A T T T T A G A C T G A	A G C T G T A G T C G T C A A A T A C T C T A G A A	T T G T T T T A T T T G G G G A G A A T G A A G G A G G A G G A G A T T T T A G A C T G A A T C [A/G] T T C T A G A G A T A T T T G A C G A C T A C A G C T C T C T C T T T G T A C T A C G G A G A C C C T G C T T A T A G C C C C A A C A G G A A T C C T C A T C T G C G G T T G C A G A C A G

WI-14379	102	CT	TGCA	GGGTTATGTCA	ATCATCTGTTT	TTTATGCTGTTGTTTCTACTGGTGGTCTGCTCACTAATATCCAATCCTAGTATGATTTTCTTT
WI-14102	22	CA	---	CACC	TGAGGTTGACA	TACTTGTGCTATTAACAGGGTTATGTACACC[C]/[T]GTCAACCTCAAACAGATGATACT
WI-15937	24	AG	---	CGCAGAGCTG	---	TAAATAAAACAAAGCAGAAA[C]/[A]CCACCATTAACAAGAGGACACTGCAGAGGCTTATGTACA
WI-15944	24	AC	---	CTGTATTTAAA	GCAGAGATCCA	ACACGTGTCGCGAGGCTGGCGCAGGACTGCCACTCACTCCAAAATTTCTTTGGAGCAGAG
WI-14124	92	AG	---	AAACTGAAAC	GGCCTTTAAGT	ACCGCAGAGCTGCTGTATTTAAA[A]/GACAAAGCGTCTGGATCTCTGCAGGGGCTGGGACCAGCTGC
WI-14125	88	CT	---	GTATTTCTCTCC	TCTACGGTG	AGTGGGGCTCGGCAGCTGCTCTGCTCTCCAGGACTCTTCCCACACCCC
WI-14136	120	GA	---	ATGTTGACCTG	---	TGAAACTGAAACGTATTTCTCTCCA[A]/CJACACCGTAGAACTTAAAGGCCGCAAAAGACTCACACCC
WI-14138	23	CT	---	CTCATGATTTT	GGCCTTTAAGT	ACCACCTAGCGGCGAAAGGAAGTTTCAGGTGATACAAGATGTCCTGCCATCACACCTGAAGGAT
WI-13551	74	GA	---	GCATGCTTCC	---	GGTT
WI-15953b	59	CT	---	ATGTTGACCTG	---	ATGTTTATGATCAATCCAAACATACAGTACAGGGGAAGGTGAAATGAGTAAGAAAAAATCAT
WI-15953a	26	CT	---	CTCATGATTTT	---	ATTTAAGTCCCGTTAACACTAAGCC[A]/GJTATTTATTCAAAATGTGTTTCAAAATACTCAGCCAGAT
WI-15953b	59	CT	---	CTCATGATTTT	---	CACCAAGCTCAGTCACTAG
WI-15953c	26	CT	---	CTCATGATTTT	---	GACAAAGAGGCGAGTTTCTGTAGTTCCAGCAGGGCCAGAGCATATCAGAACGGTGGTTTGAACCT
WI-15953d	26	CT	---	CTCATGATTTT	---	GCATAGATTTTGTACGACTA[C]/[T]GTGGCCATGCCATTCCTGTAGTGAAATTAATGAACA
WI-15953e	26	CT	---	CTCATGATTTT	---	GTTTATTTTCTCACAGTTCTGGAGGTTAGAACTGAGATGAGGATATCACCAGCATGGTTAGGTTCT
WI-15953f	26	CT	---	CTCATGATTTT	---	GGTGAGGACTCTCTGGCTTACAGCTGGCTGCTTTCTCACCATGTCTTTCACAT[G/A]GCCCAAAGAGAC
WI-15953g	26	CT	---	CTCATGATTTT	---	AGAACAAGCTCTCTGGT
WI-15953h	26	CT	---	CTCATGATTTT	---	TTGTTGTTGGCACCAGAAAAGCT[C]/[T]ATGTTCTATGTTATGTCACTGTACATACTGTAAACAAGACT
WI-15953i	26	CT	---	CTCATGATTTT	---	GCATTAATATGTTTCTTATGATTTGTTTCAATG
WI-15953j	26	CT	---	CTCATGATTTT	---	GGCAGGTTTATTCATAATTTTCAAACTTGGAAAGCAACCAAGATGTCCTTCAGTAGTATATTCA
WI-15953k	26	CT	---	CTCATGATTTT	---	GACAATC[G/A]AATATTACTTAGCACTAAAAGAAATGAGCTATCAAGTCATGAAAAGACATGCAGG
WI-15953l	26	CT	---	CTCATGATTTT	---	AACCTTAAATGGATATTACT
WI-15953m	26	CT	---	CTCATGATTTT	---	TTTTTTAAGAGTGCCTTCACATCATTTATATTGTTGTCACACAAAACCTTTTAACTC[C]/[T]GTCAA
WI-15953n	26	CT	---	CTCATGATTTT	---	AAACAACAAGAACAGATGAATAAGGAAGCCAGTGCTTTTGTGATAGAAAGCCCTTCTTCAGATCA
WI-15953o	26	CT	---	CTCATGATTTT	---	CCTOOC
WI-15953p	26	CT	---	CTCATGATTTT	---	TTTTTTAAGAGTGCCTTCACATCATTTGTTATATTGTTGTCACACAAAACCTTTTAACTCCGTCAA
WI-15953q	26	CT	---	CTCATGATTTT	---	AAACAACAAGAACAGATGAATAAGGAAGCCAGTGCTTTTGTGATAGAAAGCCCTTCTTCAGATCA
WI-15953r	26	CT	---	CTCATGATTTT	---	CCTOOC

WI-14631	82	G A ---	---	TGAATTCATGGACAGTTTGGCTCTGTTTGTAGTGAACCCCTCACAAGCACTCTGCATAGTCCGCTTTCTGTCTCTTTAAAC[G/A]TGCCTGGTCCCTCTGCCAAACITTTAGGATTGGGCTCTCAGGGCCTTGTCCTGA
WI-6053	24	A G ---	---	ATCACACCGTGTCTAAGAACAAQ/GJCTTCATGTCCAACTCATATCCCCGGGACITTTGTCAACTGCAGTACACTCTCTGCATTGAACCTGGCTTCTGGAGGGAAGCCTCTAGAGGCCAGGTAAGGGGTGCAGCAGTGGGGGTATATCTGGGCTGGCCAGTTGGAACACGGAG
WI-15964	99	T A CTGGAGGTA	GACTTCTCCAC CCTCTTGC	CAGAACTCTTCTGTGTATTAGCTGATGCTAAAGTCAGAGCAGTCCAAAGGAGGAGGCTGCCTTGGGAGGTAGTAAGCTCTCTGTCCCTGGAGTA[T/A]GCAAGAGGGTGGAGAAGTCTTGGCAAG
WI-12075	103	G A GGCAC	CCCTTCTTTC TCTTCTTC	CAGCTAAAGGATCACTGCAGCTAAATACAGATAGAGAAGCAACAAAGCCAGGCAAAATACCCATCAGAGACAGTGCACAAGAGCAGCTGGGGGCACGGGGAGGC[G/A]GAAGGAAGAGAAAGAGGGGAGGAGCCT
WI-12179	96	G A TGGAGGTCA	TCGAATGACCC TGTAGATGC	TAATTTAAACACAGCCCTTCCACATAGTGGGTGAGGCATCTGCACATTTTCTTAGAAGGACATGATAGTGATGTGGAGGTACGGTGGAGGTCA[G/A]GCATCTACAGGGTCAITTCGAGGAGGAACAG
WI-14651	49	C G ATTGT	GGAGATATTGA TCTCATTTAAA CTTATT	CACAAATAGTGAATTTATCTGAGCAAGAATCATTTCTCATTTAAATTTG[C/G]AAATAAGTCAGAAAGATCAATATCTCCCTGCTTCAAAAATGACACTCCCAITTTTACAGGTAAACCCTGTTA
WI-14666	105	T A ---	---	AATGGGACTTTCAACAAGGGTTTAAACTAACTCTAAATACAACCTCTACAACACATTTCCAGAGCATATAACAAGAAATTTTACAGGCAGCTAATGTATTAAAT[T/A]AACCATGAAAAGAAAAAATTGTATCTAGATGCACAAATGGGCTGAGACTG[C/G]TGTCTGGTAGATGCAGTGTGTATGTTTCTACTCTATTACAAAAATTAACAGAAATATGGCTTCGCTTTGTGCAATGTTTATACAGTC
WI-13967	103	A C AAAATAAAAA	TTGTGTTTCA TCTCCTAAAAG TG	AAATTAATAGCAGCTCTGTGTGTGATTTTAAAGAACAGATAAAATATGTCATTCAGCAGTCATTTAAAAATAAAAGACTACAGATACAAAGGAATAAAAA[A/C]CACITTTAGGAGATGAAAACACAAA
WI-14408	60	T A G	TTAATTGTGTA AAACTCATTTG TTACTTT	TTAATATTTACAGCAAAGTTATTGCAACAGGTTGAAAAATGCAGACACACTATTACAGGCTG[T/A]AAATAACAATGAGTTTACACAATTAATAATATTAAACACATACTTATGGGATTTGTTGAATGA
WI-13683	47	C G ---	---	TTTTGTGTTAAGAACAGCATTTTGAATAAATAAACCTATCTGCCCATG[C/G]TTTACAGCCCTTTAAATTTGTAATTTATATAGTCGTTTATGGTACATATTGATTGC
WI-13910b	63	C T CGTCT	CATTGAGATAA AGCACACTTAT CAC	TTAGAAAACTGATAAAAGCAACACAACITTTGGGAAAGCACCATGGCACGCTCTTTGTGCTA[C/T]GTGATAAGTGTGCTTTATCTCAATGAAGCAACCCCA
WI-14635	22	G A ---	---	ACATGGCAGATACAGAGCTG[C/G]ATCTTGAAGACCACCACTGACCAGGAAATGCCACTTTTACAAATCATCCGCCCTTTTCATGATTGGAACAGTTTCCCTGACCGTCTGGAGCGTTGAAGGGGTGACCAGCACATTTGCACATGCAAAA

WI-16002	59 T	GATAACATAA AATGATCATG CAGAAATTC	GCCATCTCCTC TTTGACTTTT	CCAACATTTTAAACCTATGACTGGTCAATTGATAACATAAAATGATCATGAGAAATTCATTC/GTTA AAAGTCAAGAGGAGATGGCTAATGCATGCTGGCT
WI-15361b	101 A G A	CCCACTTGAAC TCAAGTCATC A	AAACTAAAC CTTTGTGCGTA AAA	GTGGAATTTTATTAGCCATCAAAATTTCTTCACACTCAATACTGTTGAACAACAAGATAACACAT CTTCTGTGCTATCCCACTTGAACCTCAAGTCATCA/GTTTTAGGCACAAAGGTTTTAGTTTTCTCGG GAAATCAAGTTTTAACCA
WI-14759	73 T C	GCGTTGACTT GTGGG	TCCACACTGC OCC	TGAGTTACAACAATGAGCAACAAGTTAGAAAAATGGTTTTATTCAAACTTCTAGCGTTTGACTT GTGCGGTTC/GTACTCAAAATGGGGGCAGTGTGGACGGGGAGGATTGCAACAGAGTTTCATACTG CAA
WI-12535	50 A T T A T	CTAGGAGGGTT GAGGTGTAGA TAT	GCTCCACGAGA AGAGAGGAA	TCCCTAACATTTATTCAGGTGGTGACTAGGAGGGTTGAGGTGTAGATATATCTCTCTCTCTCTC GTGGAGCCTTACTGAAGACAGGATGCGCTTCTGTGTTATCAGCTGAGAAAGGCAGTCTCGCATC TTAAAGACCTGCGCTCC
WI-13805a	112 G A GGGAA	AAAGGCACAC GGGAA	CTCAGCCTGOC TTGACC	TTCCATTGATATGCTTGGCTTACCAATTTTATAGCTATTGGGAGGCAGGAAAGGGAATTTTGGC CCCAGAAACCATGAGATTTGGTTCAGAAAAAGGCACACGGGAA/G/AGGGTCAAGGCAGGCTGAG AGTCACATTTCCAGACCIC
WI-12340	18 T C ---		---	ACACAATATAATTCATTTTC/GAGAGTGATTAAACCTATTTGTTTGTAGAACCAACAAAACTAC AAGAAACATTTTCAAAACCTTTTTTTCAGGCTGA
WI-14808	52 T A CTACCTGT	ACCACACACA CTACCTGT	GAGGCATCACA ATGTTAAGATT TT	CTTTGAAACACTTTAAGCAAAACAGTTAAAAAGTACCCACACACTACCTGT/T/AJAAAACTTTAAC ATTGTGATGCTCTGCTGATCAATTTTGTAGAAAAACAAAGAAAAACAACTGAAGGCCCATGTA
WI-14816	29 A T ---		---	AGTTAAAAAAATCGAGTCAGCATTTATTT/AAAAAACTGGACACGCTTCTATATTGCAAGCTCAT TCAATGCAATTTATTTTGTATCCCAAGCCCCGAAACATGAAAAAATATTTACTAAAGGAATGTTG ATTACCAGCTACGACTTC
WI-12542c	71 G T ---		---	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAGATC ATG/G/TTAGGTGATTGATACAAATACGATCCATAA
WI-12542b	70 G T ---		---	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCATCCATGTGAGGGCTCTAGATC ATG/TTGTAGGTGATTGATACAAATACGATCCATAA
WI-12542a	45 C T TTTAA	GCTATTAGGC AACTGAACA TTTTAA	TCTAGAGCCCT CACATGGAT	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTC/TTATCCATGTGAGGGCTCTAG ATCATGGTAGGTGATTGATACAAATACGATCCATAA
WI-12173	57 C T CAAAA	GGATACAGCA GTAAAGAATA CAAAAA	CCACCTCTAGA ATGTATGCTCT ATAA	CACCTAAATCATTCTAGAAACTGGGGATACAGCAGTAAGAATAACAAAAATCCTGC/C/TTCTATA GAGCATACATCTAGAGGTGGGAAAGAGGCAATAAATA

WI-14836	28 T C ---		---	TC TTGGAGGGATAGAGGACAGAGTGTTC/GITTGATTTTCGTTTCAGTTTGGTGTGTCATT GGTTTGTGTTTGTCTAATTTGGCCACCTATAAAAAGCAGTGCCACCCAGAGGCAG
WI-14856	60 A T A A	TGGTGACAG GAAAATAC TT	TTGTTTGCTA CTTTTACAAA CTTT	ACATTTCCCTATGATAGCAACAACATAAATATGATGGATGGTGACACGGAAAACTTTAATATATTA AGTTGTAAAAGTAGCAAAACAAAATTTGAGTATATACTATAAGTGATAGAGGATGTATATGAAAAA GGCTATAAAAAGCTCCAAA
WI-14863	61 G A ---		---	ATGGCAATTTACTTTATAGCAATGAACAAATATTTGTCAAAGGGGCAAAATATTTTGTCTG/GA/JAG TTAATAAAGTTAATATCTTTTACCACAAAGCTAGAGGTCAACAGTACCACATATTATTGATTGGCCACT ACTGGC
WI-14867	46 T C A	GACATTCCAA GGCTCTCTAAC	TGGGCTGCAG ACACTC	TTTTAATTAACGTAAAAAGGCAGGACATTCCAAAGGCTCTCTAACA/T/C/GAGTGTCTGCAGCCCCA TTGGCTTTGAGATGTGAATGTGTTAACCCAGGGTGA
WI-14733	98 G A A	CCAAATTGAC AGATATTCTGC	GATGAGGTCAG GCCATTTATT	ACGGAGTCGTCTGTGATGATTTCTTTGTCAAAAAATTTGGCTGATTCATCATGAAAGAACAATT AGAAAAATCCAAATTTGACAGATATTTCTGCA/GA/JAATAATGGCCTGACCTCATCAAAAAACATCA ATGTCATGAAAAACACAAAA
WI-14898b	79 A C ---		---	TTTTGTACCTATTCCCTGTTTCAGTGCATGTACAGGAAGAGTTGTCTCATAAGGTGCCACTAAGGAAA ACTTTCTCCAT/GA/JAAGCTGCCTGCTGTGCACGTTGCCTGGCTTTTGTAAACCCCTGGTGTGCTGCATCT GCCTGTGTTCTGCTT
WI-14898a	50 A C CA	CATGTACAG AAGAGTTGTCT	AAGTTTCCCT AGTGGCACT	TTTTGTACCTATTCCCTGTTTCAGTGCATGTACAGGAAGAGTTGTCTCAT/GA/JAGGTGCCACTAAGG AAAACTTCTCATAAAGCTGCTGTGCACGTTGCCTGGCTTTGCTAACCCCTGGTGTGCTGCATC TGCTGTGTTCTGTCTT
WI-14907	48 G A	GGCACACATT GGACTCTGAC	TCTGCTGCAAG GGGAAT	TGGTATTTATTTCCGACATTACTGTAGAGGCACACATTGGACTCTGAC/GA/JATTTCCCTTGCAGCAG ACATTTGTGAAGCTGCTGGTGGCACACCCCATCAATCAGTGACTCTGCACTGCAGAGGGGCCACATG CACGATGCTCACGTGTG
WI-14911	52 G A C	CCAATACATT CAGTTCTGGT	CAAAACCAGGA AAAGGACCTT	CTAGAACTCTGGGAAGTCCAAGCTCAGTGCACCAATACATTCACTTCTGTTG/GA/JAAGGTCTCTTC CTGGTTGCAGACAGATACCTTGTCTGTATCCTCACATGGCAGAGAAAGAGAGGAAATATCT
WI-14913	88 C A ---		---	CTGATGCTTTGACATCTGGGGGATTTGCTGTCTGTAGAGACTACTTCTCTGGGACCGCAATTTC TAGTGATAGTAGAGGACTCA/C/AJCTGACGCTGCACCTTTTCATATACAGATCAACCAATCCAAAAC CTACACCTCCAACCCT
WI-14914	66 G C A	CTGGACACAG TTTTCTCTAGC	CAAGCCCAGGA CAATAAATTC	ATTTCCCTGATTGGCTGTGTAAGCCTGTGAAGTCATGCACATCTGGACACAGTTTTTCTCTAGCA/G C/GAATTTATTGTCTGGGCTGTGATGGCTTTCACAG
WI-14926	49 T C ---		---	GTTATTTTCAAAATGACACATCCAGATTGAAATGGGCACCTAGCGAAT/GC/ACTTGTGGACCACA AGACTGTGCTGAGAACATGTTCAAAGACAGTTTCAAATAAAAAATTTTCCTTAATCAGGTCCA

WI-16083	89 C T	ATGTTTAAACA CAACATATC	TGGAAGAAGATT CCAGGCC	GCATCTTTATTACCACAGAAACTCATTTATGTCTTAATCATTTGTTTAAATATATATATAGCATGTT TAACACAAACATATCAAGGATC/TGGGCTGGAATCTTTTCCATTCTATAGAAAAGCACTAACCATC CATTAAAGCAG
WI-14930	55 C T	GGAGAGTCC CTCATGGAT	CACAACCAACC AATACCGC	CAGTCTGTGTTCTGGAACAGCTCTCTTTCCACAGGAGGAGTCCCTCATGGATC/TGGCGTATTG GTTGGTTGTGGTATTGGGGAGCACGAGGGAGAGCAA
WI-14946	47 T C	---	---	TCAATCTGAAGGTGTCAAAGTGGTCTATTTGCCCCACAGACATAACA/TCTCTCTAAATCATCTCTA GATCAGGGAGTCATAAGGACCATTAAAGGCTCATTAACACAGTACTTTATGAAAGGATT
WI-15987b	80 A G	---	---	ACATTAAACACAGCACAAITTAAGGGGTCCCAACGAGGTGGTAGTGCCTTCCACTATGTGAGGACAC TAAGAAGATGGTCA/GTCTATGAACCAAGCTGCCGGTGCCATGCTCTTAAACCTCTCAGC
WI-15987a	32 C T	CACAAATTAAA GGGGTCCCAA	GGAAGGCACTA CCAACCTC	ACATTAAACACAGCACAAITTAAGGGGTCCCAACGAGGTGGTAGTGCCTTCCACTATGTGAGGA CACTAAGAAGATGGTCACTATGAACCAAGCTGCCGGTGCCATGCTCTTAAACCTCTCAGC
WI-14948	56 T C	AGGAAACTG CTAACTTGTC G	GATGATCTTAC ATCAGTTGTTG GA	GAATAAAGTTCTTATTGCCGTTCTTACAGGGAACAGGGAAGTGTAACTTGTCAGT/CJTCCAACA ACTGATGAAGATCATCTTCTGACCATAGCGAACCTGTAAAGCTGTGTTCCCTCCAGCTGA
WI-16100	52 A G	CAAAAAGCTA TTTTCTACAC TTGA	ACAGGAATGTC AGAAAACAGT ATATTAC	TTGTGTTAAATTCATCAAGGAATTGACAAAAAGCTATTTCTACACTTGAC/A/GJGTAATACTAG TTTTCTGACATTCTGTTATCAACTCTCTGAAATC
WI-14958	83 A G	AATAATTTAT CTCTTCTTTT CAAGGG	AATGCATTCT TTGGTTTTT	GTGATTGATCTGTAATTATTGGGATTATTTATCAACTCTAAAATTCGAAGATGAAAATAATTTATCT CTTCTTTTCAAGGG/A/GJAAAAAACCCAAATGAATGCAATTTTTCAGTTTCTCCAGGCTTTGAACTGC AGCAGAAAATCAAGGA
WI-14976	35 C T	GTTGATTGCT TCGTTCAAAG	TCAAACATAAT CTTCCATTCTA AGC	TATTTTTTAATTGGTTGTTTATTGGATTTTTGTCTCGTTCAAAG/C/TGGCTTAGAATGGAAGATTTAGTTTGAGGAG GGCAGGTTTGGGGTAGGCTAGGCTCAGCGGGCATAGTGGCCACAGAAGATGCCATCTCACACCTGGAG ACGTCCATGAGCACTCG
WI-14981	31 G T	TCAGTGGTGT TATTGGATTT T	CACCTCTGACA TAATACTTAGC ATAAA	TAATTGATTCAGTGGTGTATTGGATTTTTGTGTTTATGCTAAGTATTATGTCAGAGGTGGAGAAT AAAGAGGAAAAAGAAACAAGTGTGGCTCTCGCATCAACGACCTGATCTTGTACAGGAAGTTTTTGA GAGCTCACAAA
WI-14992	80 C T	TGCATTAAAT GAAGCTGCAG	GCTATGTGCTC AGCTTTCTCT	TGATTACATTTTTTAAATCATGCCTACCAGCCCCATCTAAGCCAAAATTCAAACACCACCTCTGCATTA AATGAAGCTGCAG/C/TAGGAAAGCTGAGCACATAGCACCCCACTGATCGGAAAGAAACGTA
WI-15002	72 T A	---	---	AAATCTCTCTTTACACACAGATGAACCTTTAATAAATTACAATGCACCTGAAAATGCCCTCTTGA TTTTCTT/AJTTCAAGTTAGGCTCAATGGGCTCTCTCTCAAGGCTGGACCTCAAGGCCAGTT
WI-15000	90 G A	GACAGAAAAA GACTCAGACT GTCTAA	GTTTCTAGTTC TGCACAAACTT CA	TCAAGCCAAATATCTGCAACAATAACATGTATTGAAAGGTATAGAAATAAACAGATGGATAGACAG AAAAAGACTCAGACTGTCTAAGTA/GJTAGAAGTTTGTGCAGAACTAGAAAACAAAAATCCACCT

WI-12323	68	G A	CACAATACTT CATGTACCTAT GAAATAA	CACTGGACATA TCCCTACCTG	ATTTGTTGATGTTGGTTAAATCTTATCTCTTTTATACACAATACTTTCATGTACCTATGAATAAA G/AJACAGGTAGGGAATATGTCAGTGCAACAGAGGACTCACACCTGTGCATAGACAGCACC
WI-14683	91	A T	AAGGGACGAT TTAGTATCTAA AAACA	GGCATGTCCCA GTGTTTT	CATAAGTTGCATTTATTCACGTCCAGCCCATCTAAAGCTACTGTGTACAGTAATCAGGACTGGAGAA GGGACGATTTAGTATCTAAAAACA/AJCAAAAAAACACTGGGACATGCCCCCTGAATTGCAAGT TGGAGTTCGTAAGAATCTAC
WI-13470	100	C A T	CCTGCCCTTAT ATTGGAATTC	GGGAGACCATG GGTCTCT	ATTTGTTGTTTATTAGCACCTGAATTTAGGGAAGAGAAACATTTCTACCTGAAGACTCCATGCAGT CAAAATTCCTGCCCTTATATTGGAATTTCTA/C/AJAGAGACCCCATGGTCTCCCCAAGTGAGGAAGCC AGGGCACTCAGCCCTTC
WI-14712	38	T A C A	TGAATGCTTCC AAGTACAAAT CA	TGAAAGTATGT TGTATATGGTA TTGGA	TTTGGTGCTACTTTGTGAATGCTTCCAAGTACAAAATCA/T/AJCTCACAATACCATATACAAACATACT TTCAATCACAACTCAAAATATAAAATAACCTACAAAATCACATTGC
WI-13712	40	A C T C T A T T G	TTTACTTTGTT GTCAATTTTAT TCTATTG	CCATAAGGTCT CACACTTTTCT TAT	TGGGATACCCCTTTTACTTTGTTGTCATTTTATTCTATTG/AJATTATAAGAAAAAGTGTGAGACCTT ATGGCTTCGCTTATTGGCAATATGCAATATAATTTGTTGTTTAAATTTATGCAT
WI-16163	35	C T A	TCTGGTGATGC AATTGAAATA A	GCTGCCAATTA CATTAACTTAC AA	TCTAAGATTTTACTCTGGTGATGCAATTGAAATAA/CJATTGTAAGTTAATGTAATTTGGCAGCATT GCCAAAAGTTTAAGAGGACTATTTCTTTAAACAAGACAGTGTCTGACATTTATTTCAAGT
WI-13453	88	T A T C	AATGCACAAA ATCTTGCTCT TC	TCAGATTTTAA CATCTCTTCT AGCA	TTTTTTTATTGTCATTGAGTGCTTTATTATATTGGAAATGCGAGTGTATTAACATTTGTACAAAT GCACAAAATCTTGCTCTTCTT/AJTGCTAGAAAGAGATGTAAAAATCTGCCTAGTTGAACAGTCTT AATGAACCTCATTGTCCAT
WI-16167	58	T C G A T T T T	CGCACTCTAA ATTAGAGATA GATTTT	TGCTCGTGGTG AATAAGATG	CGGATATAATTATGTACCGCACTCTAAATTAGAGATAGATTTTCTGATATACATTT/CJCATCTT ATTCACCACGAGCACACCACGACAGTAGACAGTCCACACCTGATAAATTCACAAAGATG
WI-14482	17	G A ---	---	---	GCAGAACCAATTAATAA/G/AJATCTGCAAGTTTCCCCAAGAACTCTGGAAACCATAGTGCCTAAT GCCCTTTAAATCGATACTAAAGGAGAGAGATAAAGGACTGCTTGATGTGACAGTCACTGGT
WI-15069	81	T C ---	---	---	TGTAGTCTTCAAAAGACATGTTGGCAGATAGCCAGGCCATCTATGTGTATCCCAGTATCATGTAC GCCTAAAAAAAAT/CJGTGTGCTTGTGCTGTGCTGTGAGTGAACCATTTGCTTAAGATAAA
WI-16156	97	A C C C A G A T C G C	TGAAGATTAA CCAGAGTCGC	AATTGTGTGCA TTTTGAAGAGA	ATCTGGTATTGTGTATCCCAACAAGTATACAGAATACTCTATAAAACCAACCCCAACCCCTTCAATA TTACACTAATGAAGATTAAACCCAGAGTCGC/AJCTCTTCAAAATGCACACAATTAAGACG
WI-15012	59	G T A T G T	GCAGCAAGAT TACATCAGTA	CTOCAAATAGC CTAGAGTATAG TAAGGT	CATGGCAGCAAGATTACATCAGTAATGTAATAATACAGCTTTTTCATTGAAGCTTTG/TJACCT TACTATCTCTAGGCTATTGGAGTGTCCCCAC



WI-15100	74	G A ---			---	TCATTACAGCAAGAAATAACCCAAATTATTTCCAAATAAAGCAAAATTTGGAACAGACTGGA GTGAGAAC[G/A]GGTTCCACCACCAAGCCCCTCAAGACAAGATGGACACGGCAGCTGTTCTGGGGT GCATTTCTAGTGGACTTTAT
		CCTTATTTC CCAAATATAA AATTACT			GTCAACATGTT ATATTTCTTT TAAGAC	TGGTACAGAAATGTTAATTACAGCAGGGCAGTGATTCAGTTAAATAAATAAACCCTTTATTTT CCCAATATAAATACTAAATTA[A/T]GTCCTAAAGAAAAATAACATGGTGACAGCTTT
WI-14492	92	A T				TCCTTAATTTATCGGAATCCAGGACACAACAAGAAAAACACCCCAAAACCACATGGAGACAGAAG ACGAGACACAACCTCTCCCCAC[T/C]GCCTCCCTGCTCTAGAGTGGGGACAAAAGTGGGGGTGAGAC AG
WI-12002c	89	T C ---			---	TCCTTAATTTTATCGGAATCCAGGACACAACAAGAAAAACCCCAAAACCACATGGAGACAGAAG AC[G/A]GACACAACCTCTCCCCACTGCCTCCCTGCTCTAGAGTGGGGACAAAAGTGGGGGTGAGAC AG
WI-12002b	68	G A ---			---	TCCTTAATTTTATCGGAATCCAGGACACAACACCCCAAAACCACATGGAGACAG AAGACGAGACACAACCTCTCCCCACTGCCTCCCTGCTCTAGAGTGGGGACAAAAGTGGGGGTGAGAC AG
WI-12002a	30	C G	TCGGAATCCA GGACACAA		TGGTTTTGGG TGTTTTCTT	TTTTCATTTATTTCCAGAAAAAGAAATCACATTTTCAGTAACAACCTTACATATAGAAATTAACATTTG TTCTGGAATGGAGCCCTAGTTGCAGTA[A/C]TGTCATAATAAATAATTGCATATTCAGGATTTTG TGAATAGGTGATTGGGA
WI-15116	96	C T	GGGAGCCCTA GTTGCAGTAA		CTGGAATATGC AATTATTTATT ATGACA	GCAAAAGCAAAAGCTATGGAGGCCCTAAAGGAATGGAA[C/T]GTGTTGGTGGCTTGATACTTGGT GCTTGTGTGCATGGAGCAGAAAGTCTCCTGTGTCATGCAGGGGGTCACATATTTAACTGCACATAAT TTGGGCAAACTGTCATTG
WI-12578	37	C T	GGCCTAAAGG AATGGGA		TCAAGCGACCA CCAACAC	ATTTACAGTTGGCCCAAGATCTCCCTTATGTTGGCATTGCA[A/G]AGACACTGCACCTTATCTGAGGTTA GAAAAATGTAGCTTAATAGCCCTCTTAATGTGTAGCAAGGCAAAATTACCATTTCTCTAA
WI-15153	40	A G	CCCTTATGTTG GCATTGCA		T T	CCCTTGTCTCTGAACTGGGACCAGGATGTGAATAATTTTGAATCTGATGCAGGTCGAGGTATGGC TTTGAATCAAAATGGG[G/C]TGACTTTTCCCCTGTTGGTGGAAAACCTCTGTGAGGGTTTGGCA
WI-15215	84	G C	TCAAATGGG CTTGAGGACCT AGAAAGCAAA		CCAACAGGGGA AAAAGTCA	AGGAAAGAGTGTAAAGCAAGGGCGATCATTGGATGGAATGATTATGTGTACGAGCCTTGAGGAC CTAGAAAGCAAAAC[C/T]GGAGTGATTATGCCAATCAAAATTGCAAGGTTGGAGATATGCTAAAA
WI-15225	80	C T C			TAATCACTCC	AATTTGCTAGTGCAATGGACCCAGAATTTGGAAGGGCTATGTAACACACA[G/A]TATGCACACCAC AGCCATGTCAGTGTACAGATCCCTCTGTGCATTGCTTCTTAAAAACACATCAAAAGGCTGCA
WI-15152	51	G A ---			---	
		TGTTAGTGACA GACAGATAAA			TGCTTAAGGG CAAACAGAC	TGACTGTATACCAAAATGCTGTGCTTAATGTTAGTGACAGACAGATAAATAGGATG[C/T]GTCTGTTT GCCCTTAAGCAATTTACAACCTCACTGGGGAAGAAACAGACATGCAACACGAGATAAAACACAAT
WI-15123	55	C T TAGGATG				

WI-15182	49	C A	GCACAAACCAG GGCAAAATA	GCATGGGTTAA TCCAGCA	GAGACTGCCCTGTGACACAACACTAGCTAGCTGCACAACCCAGGGCAAAATAC/AITGCTGGATTAACCC ATGCTAATGGGTTACCTTTATTAGTAATCATGGTCCCTCATAGCATGGTCCAGATCCG
WI-15198	38	T C	GGGCCCTTGGC ACTATG	ACTTATCCGTC AGCAGAGTAG	GTGGAACCTCTACAAGTACCATGGCCCTTGGCACTATG/CJCTACTCTGCTGACGGATAAGTTGGC ATATGGTTCAGATTGCTTGCTACACAGTCCAGTTTCCCTAGAGACTAGTCCGACTCTCT
WI-12601	42	T C	CATTATTGAG TATTCTTGCTT	GTGTAGTCTT ACATGCTTACG	TCAAGTGGTAAATAGCCATTATTGAGTATCTTGCTTTGAT/CJGCTACGTAAAGCATGTAAGACT ACAACTTACGACCCCATCTCTCAAGAGGAAGCTGGTATTATGGAAAAACAATTTGTCAATTCAGAT T
WI-14510	104	A T	TGGCAAAATA TGCATAACAA	TTGAAAATGGT TAAACTGGCA	ATGTTGAGAGTAATAATGCCCTACATATTAGTGTAAAGTACACCCAGATATTTTGGGGAGAAGAG TTGTTTGCCTTTTGTGGCAAAATATGCATAACAAAAAT/ATJTGCCAGTTTAACCAATTTTCAAGAGT
WI-15239	57	T C A	CATTGCAAT AAACACCATC	GGACCTTATCT GTGGACTCAGG	CAGTGTGATGACATTTCAATGGGAAAAAGATTGTGCATTTGCAATAAACACCATCAT/CJCTGAG TCCACAGATAAGGTCCCGGAGAAAGGGCTTCCCTCTCTTCTCGCTGGTTCAGCTTCCAGCGGAGT GAAGCCTTTTCTGGAATG
WI-12634	52	T C	GCATCATATG AACTGTCTAGC	GGACAAATTGT AAACATAGCT	ATGAGTTTATAAACTGGAGACAGCGCATATATGAACGTCTAGCAGTATTAT/CJGCTATTAGCTA TGTTTACAATTTGCTCTGAAGGGTCTAGATGTGTACACCCAGAAAGTGGTGAATCCTGA
WI-15249	34	T C	GGGCTTGACAC AAAGTTCTAA	GGAAAGCCAG AGATTTTAAAC	TTTGCTTGAAGGGCTTGACACAAAGTTCTAATTTTAACTT/CJTGTAAAAATCTCTGGCTTTCCCTGGCTGG TGAGGAGCACAGGCTGGGGTCTTCAGGTATCCAGTGGTGGCCCGCATCTGTTCCCTCCACTCCCCAG CCACATCTTGGCTCT
WI-12159	28	C T	AAGACACCGT GCAAATGC	CCCTCTCCTCA GTGCACITT	CTGTCCGGGGAAGACACCGTGCAAAATGC/CJTAAGTGCACCTGAGGAGAGGGGGTCTGTGACTC CCAAACCTCGAATAATTTATGAATCTAAGAGTCCAGACGCAGTTTCATCCACGGAGATCTGC
WI-12648	41	A G	CCTAGTGGCAT TAAGGATGC	TTGCTACTAAA AGTGGACATCC	TCCCCAGATTGTATGGAAATGCCCTAGTGGCATTAAGGATGC/CJGTAGGATGTCCACTTTTAGTAGC AACCGATGTTAATTCACACTACTCCATGTTAGGTGCTTTACTTGGATTATCTCACTTAAAAACCACA
WI-12684	64	G T	CATGCTGTAA ACAGCTGTGC	GGAACAACAA AGCCTAAATGG	ATGAGAGGTAAGTGTCAACAGTAGGCTTAAAAATATTCAAGTAAACCATGCTGTAAACAGCTGTGC/G/ TJCCATTTAGGCTTTGTTGCCATTTAGAGAGCACAGGAGGAAATTTAGCATAATTTCTT
WI-15260	75	G A	AAAGGATGAA GCTAATCATG	TCTCTCCAGGG AGCTTGC	TTTATAAGCTGAATGAAAGAGTCCACACAGCGGACACTGTCATAGTGGAAACAAGGATGAAGCT AATCATGGA/GA/GCAAGCTCCCTGGAGAGACAGGGACAAAATCAAGAATGAGCTGGAGAAATTA TCCCTG
WI-15325	39	T C	CATGTGGCTGG GAGGC	CCTTCCACCAT GATTGGA	AAGGTTTAAATGGACTCACAGTTCCATGTGGCTGGGAGGG/CJTCACAATCATGGTGGGAAGGCAAAA GGCACATCTTACATGGTGGCAGTCAAGAGAGAAATGAGAGC
WI-13936	123	C T C	AGTTGGCATT AATAGCCTAT	TGAAACTCCCA CATGGAGTT	TATTTGAGTATTTTCCATGGCGCTTCTCACTCCCTATACATCTCCAGGGTTGAGGTAGTCTACCC CCATAGGTTTCAAGACCTATGACCTGTATCTCAGTTGGCATTCAATAGCCTATC/CJTAAGTCCCATGT GGGAGTTTCATAATAA

WI-14528	62	T G T A A A T	TTTAACTTTT TCTGGATGGTA	CTCGATTAGCA CTTATTATAAA AATTAAAA	TATGCTTTATTGAAGAGAAATAGGCTATTATAATATATTTAACTTTTCTGGATGGTATAAAATTTGJTT GAATTATAAATTTTAAATTTTATAATAAGTCTAATCGAGACATCACTGGGTATAATTGA
WI-15347	74	C T A A T T	GACTCAAAG GAAAAGAACA	TCAC TCC C C C A AGTCTTTG	TATTTCTTCGGTTCCGGATGCAAAACAAAAATTTTAAAGAAAAATGTGACTTCAAAGGAAAAAGA ACAAATTTTC/TC/CAAAGACTTGGGGGAGTGAAGCGAGAGCCTGGTGCAGATGGACGAGGTCTGCAGA CG
WI-14546	95	C A G G A C T C A	CCAATTTCTAG TGATAGTAGA	AAGGTGCACGT GCAGG	GTATTTCTGATGCTTTGACATCTGGGGCATTGCTGTCTCTAGAGAGACTACTTCTCTGGGACCAGC CAATTTCTAGTGATAGTAGAGGACTCA/C/CTCGCACGTGCACCTTTTATATACAGATCA
WI-15353	37	G A ---	---	---	TTTATGGCTGCTCTGTAATACAAATGTGGTGAACAC/G/ATCTTAATTCAGGACATCTTCCACCTTG TTTGGCTTCCAGTTGACTGCAAGACCAGTGTGAGGACATAGGCTGATTAATCAGTGG
WI-14580	100	G A G T C T T G C A	CATTCCCATCT GTCTTGCA	CCGACCAAGAT OCTOC	AGAAATTTTCTCTTTTAAACAGGACAAGTAACAGATTACATCAAACTTCAGAACTTCTCAATAC CTAGTTATTATACACATTCCTCTGTCTTGCA/G/AGGAGGGATCTTGGTCGGCTTAACA
WI-8540	73	T C G G C T T A	GGCCTGCATTT GGCTTA	GCCTTCTTTT TCAGGCAC	CCAGCTGGAGGTGGAATAATCGGGCAACCACAGAAAAACACACAGCTACACAGGCCTGCATT TGGCTTA/T/C/GTGCCTGAAAAAGAGGGCCGACCTCTTGATAAAGAAATGTCT
WI-8039b	97	T C ---	---	---	AAGTAGAACACAATAAGATGGCTCAAAAATATCAGAAATGCACACTACGCACATCACGAGTAAATACTG TTTGGTAAACTTTGTTTCAGTTT/C/AAATATGTATGTGTCGGTGCATGTCAATTAATATCCTTCT TACCACAGTCACCTAAAGAACCAAGCTTAGGACTAGGACACAAACCATGCAGAAAGAGCAGGGA GACCAGACACTCTGGGTTGAGATGATGATTTAATGCCGAGCCGACACCCACA
WI-8039a	87	T C ---	---	---	AAGTAGAACACAATAAGATGGCTCAAAAATATCAGAAATGCACACTACGCACATCACGAGTAAATACTG TTTGGTAAACTTTGTTTCAGTTT/C/AAATATGTATGTGTCGGTGCATGTCAATTAATATCCTTCT TACCACAGTCACCTAAAGAACCAAGCTTAGGACTAGGACACAAACCATGCAGAAAGAGCAGGGA GACCAGACACTCTGGGTTGAGATGATGATTTAATGCCGAGCCGACACCCACA
WI-8044	107	C A ---	---	---	CACAACATTCAGAAAGTTTCTGCAATTTGCTCTCTCTGATGTCTAAAAAGATTGAGCTTTGACTAT ACGATTTCCACACTGAACGCAATTCATAAGGTTTCTCC/C/AGATATGGATTCTCTGATGATTAATA AGCCCCGAATCTGGCTAAAGGCTTCCACATTCAGACATTTGTAAGGTTTTCTCCAGTGTGGAC TCTCTGGTGTGCACAGAATGGAATCTGGCTGAATGCTTTCCACACT
WI-8550	32	G A A T G C A A C A A G	GGGAACATCA ATGCAACAAG	TTTGTGGCTTG AGTTTACAAAT T	CTTACTACATGGGAACATCAATGCAACAAGTA/G/AAATTTGTAACTCAAGCCACAACCTTAGTTA ATAATCATGTTAAGGGACATTTGCCAAAGAGCAACTGATGCCTCAGTGAA
WI-8057	87	T A ---	---	---	TATTAGATAAAACCTTTGTTCCCGATTGAGGATGTTTAAATTTGCTTCTCTTTAACTCTGTGACTTTT CCTGGTTCAAAGGACAGT/A/GATGGACAGCAGCAGGAGGTGGGGTCTGAAAAATGTAATCTTT GTGTCAAGGCACCTGTGGCTCACAACCTGCCCTGTAGAGGGATGCTGCCCTTCCAGCCCTAAAG ACACTAGGGCTTTTCAATGGACGGGGTGTGAAGCAGCCAGATGGTAAGG

WI-6192	91 A G	GACTGCTAAG GATTTAAATTTG GAT	TGAAGTGTAG ATGGCTAAGTA TTAAAA	AAGAGGAACAAATTAGCTCAGTCCACATGATTGGCAGTTGGCATAATCTAGTGAAGCAAGTGTCT GACTGCTAAGGATTAAATTTGGATJAG/ATTTTAACTTAGCCATCTAACACCTTCAAGCATAAC AAGTGATGTGCTCTCACAAATACATTTCTCAAACTCAAAACATCATGCTTGAATATCACTGAACCTT GTCACCAAGAAGTCACATGGCAATGATAATAAAGAAAT/ATATGCAGACTACACTCTGAGGATAG AGCTCTAAGAGTAAAAACAATGGAATTTGGAAAAAATAGGAGTAA
WI-6194	105 T A	CACATGGCAA TGATAATAAA GAAA	TCATCCTCAG AGTGTAGTCTG CA	CATATGCTGCTTATTTCTGTAAGGATACACTGAACGTTAGATGATAATAGCTAATGACAGAATGT AGAAATGAGGCATCAGCTCTCTAACCACTCTCAAGAAATGTTAGTATGTTGTCATTACATGTTT ACTTTGATATTGCTCATTACTATGTCT/ATATAATAATAGTAACATACAGTAAGTAGGTGATCC TGCATTTGAGGTAAAGCGTAGGTGGAAATCCAGATTTCCCTTGAGGAAAA
WI-6213	164 C T	---	---	CGGGTTAAGAAATACCTTTAAATTTAGTAAATAAAGCTCAAGGAGTGGGGCTGTCATCTGTGGTG TCAGTCCCTTCTGGCCCCCTGGCTGTCAGTGTGCTCCAGGGCCTTGACAAGCAGCTCATTCAAG[C/T] GGCCACCATGGCCCTAGGGTGTGTCACAAAGTCCAGCAGCAATCATGGGTTCTCGTATATCTGATCC AC
WI-6217	131 C T	---	---	ATAGTCTTATTGTCAACGAAGGCTACACGGGATCACTTCTGGTTTGTGTTTTTATGCTTTTTTTTC TAGAAGGTATCTACATCTGCATTTATTTACAGCCTTGTGGTATTTACAGATCAAGATACAGTGTTA GAAACACAAAGTGTGAGAAAAAACTTCTCAAAATTTG/ATGTTCCAGACTTCAGGAAAAATGATT TCCACATGTTAAGGCCAGAGTCTCCAGTGTGGTGTGTCATCCAGAAAGCAGCTTG
WI-6238	175 G A	---	---	CTTGATTAAATCAGGGCTTTGGGGTCATAGGGGATTAGTCACTGTACAGTCATAATAATGCATTTA TTCAGGGAAAACTTTAAATTC/TTTCTTTGTCTTCTCCAAAAACAGCTGCTGGAACACCTCAAAATTA GGGATGTTTCATCTAAAAACACCTTTTACTGAACTTGATTCCTTGGGCCAGAGAGGCTTTTACTGTAG CAGAGGACTTAATGCAATGCCCTATTCCGGGCAATAAATGAATACTTGATGCATTCACAGGCAAGAA TCCCAGCATCCAGAGAGGCTGTGTGTC[G/AT]GCAAAAGCATGGCTGCAGACATCAGGGAAGCT GGTGCAGTTCTAGTCTCGCCTCCTCGATTTCCCTGCCAGCAGTCTCTCTCTCTCTCTCTCTGCCCC TCTG
WI-6303	96 G A	CCCAGAGAAG CTCTGTCTGC	CAGCOATGGCT TTGCAG	ATGCTTTTGCATGATTCTAATTATGCTTTTTCAGAGCTCTGCTGGTAAAAAGTGGGTGCCATACA AACAGTCCCTTTTCAAGCCAGCGTGTGCATGCATCCTGCCAATCAATCACTGTAATGTCCATTGTCCA AACAGGTCAACCGTTGTCTCCATGAAAACTGGATAAAGAGTTGCTGATAGTGT[C/AT]CTGGTT CTTCCCTTTACATCTTTTGGGGGA
WI-6315b	193 C T	---	---	ATGCTTTTGCATGATTCTAATTATGCTTTTTCAGAGCTCTGCTGGTAAAAAGTGGGTGCCATACA AACAGTCCCTTTTCAAGCCAGCGTGTGCATGCATCCTGCCAATCAATCACTGTAATGTCCATTGTCCA AACAGGTCAACCGTTGTCTCCATGAAAACTGGATAAAGAGTTGCTGATAGTGT[C/AT]GAGTGTCTGGTT CTTCCCTTTACATCTTTTGGGGGA
WI-6315	187 T C	---	---	CTTCCCTTTACATCTTTTGGGGGA

WI-6375	28 A G A A	GGTTTATTGCA TATGGAATC	AATGTGAGATC TTTATTCTAAC CTTTTT	AAGGTTTATTGCATATGGAAATCAATAG[A/G]TATCTTTTACAAAAAAGGTTAGATAAAAGATCTC ACATTTGTAAAGGCACATATGAACATTTTATAGCAAGCACAAGGGCAGTGAGACATCAACAA TTGTGCTCAACAGATGAAATTCATAACCTTGTTTTCTGATAAGACAAATTCAAACATACAAATCAAT TACAACAATGTGCTTATCAGCTCCCTCCACCCCTATATTTAA[T/A]GCCAAGTACAGTTTTGAAG GACACCAAGACAATAGGGCT
WI-6409b	112 T A ---		---	TTGTGCTCAACAGATGAAATTCATAACCTTGTTTTCTGATAAGACAAATTCAAACATACAAATCAAT TACAAC[A/T]ATGTGCTTATCAGCTCCCTCCACCCCTATATTTAATGCAACTGACAGTTTTGAAG GACACCAAGACAATAGGGCT
WI-6409a	73 A T ---		---	CTAATATAATCCTGGGCACATGGATTCCAAGAGAGATTTTGCAGCAGATTTTCAATATAGTTACTTAA CAGCTAAATAATAAGGGTGATTTAACTTACTTACAGAGTCACTAAATAATGGAGGGGAAAGGAAA GAGTAGGGCTAATCCAGTAGAGACTGAAGCTG[G/T]ATCAACCTTCCCTAAGCATCTGCTGCTCCG CAGC
WI-6523	165 G T G C T G	GCTAATCCAGT AGAGACTGAA	AGATGCTTAGG GAAGGTTGATA	TCTCTAGCCCTATTAGGCTACACTGTAGTCACCTTCTATGAGAGCAAGGAAACAGGAAGATGGGC TCTGGAGTCCAAACAGGATGTGGACGTCCTGGTGTCTCTCTTTTACACAACTTTTCCCTGAGA ACTGTCCAGTCAGGTGACCTTCAACAACACGAGCTAAACTCTGAGAGAAAAAC[C/G]CTG ACTTTCAGAAAGCATAAAGCTGAGAAAAA
WI-6554	195 C G ---		---	ATTGTAATTAAAAATTTACATGGGCCTATTATTAAAGGACATTGTGTAATGTTTCCACTTTGTTTTAAA [C/T]AATTACAAACATGTGGCTTAAAAATAATGTACAGATCAATGTAAACAAGTTTGAAAAATGGGCG
WI-6558b	68 C T ---		---	ATTGTAATTAAAAATTTACATGGGCCTATTATTAAAGGACATT[G/C]TGTAATGTTTCCACTTTGTTTT AAACAATTACAAACATGTGGCTTAAAAATAATGTACAGATCAATGTAAACAAGTTTGAAAAATGGGCG
WI-6558a	42 G C ---		---	AACCAACAAAACTAAGAAATGGGAAAAAGAAATGGCAGGTGAAGAACTCTTTTTCAGAGAAATAAA AGTTGTCATA[T/C]AGCAATGGATGCTGTGTCAGAACATACTGCCAATAAACTTTAAGAAAAAAGGA ACTCAATGAAGTTACTGTATATAAAACAGGAGCTCACAGCAGGATGTAAAGATTAAATGGAAGAT ATCGTGAGCCAAAAC
WI-6629	75 T C G C A T A	TCITTTTCAGAG AATAAAAAGTT	TGACACAGCAT CCATTGCT	CTGCCCTGAACCAATCAGATTTAGTTTAAATCAAAATCAATCAAACTCCAGCTGTTTCTCTTGCTTT TTACTTAGCAAGGAAAACTTTAGTGAATGCTACTTGACAAGAAAGAAAGTCAATTTCTCAAGCACA T/CJACCCAACTTGAAGGTGATTGAACCCAAAATAATGGTGGAAACACCAAAATGAGGTGGAGGA ATGAGAAAGATGTGTGGGCCAAAGCTATCTGGTTATATTTGATGTTGCCAAT
WI-6644	134 T C ---		---	TGCTAAACACCACCATTTATTAAAGGAGAGTACTAGGAAAAAACTACCAACACAGCATGTGAAACAGT TGGGCACGGTGGTAAAGGACAGACTCTGGAGCCACAG[C/T]GGCTAATACACTGCAATATTTTA TGTTTAGCAAAATTATAGCTGGTCTGTGTATATAACCAAGAGCGGTATCTGG
WI-6690b	106 C T A G C C A C A G C	CAGACTCTGG	TAGCC	

WI-6690a	28 T C A G A G	AAACACCACG ATTATTAAGG	GCTGTGTTGG TAGTTTTCCT	TGCTAAACACCACCATTAATTAAGGAGAGTC/ACTAGGAAAAAATACCAAAACACACGATGTGAAAC AGTTGGCAGCGGTGTAAGGGCACAGACTCGGAGCCACAGCCGGCTAATACACTGCAATATTTTA TGTTAGCAAAATTAAGCTGGTCTGTGTATACCAAGAGAGCGGTATCTGG
WI-6770	53 A G A A C A T C A C A	CAAAACCCAA AACATCACA	GCTTTGGAGT GTATAATAGTA TGAATAA	GATGTTTAATGACACAGATCTTCCCAAAGTAATCCAAACCCCAAAACATCACA/AGJAATTATTCAT ACTATTATACACTCCAAAGGCAAAATACCTCAACTGCAATCC
WI-6886	151 A G A	GCAATCTTCCA AAAACAAAGA	CCITGTAAGTG ACTATTCCAAT GTT	ATTCTGTAGGCAAGGTCAGCAATCAGTACACTAATCTTGACCAAAATGGGTGAGTCAGCCTCA TCACAGAGATTTTTTTTAAATTTAGATGAAATTCACATTTAAACATGGTAACTCCAAGCATTCCT TCCAAAACAAAGAAT/AGJAACATTGGGAATAGTCACTTACAAGGAC
WI-6761	32 C A G	GATCTAACAG CTGCAGAAATG	AAAGCTGGG AAGGAAGAAG	CCTGAGAGGCAGATCTAACAGCTGCAGAAATGG/CACTTCTTCCCTCCAGCTTTTGTGAACAAAAC AATCTCCTAAGGCATCAGAAAGCACTGAGTGCAAAATGGGTGTCAGGTACAAGGTCTC
WI-6844	225 T C ---		---	TAAATACTGCCAACTAGCATTACGTCCACTCTTGCAATCAATTAACAAACAAAGGATTTCTCCTCTG GTATTTTCAATGATGCATTATACATAAACGAAGTTAGAATTAACATGACCCCTGATTAATATG TAACTGGTAATTTGTTTAAAGCATATAATTTGGTCTCTTTCATAAATGGAATTTAA TATTTCTCTGATAGCTTGAGGT/CACTCATATGAGTAGTGCAAAAGTG
WI-6824	112 A G ---		---	CGGTTTGTCTACACTTAATGGGTTTTTTTAAAGGATTTTTTTCAGGTCTGTCAGCAACATCAA ACAAAGGTACTGAGTACTCCACAGGTACAGAGTGCTGCCAA/AGJACCTTAGAAAAATTACAT GACACGGAGAAATGCGCTCTTGCTCTGAAAGCTACAGTCTAGGGATTTGACAACTCACAGT CTTAGGAACTGGGCAAGTAAGGCAAAATCTTCATCCCTAGAGCTATTGTG
WI-6889	139 T C A A T T C	GAAAAATGAG ATGCAGTTAA	TCACTTTGTGG CTTTAATTAT TCT	GTACAAAAAAGCTGAGAAGAGCCCAACATGGAAGTGCAAGAAACATTTCTGATAGGTACGGACAA AAGAGCTCCTCAATCAAGAGGAGTTACATATTAGTTCTCACCATGCTAGAAAAATGAGATGCAGTTA AAATTC/CAJAGATAATTAAAGCCACAAAGTGAAACTGTTGTTCTGGGCCCTATGTTGTAGATT CTCT
WI-6911	216 T C ---		---	TCCCAGCTCATATTTATTTGGGCACAGAGTGGGCACACTCAATATCTGATGAACCTGATGAACGTGAA AAGAGGTCTCCTTAAACAAGATATCATCTCCGAAGAGAGAGTCCCAACCATATAAAATGTATGAT CAAGTCCCAGAAAACTTTGCCCTCCCAAGGAATGTGTTCTAATTTGGTTTCAAAGCACACTGGTTCC CACTTTTACCACCTT/CACTGACATTGGACAATAGTACTACTCTTTCTAC
WI-9413	112 G C ---		---	GCCAGTCTAGTAAGTCTTAGGGACATGACCAGACCAGAGCCCTGTTCTATATGAAGACAAAC AGGTGCCATACTGGGTGGAGGATACCGCTGCTATCCCAGAT/CAAGATTGGTGGGAAGGAG ACCATGACAGATGACAAACGGAACAGTTTCTCAAAAACAGAGGTATGA
WI-9557	74 C T ---		---	AAAAGCTTTAAAAAAGTGGTGCTATCTTTAGAAACACTTTCAGCAAGATCAAGTAGCCCCAGCT ACAGCC/CT/CGGTGCATCTTAACCCCTCTCTCTTT

WI-9617	37	G T ---				TGCTCTTTTATTCACGTTTCACAACACACGCCGTG/GTJGGACAGTCTACCAAAGTGCCCGCAG CGCCACGCTTGGCCGGAAGGTCTATTCTGTCTCTATGGACTGATTGAATTTGGGATGGCCAG CTCCAGAATGTTCCACGTGGGGCAGCTCTGTGGGCAGAGAGGCTAGCCCTGCCACACTGGCAACCA AAGAGGTTCACGATGCAGCTTCAGTGGTCCAAAGCCGGTGTGCTGTG
WI-9657	121	T G ---				AATGCTGGAGAAAACATCAACATTGAGTTGACATTTGTTTGTCTGAAGTATAGCTACCATCCACTAT CATGAATTTTGTTCATTACAAATGATAGAAAGCCAGATTCTCAAAATAAAGT/GJATAATTCTT TGTAATTAATAAATGTTTATAAATGTTTATGAAGCTCATTACATTATCTTTTAAAAAAGTAAAAA TTTTAGAACATATGACGCTTTTCATAATTAAATGCTTTTGATATAGATTGAGG
WI-13119b	114	G C GCTGGGA			AAAAATTAAAC CAGGTGTGGTG T	CAGGGTCTTGCTCTGCTCCAGGCTAGAGTGAGGTGACACAATCAAGACTCACAGTAGCCTCAACCT CCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGCATGT(G/C)ACACACACCTGGTTAA TTTTTTAATTTTTTGTAAAGATAGGCTCTCACTATGTTGCCCGCTCAAAAAACAAACCACTAAC CAGGGTCTTGCTCTGCTCCAGGCTAGAGTGAGGTGACACAATCAAGACT(G/C)ACAGTAGCCTCA ACCTCCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGCATGTGACACACACCTGGTTA ATTTTTTAAATTTTTGTAAAGATAGGCTCTCACTATGTTGCCCGCTCAAAAAACAAACCACTAA C
WI-13119a	51	C G ---				ACAGGAATCTGAAAGTTACCAAGGCAATTTCCCTTTTAGGATCATAAAGACTACAGACTTAAGCTT TTTT(C/T)CTTTTCCATATAATACACAAAATTTCTAAATATCCTTAAAAAGAAAAATATAAATAGT TTCAGTATGTTATGTAGAGTCACATACACTATGGCAAAAATATTTTATTAATTGAGGGAATAGGCCAAT TT
WI-13112	71	C T AGCTTTT			TTAGAAAATTTT GTGTATTATAT GGAAAAAG	TGTTAACATTTTATTGGTACGTGCTCTCAGTACAA(C/A)AAACAGCATCAGTAGTGTACACTTTTGAT AAAAAGGAATTTTAGCTTAGTAGAAAAAGAAAGCCCAAGGTCAGAAGTATAATGAATATGTACAT CTTTATGGAAACTGTTTGTGTGACCATCTTTATCTCCCTGTGGATGAGATGTATGCACACACAAGT AAA
WI-12988	36	C A CTCAGTACAA			CAAAGTGTACA CTACTGATGCT GTTT	TGCTATTTCATGACAGACACGTCGAGACAAAATATTTCTATTACAGATGGAATAGACCCAGACATTA TTCAGTACTTTAAACCACATAATAGTGGAAACCCCTGAGACTTTA(G/A)ATCTGCAAGGGGTTTAAATAAT GCAAAATATCACATATATTTCCATTTTAAACACCATAATTTAAGTTTCCATTTTCTTAATAGAAAAATGA TAAAAAATGTTTCCCAATAT
WI-13020a	108	G A CTTT			CATTATTAAC CCCTTGCAGA	TGTATAAAAAATCCAACCTGTTCCACAAGTACATATGTCCTATGATTTTATGCATACATCCATATAC ATATATCAAGGTAAAGTCCA(A/G)TACAAAAAACAGCATTTCCCTATGGCCAGTGTCTACAGAAGT AAGACTGTGCAAACTTTATCGTATAGTCAAAATGAGATTGCACACTAAGGCAGGATGAGGCAGAAGCA AGTTGTGTCCA
WI-12837	87	A G AAAGTCCA			GOCATAGGAA ATGCTGTTTTT	

L42611b	50 G C ---			---	GTCTCAGGCCCTTCTCTGGCTGCAGAGCCGCTTCTCAGGTTGCCTGTC[G/C]TCTCCTGGCCTCTAG TCITCCCTGCTCTCCGAGGTAGAGCTGGGTATGGATGCTTAGTGCCCTCACTTCTCTCTGTCTATAOCT GCCCATCTGAGCACCCATTGCTCACCATCAGATCAACCTTTTGATTTTACATCATATGATTTCAACCA CTGGAGCTTCACCTTGTITAC
L42611	34 T C ---			---	GTCTCAGGCCCTTCTCTGGCTGCAGAGCCGCTT[C/C]CTCAGGTTGCCTGCTCCTGGCCTCTAG TCITCCCTGCTCTCCGAGGTAGAGCTGGGTATGGATGCTTAGTGCCCTCACTTCTCTCTGTCTATAOCT GCCCATCTGAGCACCCATTGCTCACCATCAGATCAACCTTTTGATTTTACATCATATGATTTCAACCA CTGGAGCTTCACCTTGTITAC
WI-1172b	179 C T A	TGAAGAAATG GCTGATACCA	ATGTGCATTTT TCACTGCAG		TGAACGTGTGGTTAAACTAGGCAATTGGTTAAAAATCAATTTAAAAACAGGCCCTAGAAACAGTG ACCACACCTCAAGCAATGATTATCCCTAGCACTCAGATTATGTTCTTGAAATACCATTTTCTGCTTTC AAAGAAAGACATGAGGGCTTCTTGAAGAAATGGCTGATACCAAG[C/T]TGCAAGTGAAATGCA CATGATGAGCCTGGAACATGTTGT
WI-1172a	17 C A ---			---	TGAACGTGTGGTTAAAC[C/A]TAGGCAATTGGTTAAAAATCAATTTAAAAACAGGCCCTAGAAACA GTGACCACACCTCAAGCAATGATTATCCCTAGCACTCAGATTATGTTCTTGAAATACCATTTTCTGCT TTCAAAAGAAAGACATGAGGGCTTCTTGAAGAAATGGCTGATACCAAGCCCTGCAGTGAAAAATGCA CATGATGAGCCTGGAACATGTTGT
WI-1177	35 G C A	GCAGATTGGA AGTGTGAAAA	CACTTACATTT CTGAATATTTA GACTCTTT		AGAGGCAGATTGGAAGTGTGAAAAAATGAAAGAA[G/C]AAGAAAAAAGAGTCTAAATATTGAG AAATGTAAGTGTGCTGCCCTCAACTGTTCTTTACCCACTTAATTTCTGCAATTTTGAAACTAGATTGAAT TCCTTTGCAAAACCCCTTGATCATGATGATACCCGAGTTAAACCGTTAATTTAAAGACATTTAAACATGG CCTGGTG
WI-1231b	141 G A ---			---	TCCATGGTTTGGTTGCTACTGACTTGTAGCCTTACTGCCCACTATGCATTGGAACATTCCTCATATTG CAACTAAGCAGGAGTGTTCACAATAAACACATAGGCTCTTTATCTCCTTCTTCAATTAATTTCTT TCAC[G/A]TTATTCCTCACCCTGAACGCCCTTCTTCCCTCGTAGTGACATTTTAAATCCACTTTAC ACATTCGGACC
WI-1231a	126 T C A	GGCTCTTTATT CTCCTTCTTTC	CGTTCAGGGTG AGGGAATAA		TCCATGGTTTGGTTGCTACTGACTTGTAGCCTTACTGCCCACTATGCATTGGAACATTCCTCATATTG CAACTAAGCAGGAGTGTTCACAATAAACACATAGGCTCTTTATCTCCTTCTTCAATTAATTTCTT CTTTCACGTTATTCCTCACCCTGAACGCCCTTCTTCCCTCGTAGTGACATTTTAAATCCACTTTACA CATTCGGACC
WI-472	114 G C ACAGAAAAG	ACATACATAT CCATTATACA	GACCTTCTTT TCCAGGCC		GAAGCAGGACTGTGTTTGGAGGACAAAAGTAAATCTTTTATCTTTATTTTAAATTTATT TTTTTTCAGGCATATAGACATACATATCCATTATACACAGAAAAG[G/C]GGGCTGGAAAAAGAAAG GTCAAGTGAGATTTCAGATATCTTAAATGCAAGGCTGACAAAATTTGGGCTTGATT



WI-478	46 C T	GCATGCTGTG T TACTCTATTT TGTTCT	AAATGCCACAG GTGGCT	AAACCACCTGCAAGCATGTCTGTGTACTCTATTTTGTTC/TAAGCCACCTGTGGCATTTC CAAAATATGATAATCTCTGCCACCATCTGCTTTAAACACAAATAGAATCTGGCAGCAAAATATAGC ATAAGCTTACTTCTAAATCAAAGGCTACCATCAGTACCTTAGCACAATTTAAAAAATAAAAAACCAAC ACTGCCCA
WI-533	29 T C	ATCACAGCAG AGTACCTTTCT AACT	CTTCCAACT CTACACAATCT T	AGCCATCACAGCAGTACCTTTCTAACTT/CJATAAGATTGTGTAGAGGTTGGAAGGAGGACAGGA CTGTCTGTGGTATAATGACCTGTGTCCAGTTAATCCA
WI-601b	112 T A	---	---	TCACCTATCTCTTTTGTGGTGAGAACACTTAAATCTAAGAATGATCAATTTCAAATAAAGATGG TAGTGAGCGAACAGAGAGGTTTCAATTGACTCCTAACTGAGTACT/AAACAAACGAGCAGGTGCT CACAGTCAGGAAGCAGGTGCTGAGTACAGGAT
WI-601a	74 C T	---	---	TCACCTATCTCTTTTGTGGTGAGAACACTTAAATCTAAGAATGATCAATTTCAAATAAAGATGG TAGTGAGC/TAAGACAGAGAGGTTTCAATTGACTCCTAACTGAGTACTCAAAACGAGCAGGTGCT CACAGTCAGGAAGCAGGTGCTGAGTACAGGAT
WI-863	107 A G	CTCCTTCACAA CCTCACCA	CTTCCGGTAA GCCAAGT	AACAAAACAGACACCTCGGCTTCTCACCAGTCCACATGGTGCCAAACAATCCCACATTCTCT ACATCTCCCACTGGGCTGCTCCTTCAACACCTCACCAG/AGTCTGGCTTACCGGGAAGCATAAA GCCAAAGCATTTAGTCTTTTATTGCAACATGGTCTGGCTGCAATAC
WI-919	36 G A C	ACTGCTTGCTT GTTGATTTAAT C	TTATCTAATC CCACATGACAG C	ACTCACTGCTGCTTGTGATTTAATCAACCTAGCCG/AGTCTGTCATGTGGGATTAGATAAAATA AACACAAAATGAAAAACACACGATTGCTAACAAAGCAGATTCTTTTCAAGGCACACGTTAAAGAT AATAACTTCAA
WI-991	37 A T	---	---	TGCATTCAATTATGCCAAATAATAACTCTGTACAT/ATGATTATGATTTCATTATCACAATAAT TATAGTGAGGGATGATTGTTATCCCTATTTACAGATGAGAACACTGAGACTTAGAAGAAGTATCT TTCCAAAGTCACAAAGTTAGTGACAGAGCCGGATTGGAATCCATCAACTTGAATCCAGAGAAAAT GTTCTGCATCACTGTACACACTGACTCTCTTTTCTCTTTGAAAACAAGGC
WI-1011	70 G C CCA	CAGTATCTGA AGTTTTGTCT CCA	AGGAACACCTA CAAAATGACTT CT	CTTCTGACCTGTTGCAGTGGATGTTTGAAGGCTCTGTCTCAGTATCTGAAGTTTTGTCTCC A/GC/JAGAAGTCAATTTGTAGGTGTTCTGGCGTTTTTGTACGTTTCCATTTCTTAATACACTGC CGTCTAAGGGAGGGCTTGCAGAGCATTTATCAGATGGCTGTTTGTCTGCTGCTGCACTGAAG
WI-5381	178 A T	---	---	TTATGCAGAAGGTCATGAGTTTACAGAACTCAAGGAAGAAAGGCCCTAGAGATGACACCAGAA ATGAGAGTGGCTTGTCTCATGAAATTTGGACAGCATGTTCCAAAGCAGAGGGAACAGCATGGAGAAGA AAATCATACTCTATCCACGTGCAGAAACTGGCAATTAGTTTTGT/ATTTACTAAAACACAAATGT TTAATTTGGGGTCCACAACAAGGATATGTTGGCAATGGTATTTCTGTGATG
WI-5791b	76 G A	---	---	CTATGATTCCATCTAGCAAAAGCAAGACTATTGGATAAGTTTCAAAAGATGAGAACAGGTCCTA GAACCTCAG/G/ATCGAAAGGAAGTTTCATCTAGTCCATAGACCCTATCTCACTGACCCAAAGGTA AAAAAATAAAATAAAAGTAAAGAACTTACATCAGATTGTGCATTTCTTATTTTGGCCACCCTGTTTGT TAGGAA

WI-5791a	44	C G	---				CTATGATTCCATCTAGCAAAAGCAAGACTATTGGATAAGTTTC/GIACAAAGATGAGAACAGGTC CTAGAACCTCAGGATCGAAAGGAGTTTCATCTAGTCCATAGACCCTATCTCACTGACCCAAAGGTA AAAAATAAAATAAAAGTAAAGAACTTACATCAGATTGTGCATTCTTATTGGCACCCCTGTTTGT TAGGAA
WI-5406c	120	C T	---				CACCTGCTGTTGTCCATGGTGCCACAGACTCTTCCAGAAGAGCCACTTCCACAGATGCAACAGGCC TTTTGAAGGAGGCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAACCC/C/TJATGAGCCAC ACTTCTCATTTCCCTTAGAATTTCTTGACCTCTGTGAAGAGGAAGGAAAGGAAAGAAAGAGAGGCAA GG
WI-5406b	118	C A A		CCAGGATGTC AAGGTGAGAA	AATGAGAAGT GTGGGCTCAT		CACCTGCTGTTGTCCATGGTGCCACAGACTCTTCCAGAAGAGCCACTTCCACAGATGCAACAGGCC TTTTGAAGGAGGCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAAC/C/AJCTATGAGCCAC ACTTCTCATTTCCCTTAGAATTTCTTGACCTCTGTGAAGAGGAAGGAAAGGAAAGAAAGAGAGGCAA GG
WI-5406a	42	A G	---				CACCTGCTGTTGTCCATGGTGCCACAGACTCTTCCAGAAGAG/GJGCCACTTCCACAGATGCAACAG GCCTTTGAAGGAGGCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAACCCCTATGAGCCAC ACTTCTCATTTCCCTTAGAATTTCTTGACCTCTGTGAAGAGGAAGGAAAGGAAAGAAAGAGAGGCAA GG
WI-5798	48	G C	TG	TTATTCTCCC TTGTTTCTTT	ACTGTTAGAAA ACCAGTATTTT TCAAT		CCATTCTCTCTCCCTCCCTCTTATCTCCCTGTTTTCTTTTG/CJATTGAAAAAATACTGGTT TTCTAACAGTGTGCTGGTATGGATACTATGTTAATACATGCTATGTTCTATATGGGTATCA
WI-5415	54	T A	TTT	TCTTCATGAAT TCATCTTTCAG	GGACTAATTCA TGATCCGATCT		CCTGCTAATAATAATTTAAGCACGATTGTCTTCATGAATTCATCTTTCAGTTT/AJTAGATCGGAT CATGAATTAGTCCAGGCTTTTAGTTGTAATCGAAATTGGA
WI-5437	41	C T	G	TCCAGAGAA AAATCCAAGA	AGTTTCTAAAC ACAAAATATG GTTTAAG		TGTTTTAACCCAGGCAGACCTCCAGAGAAAAATCCAAGAG/C/TJCTTAAACCATAATTTTGTTTTA GAACTCCTGTGCCCCAACCTCTTGATGTGAGTGAC
WI-5481b	131	A G	CTG	TGTCATTTATG CTGCAGTCG	TTACTTCCAGG CTCCAAGTATT		AAGCCAAATTCACATTAGTTGATGAATTTGAATTTTACAGTATCTAATGCATGGGCATCTGTTTCAAC TCTCTGTTTTCAAGAGGAGTAGTATATGCTGAAAAATCTATTTTGTCATTTATGCTGCAGTCG/A/GJA ATACTGGAGCCTGGAAAGTAAAGACTTGGCTATTTTACAAATTA
WI-5481a	29	G A	AATTT	CCAAATTCAC ATTAGTTGATG	CCCATGCAATTA GATACTGTAAA ATT		AAGCCAAATTCACATTAGTTGATGAATTTGAATTTTACAGTATCTAATGCATGGGCATCTGTTTTC AACTCTGTTTTTCAAGAGGAGTAGTATATGCTGAAAAATCTATTTTGTCATTTATGCTGCAGTCGAA ATACTGGAGCCTGGAAAGTAAAGACTTGGCTATTTTACAAATTA
WI-5492	38	T C	---				TCATGAGTCTTTCTTCAAGATGCTTGTAAAGTCCCAAT/CJCAAGAAAGGATCCCATGCGCCTAAT GAAGATGTACCTCCACCTTAGGATAATTTTGACAGACCAA

WI-5826	134	T C	---			TAATTTTTTTTCTCAATCCTGGAGCACACCATGCTCTTTCTATTTTCATGCTTCACATTTATTTTTT TTTCACCTAGTTAAATGCTTTTTTCCCTTGATCTAGCAATGGCCAGTTTATACATATCTTTAGTCG TTTCAATTAATGCCACCATAGAAATAATTTCTAACCAACAGCCAAACAGCCTCACTCTTCCTT CCTGGTGCAATTACTCTTTACAC
WI-5546	40	C T A	CCCAATACITTT TTCAGGTGAA	CCTGTATTTTA GCAACATGGG		CCTTATAACCCCAATACITTTTCAGGTGAAAAAGGGAAAA[CT]ACCCATGTTTCTGCTAAATACAGG AGTATAACAGCATGACATGTTAAGGGAATTACAAATGCTTGAGTGTAATTTCTGATGTGGGAAATAT TAGAAAAATTAAGCGAGAGAGGCA
WI-5552	97	C T	GGCACCAGCCT TTTTAGAGT	TGCACAAATG CCAGG		TGTTGTCTGCACCTCCCAACAAGTGGTCAATGAGCCTCAAGGGTTTTGATTGAGCGGGTATGGGT GGGGCTATCGGCACCAAGCCTTTTTAGAGTCTCTGGGCAATTTGTGCACCTAGTGTGAGA
WI-5836b	161	C T	---	---		TAAAGTTGATTTAAACACTCTGTGCCCTCAATTTTCTCACCCTATAAAAATAAGATAAGTATCTAAAA AAAAAGAGAGAGAAATTAAGGTGGATAGACATGAATAACTCTGATGATCTGTTGATCCCTGAA TCCTGCAATATACACATGATTCAATGATCTTCCATTTTGAAAAATTAAGCTTTTGAATTTGTTTCCCA ATG
WI-5573	58	C T	GTTCATAAGG AGGTGGGA	TGAACAGTTGG AGAGTAATGTG TC		TCGGGTATTAGGATGCGTTCAACCTCGATGATGATGGGGTTTCATAAGGAGGTGGGGA[CT]TGACAC ATTACTCTCCAACTGTTTCATCAGAACACTTCAACAGCG
WI-5850b	134	G A	---	---		CAGACCTTGGAGCCTTTGCTGTTTGTCTTCCACCTCACTCTTCTCTGCTGCCCATGGGTGGAGC CTCTCTCAGGCTTCCCTCTATGCACTGCGTCTCTCTCTATATGGGGCAATATCCAATGTCCCATTCG/A TTTTGGCAATTTCTGTATATCAACAGAGAGAGGAGGTTGG
WI-5850a	92	C T	---	---		CAGGACCTTGGAGCCTTTGCTGTTTGTCTTCCACCTCACTCTTCTCTGCTGCCCATGGGTGGAGC CTCTCTCAGGCTTCCCTCTATGCACTGCGTCTCTCTCTATATGGGGCAATATCCAATGTCCCATTCG TTTTGCCATTTCTGTATATCAACAGAGAGAGGAGGTTGG
WI-5612b	125	A T	CTATTAATGA GCATCGTGTCA	TTCTCTTGAGA AACCTAAAC ACTG		TGCCCTGATTGACACATAGTTATCTGACAGTAATCATTTCAACATCACAATAATCTTATTTCTGCCCTG TCACACTAATTTGCCAAGCATTCAATGATTGACTATTATGAGCATCGTGTCATTCTATTCAGTGTT TTAGGTTTCTCAAGAGAAATTATGCTGTTCTCTCTGTAACCTCAAGTA
WI-5612a	44	T A	---	---		TGCCCTGATTGACACATAGTTATCTGACAGTAATCATTTCAACATTTCAACATAATCTTATTTCTGCG CTGTACACTAATTTGCCAAGCATTCAATGATTGACTATTATGAGCATCGTGTCATTCACAGTGTT TTAGGTTTCTCAAGAGAAATTATGCTGTTCTCTCTGTAACCTCAAGTA
WI-5636	26	A C	GCCAAATTTTAT CCGCAATAAA	CATCGAGGACT TTGGGAA		TGAGAGCCCAATTTTATCCGCAATAAA[CT]TCCCAAGTCTCGATGGAGGCAATTCAGAATCGGG GCAGGGGAGGCAGAGGTGAGACAGATGTGAAGAAC

WI-5865c	103 C G ---	---	---	TTAGAAACCTCCATTATTCTGCCATGGTACATCTTTTAAAGAACTCTTTTTCATTATGCAATTC ACTGACTCACTCACTGCTCTATCAAAAATTAA[C/G]AAATATTAATATTTTATTTACAGAGGAA CTCAGAAGCCAGAAAAATGACCAAGACACAGTCCAGTCTCCATCTTCAAAAGGTACAGTCCCTTCA GAGAAGACAGACAACATAAATCCAGG
WI-5865b	99 T A ---	---	---	TTAGAAACCTCCATTATTCTGCCATGGTACATCTTTTAAAGAACTCTTTTTCATTATGCAATTC ACTGACTCACTCACTGCTCTATCAAAAATT[A/J]AAACAAATATTAATATTTTATTTACAGAGGAA CTCAGAAGCCAGAAAAATGACCAAGACACAGTCCAGTCTCCATCTTCAAAAGGTACAGTCCCTTCA GAGAAGACAGACAACATAAATCCAGG
WI-5865	165 T A ---	---	---	TTAGAAACCTCCATTATTCTGCCATGGTACATCTTTTAAAGAACTCTTTTTCATTATGCAATTC ACTGACTCACTCACTGCTCTATCAAAAATTAAACAAATATTAATATTTTATTTACAGAGGAACTC AGAAGCCAGAAAAATGACCAAGACACAGT[A/J]CCAGTCTCCATCTTCAAAAGGTACAGTCCCTTC AGAGAAGACAGACAACATAAATCCAGG
WI-5874	76 T G ACAGAAAA	CATAGCATGG ATAATATTAT	CCTAGTAAGTT TCAGTCAATTTG ATATGT	CTCAGACATTCATTTTCATTAGTTGTTAATTTTGTGTATTTTCATAGCATGGATAATATATACAGAA AAAAAATTT[G/J]ACATATCAAAATGACTGAAACCTACTAGGTAGCAATTTGTTTGTCAATTTGCT CATGGAGCCGACGTTGAGCTCTCAGTTTTTCCATC[A/T]TTTTTCATAATTTACTCTCTTTTCTGTC ACAATGTTCTGCTCGTATTTCAACTCTCATTTGCTGATTGGATGGTAGTCATAAAAATATGGGTGATTCT AGAAAAAAGTAAATG
WI-5752	36 A T TTTTCCATC		ATGAAAA	TTAGCAGAAACAACAACAAAAATGTCAACACTGCAGTAAAGAAAGTGTTCCTCCGATAAATA[C/G]C CATTAGGTATTAGATAAGCATCCCATAAACATTTGTTGAAACGAAAGCCGAGTTTCGATTACACACA GTTGCTGTTTAAACCTCTCTAAATCCCGATAAATAGCCATTAGGTATTAGATAAGCGTCCCAAGAA CATTGTTGAAACGAAAGCCAGTTTCCGATTACACAGTATTGTTCTGTT
WI-5760b	61 C G ---	---	---	TTAGCAGAAACAACAACAAAAATGTCAACACTGCAGTAAAGAAAGTGTTCCTCCGATAAATAACCCAT TAGGTATTAGATAAGCATCCCATAAACATTTGTTGAAACGAAAGCCGAGTTTCGATTACACAGTT GTCTGTTTAAACCTCTCTAAATCCCGATAAATAGCCATTAGGTATTAGATAAGCGTCCCAAGAA ACATTGTTGAAACGAAAGCCAGTTTCCGATTACACAGTATTGTTCTGTT
WI-5760	187 G A ---	---	---	AAATATCTGGCCTTTTCTCTTAGGAGGAGATTCTCACCATGGGAATCTT[G/A]GTGCAAGTTAGAT CCCAACCTCACTATTGAGAAGCTAAAGTGAAGACTACTCATTTCTCAGTCTTCTGCTG
WI-5944	52 A G GGAATCTTG	TTCTCACCATG GGAATCTTG	GGGTGGGATCT AACTTGCA	GAGTTTAAATGAATCCTGTTCCCTCCTAAAACCTCCTGTTCCCAACCTCATTCTCAGTCTTCTGCTG CTTTCATGGGTTATTTGCCCAAGTCATGAGGAGATGCATGTAATTTGTGATCATTTTCAAGAGTGTGAG TAATGCTTGGT[A/C]TTTGTCTGTGCGGTATCTGCTCCAATCACCCTTCCACCTTTATTTCTCTATTAT GCTGAATGAACGGTTATATTACAG
WI-5967b	148 C T ---	---	---	

WI-5967	165 C T ---			---	GAGTTTAAATGAATCCTGTTCCCTCCTAAAAACCTCCTGTTCCCCAACTTCACATTGACGAGATATT CTTTCATGGGTTATTTGCCCAAGTCATGAGGAGATGCATGTAATTGTGATCATTTCAAGAGTGTGAG TAATGCTTGGTACTTGTCTGTGCGGTAT[C/T]TGCTCCAATCACCCATTCACATTATTTCCTATTAT GCTGAATGAACGGTTATATTACAG
WI-6093	53 G C ---			---	GGGTAAAGTCCAGAGCCACAGGTGAACTCGCCGGTATTGAAGTCTTTGGGCCA/GC/GTCTGTAAATG ATCTGACTTCTCCAGAACCCCTCTCTCTGGAAGTCCAACTGTGCACTGAGCCCATTTGTAGGGA GCATTTGAACCAAAACCCAGCGACACTGCTGACATTTGACTTTTCAGCAAAACCTTGATTGACGGTGAC ACACCATGCTTCGAGAGGAATGAGG
WI-6141	80 T C AGGTACTT	CTTCTTAATTA AGCATCTACA		TGAAAAACCCCA GAACAGTG	GACTCTGTCTCAAGAAAAAATAAATTGAAAAATTGAATAATTATTAAAGCACCTTCTTAATTAAAGCAT CTACAAGGTACTTAT[C]CACTGTTCTGGGGTTTCAATCCTCTTCACCTTTTAGACTTCAGGAAATT CAGAAAAATGCATGAAAAACAGGATTGTTACATGCAGAGAAATAGGGGGAGATAAAAAATTTGTCTTTT CTC
WI-6450	45 T G TGTCACA	CCAATGACTT ATTCTATATCT		TTGTTTGAAT GTGTGGTACTT CT	ATAGGACAGTTTTTCTTCCAAATGACTTATCTATATCTTGTCACAT/GJAGAAGTACCACACATTTCA AACAGAGCCAGGCTATGCCAGGGTGGGATTATTTTCACGGTCATGGTAATATGCATGTAAAGACTA TTTTACTGGCCTCTTTTATGCATAAAACAAGGTTTGGTCTATTCACAAACATGTGTCAATACAG CAGTTGTCATGTCCTCTGGTACTAGAATATAGTCTTTTATAGAATATGTGGTTTAGAATAAAGCCACA AATTATCTATAAAACAACA[C/T]AAGGAACGAGGCTCAAAAGTGAACAAAAACGGCCTTAGTTTC TAAGTGAAGACTAAGACGATATAGGAAATATAATCCGTGACCCTTA
WI-7466c	141 G A TTGTCTCTGG	TTTTCACAGTC		AGTCGCATGCC AATTATAATT	GAACTATCCTTTAGTGGTCCACATTTTCTATTTCTGATCTTTGGTCACACAGGGACTTTCTGGGCT ATGAAATAGTCTATTTCAGTGAAGTATCATATAAAGACATGCAAAACCTTTTCACAGTCTTTGT CCTGG[G/A]AATATCTCACAAAATTAATTATAAATGGCATGCGACTTTCTGATTTAGCCTGACAGG ATTGTCTCTT
WI-7466b	80 T C GTC	GACTTCTGGG CTATGAAATA		TGCTTTTATG ATACTAGTTC ACTGAA	GAACTATCCTTTAGTGGTCCACATTTTCTATTTCTGATCTTTGGTCACACAGGGACTTTCTGGGCT ATGAAATAGTCT[C/A]TTCAAGTGAAGTATGTAATAAAGACATGCAAAACCTTTTCACAGTCTT TGTCCTGGGAATATCTCACAAAATTAATAAATGGCATGCGACTTTCTGATTTAGCCTGACAGGA TTGTCTCTT
WI-9814	104 C A ---			---	TGCTTTTAAAAATAACAATGACCACCCTGACACCATAGTCTGTCTCCATTTGCCACGCTCTCCTC AGTAGAATAAGACAGGACTTTGCTGGTGTCTAT[C/A]TTCTCCTTCAGAAGAGCACTTTGGCCCT CATAGGCATTCCATAGATATTGTTGAATGAATGCTTTTTCATATTGATTCCTACATTGATACA TTCTCAGGAGGACATTTGGCCTAT
WI-9720b	55 A G ---			---	CCTCTAACAAAGAAAACTTGACTTCTCAACTCAAAATACCCCTCTCTAATAATTTTJAGTAGTAACCA AAATATTCTTCAAAATAAATTAAATCTTTTAATTAGAAGAAGCAACAGTGTAGAGGTAGTACATTCA CCACC

WI-9720a	47 A G ---	---	---	CCCTAACAAAGAAACTTGACTTCCTCAACTCAAAATACCCCTTCTCTAGJATAATTTAAGTAACCA AAATATTCCTTCAAAATAAATAATCTTTAATTAGAAAGAACACAGTGTAGAGGTAGTACATTCA CCACC
WI-9825	123 A T ---	---	---	CACGCTAAGGCAGGATGTGGCTATGAGATACTTTGCATTGTCTGTCTGCACACCTTGAATCTGCC TGCTGGCTCCCTTACTTTACCTCTGTCTGTATGTCAGATGAAGGCTCAGGGTGCTATJGAGGATTAG TAAGATCTCTTTCTAAAGACAGGAGAGATTATTACAAGAAGAACTCACACAGGTTAGTTTGCAAT TAAGAAATGCCAGCTTTTGCTGTGCATCATCTTGAACATTAATCCACATG
WI-9748	74 C G ---	---	---	CCACTCAGTAAATCAATTTGTAGCATTATTTCTAAAGATTCTAAATTTTATATGTTTACCCCTTT GTCATTTCGTCAGACCAAGTACATGTTTTCACACAGCCATCTTCTTTTCCCTGGAATCTTTCAGAAT TACAGTTATGATGTCTCTTTTATATCCCCA
WI-9943	91 T C ---	---	---	TGAGGCTATGATTCAGATTGTGTAGTACTAATACTATTAAAGCAATTTCAATGTTGTGGCACTGTT CGTTGTGTTTATATCCATCTTCCTCTATTTTAAATTTCTACTGAGCAGAAAAAATAATGTATACATT AACCTTGTCTCCCTATTGTACCTTTTAAATTTGCAATTCACACCTTCTCTTTTGTCTATTTAGGGA
WI-9891	39 T C ---	---	---	AGGGCCCTTCACAGATCCGTGAGCTCAACACTGCCTCTTTCJAGTGAGCCTGTGAACCCCAAGAC GGCTGGTCAATCAGTGTCACTCTCTCTTTCCGGACACTATCTTTAAAGAAAAAAGAGTGT CTTTGAATGTATCCATTTATCCCCAAATAATCTTGTTTAATAAATCCCTATTAGGCCAAATCCAAT GTGCTGAATAATCTGCCAAGCATGTCTATCTACACAAAAGGATTGCAAA
WI-9897b	84 C T ---	---	---	CTCAGAAATTAATCAGATCTTCCCCAAATGTCATGATTCCTTGTCTCAACATCCTATTTTCCCTCAAAC ATTTATCTAGCCTGTATJCAAGTCAATCCAGTGAGGCTGTTTATTCAATCTATGTGAAATTTTGAGCA ACCCACAGGATTAGAATTAGCATCTTATTTTGTACCCACATTA
WI-9897a	83 A T ---	---	---	CTCAGAAATTAATCAGATCTTCCCCAAATGTCATGATTCCTTGTCTCAACATCCTATTTTCCCTCAAAC ATTTATCTAGCCTGTATJCAAGTCAATCCAGTGAGGCTGTTTATTCAATCTATGTGAAATTTTGAGCA ACCCACAGGATTAGAATTAGCATCTTATTTTGTACCCACATTA
WI-9935b	115 C A ---	---	---	AGATAACCCCTGGAAAACTAGAAGAAATTAATAACGTGTGCACTJACCTCACCAGAACTGGAAAGG CTGACTGTGTTCTTATGGGTGCTTGACTGGCAGGGGGAGTTCAGACA/CJAGCCAAGAAAAAGCC TGATAATTAAGAGGCACCTTGCAATTA
WI-9935a	42 C T ---	---	---	AGATAACCCCTGGAAAACTAGAAGAAATTAATAACGTGTGCACTJACCTCACCAGAACTGGAAAGG AGTCTGACTGTGTTCTTATGGGTGCTTGACTGGCAGGGGGAGTTCAGACA/CJAGCCAAGAAAAAGCC TGATAATTAAGAGGCACCTTGCAATTA
WI-9983	146 C T ---	---	---	CCTGTTAGGTGCCAGAGTCCATGCTCTTGGCCACAATGTTAGGCTGCCCTCCCATTTTCTTGTCTTGA TTCCCAAAACCCCAAGGTTCTCACCCCAATCTGATCAATGCTAGTGGTCAAGGCTGTCAGGGTAA AGCAATTATGA/CJTAGACACAAGACAAGAGAGTAAAGTTGCTGCTCAAGAGAGAGACATAA AAACAAATGGATCTGGAACATAAGTAAGGCTTCGAGGAGGAGGTGAGCAAGG

WI-10019	139	A T A T C T	TGATGTAATGC TATGTAGCAA	TTGATTACTGT GCTTAGGGGA	ATATCAGTGGGTGAGTATACAGCAATCTATTTTGGTTATTTATGTGTGCTATAAAATCAATGGTTCTA ACATTTCAAATAGATCTTTTGGCTTCTGCTCAGATGCTTTCAATGATGTAATGCTATGTAGCAAAAT CTA/ATTTCCCTAAGCACAGTAATCAAGGCCCTTCTACCCCA
WI-10020b	122	T A T T T	GCGAGAAAAG AAATCATGAC	GACTGTTAAT TATTTAATCAT TAGTCTGG	TTTACTTCATTGTCATCTTGACTCGTATTAAATAAAATATGTTAACTGGCTCTGAAAAGAATTTAGGC ATGCATAGAGAAATAGCAGTGTTTTATGGCGAGAAAAGAAATCATGACTTTT/TA/AAAAATACC AGACTAATGATTAAATAAAATTAACAGTCTAGGGTCCGGAAGTGGCTAAAGCAGTAGTAGCCCT CCTTAGA
WI-10020a	39	T C A T A A A T T	TGTCATCTTGA CTCGTATTAA	AAATTCCTTTTC AGAGCCAGTTA AC	TTTACTTCATTGTCATCTTGACTCGTATTAAATAAAATAT/CTGTTAACTGGCTCTGAAAAGAATTTA GGCATGCATAGAGAAATAGCAGTGTTTTATTTGGCGAGAAAAGAAATCATGACTTTTAAAAATACC AGACTAATGATTAAATAAAATTAACAGTCTAGGGTCCGGAAGTGGCTAAAGCAGTAGTAGCCCT CCTTAGA
WI-10064b	170	C T T T T A C A T G	CCTTTAGATAT ATTGTGATTGT	ACCTTTCTGAA GCCAGATTTC	TCTGAGTCTTTCTGAGACACTTGCCATGGTCAAGGGTAGCAGGATCAGGAGGCATTATAATAAT ATAATTTGCAGAGCATCTCTCTCTATGCACCAGATATTGGTGACACTCTGTTTAAATCCAGTATCC CTACTCCTTTAGATATATTGTGATTGTTTACATG/C/TTGAAATCTGGCTTCAGAAAAGGTTAGGTGTT T
WI-10064a	54	C A C A G G G A A G G	GTAGCAGGAT	C A A A T T A T T T A T T A T	TCTGAGTCTTTCTGAGACACTTGCCATGGTCAAGGGTAGCAGGATCAGGGAAGG/C/AJATTATAATA AATATAATTGCAGAGCATCTCTCTCTATGCACCAGATATTGGTGACACTCTGTTTAAATCCAGTA TCCCTACTCCTTTAGATATATTGTGATTGTTTACATGCGAAATCTGGCTTCAGAAAAGGTTAGGTGTT T
WI-10289	29	T C C A A A C T C T T	TCTCTGTCCC	ATTCTTGTGT ATTGAATGGAA TTAA	CCAGGGATTCTCTGTCCCCAAACTCTTAT/CTTTAAATTCATTCAATACAACAAGAAATTTATAGAA TATGCACCACATGCCACAAAGACACCCCTTATATTAGT
WI-1319	40	A T A T C T T T	TGGCACTTAG AACATAGTTT	GCCACACACCC CTATGGT	AAGAAATCCTTGTGGCACTTAGAACATAGTTTATTCTTTT/TTJACCATAGGGGTGTGGCTTATCT TTTACCTGGCATGGCTTAGGTCTGTTTATAATTTGGTATCTTTTGCCACAAAGAGTCTGTTCTGAC AGTCTTATGATCTCTATTTTAAACATTAACTGGTGCAGATGTTTAAAACTTGTGAACCTGCAGC
WI-10316	104	T C C T C T T	CTGTTGATTT CTACCTCTATT	GCTTTGGAATG TATCCAAAAGT TT	AGCAACGTGTACAACCTTAGTGAGGTGTAATCAGAGGATCTATATTATTCACCAGTCACCAACCCCTG GACTATAGTCTGTTGATTCTACCTCTATTCTCTTAT/CTJAAACTTTTGGATACATTCCCAAAGCAT CATGGTCACTTCCAGTATGAAAGGATGTTTAAAGCCCAAGCC
WI-2572	61	C T ---	---	---	AGTGAGTTGTGCACAAATTTGGAGACATCTGTGACCCCAACTTAAACACTTCTCCCAACA/C/TTJAC AAAGTTAACACTTCAGTTACCAGGTGATGATTGAGCAGA

WI-10368	31 C T	TGAAGCAACC	CAAGATATTAT	GAGGAAGCTGCCTGAAGCAACAGGCTGTGTTGCTACCCCTCTAGAGAAATAATAATATATCTT GAGATAGGGAGGAGCAGCCTGAGGACAGTCTGGGTTTTGTTCTACCCCACTGGGAAGCAGAATATCC TTCAAAGCTTTTTCCAGTGAGTCATGTTGCTGCTAACTATATGACCCCTGATGGATTGCCCTTTTCAGGG T
WI-10391	32 A G	ATGACTCCCA	GGGAGTTAGGA	CCTCCGTTCTCTGTCTCAGGTATGACTCCCAJAGTCAACTCTTGACTCCTAACTCCCATCTCGGTG TCTGCTTCCAGGGGACGCATCTGACACAGCCTTTTGCTGCTGTGACAAACAGAACATTGCGAGAAG TGATGCTGCGTGACCTCCAGGATA
WI-10567c	146 A C	GCAA	TGCCGCTTCCA	AGCGATGAAATTTATATGTTATGCTGACTGACTTACGGGGTGTCAATAAATAATATTCTTTTTCATATT TTCCAATTTAATACTAGAAATTTTACCACACAGAAATTTTAAACATTTTAAAGTTACCCAGAGCTTT CTAATAGCAAJACJAGCTACTGGAAGCGGCAAGAAATTTAAACCTT
WI-10567b	82 A C	---	---	AGCGATGAAATTTATATGTTATGCTGACTTACGGGGTGTCAATAAATAATATTCTTTTTCATATT TTCCAATTTAATACTAGAAATTTTACCACACAGAAATTTTAAACATTTTAAAGTTACCCAGAG TCTTCTAATAGCAAAAGCTACTGGAAGCGGCAAGAAATTTAAACCTT
WI-10567a	60 T C	CTTTT	GGTGAATAATTC	AGCGATGAAATTTATATGTTATGCTGACTTACGGGGTGTCAATAAATAATATTCTTTTTCATATT ATTTTCCAATTTAATACTAGAAATTTTACCACACAGAAATTTTAAACATTTTAAAGTTACCCAGAGT CTTCTAATAGCAAAAGCTACTGGAAGCGGCAAGAAATTTAAACCTT
WI-11153b	84 C G	TACTTTA	AAATCCAACA	CGTTGGGAATTTTCTATCTCACCTAAATATATGCGTGATTAATAATATACATTTTAAACAACTTCAAA TTGCTTTAAGTACTTTACJGJGAAGACCTTGACTGTGGATTTTGGAGTTTTTCTTTTATTTCTTAATA AAACATGCATATTTAAGTTGTGACGCAAGATGACTTATATGTTAATATCTGATATCAGCATCCCTT TATGTATT
WI-11153a	33 C A	AATTATG	GCAATTTGAAG	CGTTGGGAATTTTCTATCTCACCTAAATATATGJAJGTGATTAATAATATACATTTTAAACAACTTCTC AAATTTGCTTTAAGTACTTTACGAAGACCTTGACTGTGGATTTTGGATTTTCTTTTATTTCTTAATA AAACATGCATATTTAAGTTGTGACGCAAGATGACTTATATGTTAATATCTGATATCAGCATCCCTT TATGTATT
WI-2616	125 T C	ATCC	CCATGGCTGTA	GTTGTGAAACTCCAGTATCATTTCCCTCAAAACCAGCTTAATCACAATCACTTTTCTTTCTGTA GAGCTCAAACTCAGTCTGAATGAATTTGCTGCACAAATGTAACAAGAAATGATGATCTATTCJACTGGG ACTACAGCCATGGAGAAAAGCAATGTAGTCAGCAAAATGTTAACAG
WI-11163	58 C T	TGAGA	TTTGAGGTTTT	TGACTCAAAGGAAACACACAAAAAGTTTACCAGTGAATATGACCAAAATGAGAJCTJAAAT TTGTTAAAAAAAACCTCAATGAATGAAGAGACAAATATAGTTCAAAGATTCAGGTTCAATATTGT ACCTACAAAATAGGGATAGTCATGGGTTTGGCAGACTTTCTTTCTTTCTTTTCTTTTGTJGJCTCTTA GAATCCATTTTGTCTTTTGGCCAGCATCCCTCTCCCATATTTTAAAGGAGAGAAATTCACCTTTTCTCT CTGTTGGATGATCACAGGTTCTGCTCTCCCATCCAGAGGAGGAGTACTATTACCCCATGGGGTGCAT AGAGAGGATTAAACAGGGTGATGCCTGCAATGGGAATATTGAAAAACC
WI-10656	59 T G	---	---	



WI-11169b	154 T G TTTT	TTAACCAAGA GTTTTTCATTC	CTAACTTAAA ATCCTCATTC	AAATATAA	CAGCATAGAGGCTGTAGTACCTTGAGTTAGATTCTCTATCGAGAAAGCAATAAGTGAAAGTAA CTGACTTGAAAAAATAAATAAAGCCTAAAGTAGTGCCTTTTAAACCAAGAGTTTTTCATCTTTTT TTTAAAAAAGAGCAGACATG/GTJTATCATGTGTTCTGATAATTTTTTATATTTTGAATGAGGATT TTTAAAGTTAGCAT
WI-11169a	95 A G TTGAAAA	AATAAGTGAA AGTAACTGAC	AAACTCTTGGT TAAAAAGCAC	TACTT	CAGCATAGAGGCTGTAGTACCTTGAGTTAGATTCTCTATCGAGAAAGCAATAAGTGAAAGTAA CTGACTTGAAAAAATAAATAAAGCCTA/GJAAAGTAGTGCCTTTTAAACCAAGAGTTTTTCATCTTT TTTTTTAAAAAAGAGCAGACATTTTATCATGTGTTCTGATAATTTTTTATATTTTGAATGAGGAT TTTTAAGTTAGCAT
WI-10685	25 A G ---		---		CAAGTGCTTGGACCTTGGATAGGTC/GJACCGGCTGAAGTTGGACAGTTGTTGGTTAGGTTGGAG ACCAAAATTCAGTCATCCTGTAATATAGATCTTGTCTCTGCTAGAACTCTGAAATCTGATGCCCTGTCCAAGG AGAGATGGGAGACAGTCTCAATCTTGTCTAAATAATTCAAAATAGCCATGGGTTGGACAAAATAC AAGGTTAGTGTCTCTTAACCTTAAATGGGCATA
WI-10686	133 C T AAGG	TGCCCTGTCC AAGG	CAATCTCTAAA TTCATGTGTAG	ACACA	AATAACCTGTGGCACATAAGGCAAACTACTGAGCCCCATACAGAGTGTGTTATGTTAATATTATGAAA AAAGTCAAGAGAACAAAGATGATATAGTTCTGCTAGAACTCTGAAATCTGATGCCCTGTCCAAGG C/JTGTGCTACACATGAATTTAGAGATTGAATGAAATGGCAAAATTCAGAAAAAGGG
WI-11175	77 T A A	AAATGATTCTT TCTGCTCAAG	CTGTTCTCACA TTCTTTTTGAA	AA	GGTAGGATGATTCTAGATGCCACTTTACAGCCACTGAAATATATGCTCCCAATGATCTTTCTG CTCAAAAGAGT/AJTTTTTTTAAAGTATCTACTTATTAATCTGCTTTTTTCAAAAAGAAATGTGAGA ACAGTACAAAATGTGTTTCAGTATAGCAAAATTAATAATTAATTAANAAGTAAGAAAAAGGCCAAAT TGGGC
WI-10694	144 A G TATGAGTTTC	TGCAAAATGCTT TATGAGTTTC	GGCATTTTGT AAGGAGGAAA		TAGAGAGGCTTTTCAGTTTCAGGTTGGAGGGTGGTGAGGTGAGATTCACTTCTTAGAAGCACTGGC TATGTACAGAAAGATAAACTCTGAGAAGAACTCAGTTCTTAAAGTGTTCAGTCTTTGCAAAATGCTTTA TGAGTTTTC/GJTTTCTCCTTTACAAAATGCCATCAATTCCTCAAGGAAAAAAGGCTTTCT T
WI-2716	23 T C C	TGAATTCATCC AGAAAAACAG	TCTCTTTTCTC TCTTGTGTCA	TTC	GTGAATTCATCCAGAAAAACAGCT/CJGAATGACAACAAGAGAGAAAAAGAGAAATAAAGGTTTTTGT ATACGACAAGTGGCTCAAGCAATTTCTCTGCTCCAGTGCATGGAGCAGTG
WI-10719	115 T C GCCATTCTAG	TGACTCTCAAG GCCATTCTAG	GCACTGCCAGC AGCC		CAGGCCCAACTCTGTGCTAATTAAGTGTGTTTAAACAGACACCTCAGTCACACAAAGTTCTCTGTATGT GCCCCACATAAACAGTTACTGGAGGATGACTCTCAAGGCCATCTAGT/CJGGCTGCTGGCAGTGCTT TTCAGCCTGCTGCCATAACTAA
WI-10721	40 A G CTTGCCA	TGGCTCTGCTA CTTGCCA	GAACTCCAC ATAAATAAT	CTCA	CAACCAATTCAGATTATTTTTTGGCTCTGCTACTTGCCAA/GJATGAGATTTATTTATGTGGAGTT TCTGAAGATCCCATGGTAAATAGATTCTCTCCCTGCTTAGGTTTGAAGAAGTTGAA

WI-11204b	88 T C ---			GCACACGAAATTGATTAAATTTGGCTGACCTTTGAGGAGGAGAACACAGGAGTTGAGGTAAAAAGGGTG AAAAAGAAAACCTTCCACCTTTT[C]JATTTAAAGTAACATAAAGGTATTATGTACATTTTAAAGTGAT CAAAAAATTTAAATTTGGGAAGAGATTTAGTGAATCAGAAAAATAGCTGAGGAAATTTATTCAGAAG GCAACATC
WI-11204a	80 T A AACTT	GTAAAAAGGG TGAAAAAGAAA	TGATCACTTAA AATGTACATAA	GCACACGAAATTGATTAAATTTGGCTGACCTTTGAGGAGGAGAACACAGGAGTTGAGGTAAAAAGGGTG AAAAAGAAAACCTTT[A]CACCTTTTATTTAAAGTAACATAAAGGTATTATGTACATTTTAAAGTGAT CAAAAAATTTAAATTTGGGAAGAGATTTAGTGAATCAGAAAAATAGCTGAGGAAATTTATTCAGAAG GCAACATC
WI-10732	80 C A ATTGGTCACT	GCTGTGTCTTC ATTGGTCACT	AAGAACAAATG CATAACAGAA CTTTAA	ACATGTAATTCCTTTAGTGGTCAGCCTTCCTTACCCCAAGAAATATCCCTGGTTTATGTGTGTCTTC ATTGGTCACT[C]JTTAAAGTCTGTATGCAATTTCTTGAGTCCACATAGGTGTTAATCATTTCCA CACCACCTCTGTTTAAACGTGIC
WI-11206	127 A T ACTC	GGTGTGTTTT CTGTATGTACA		TAGTCTTTTCTTTGTACGAGTGTCAATAAAGAAATACCACCTGTGCACATTTGTAAAGATAGCACAG AGAGAAAGCATTACAGGGCACAGCACAAACATGAGGTGTGTTTCTGTATGTACAACCT[C]JCCAA CCATTAGGATTGTCACTCTCATATATAGACAGAATTCAGTGGTGTGATTGAAATTCACACACATGGA ATAAGTCTA
WI-11215	68 C T ---			GAAAAAAGTTTTAATTGGATTGCTTAGTTTGTCTTAAATTTGACCTACTTTCAGATTTTATTTAGT [C]TJATTTTTTCTATAATATTTCTTGAAGTGATGGATTTCTATAAATTAAGGAAACAGATATTT ACACAGAGAAGACAGGATTGCTTGAATTAGTATAACATTTTATTCCAAGCCCCCATTCACCATGT TTT
WI-11219b	89 G A AGAGAAA	GAGAGAATAT TCCAAAAAGT	GGTCTCTAAT TTTTGTACACT TTCT	ATGAAAAATGCATTAGAAAGAAATGGAGGATAAAATTGAGAGAATATTCAAAAAGTAGAGAAAAA GAGACAAAGAGATGAAAAATAGGA[G]AJAGAAAGTGTAGAAAAATTAGAGGACCATTTCTATACAG TCCAATATTTGAATAATAGTTATTCAAAAAAGAGGCAAGAAAAATGAAGGGAGAAAAATCCAC AAAAATCTC
WI-11219a	18 G A ---			ATGAAAAATGCATTAGAA[G]AJAATTGGAGGATAAAATTGAGAGAATATTCAAAAAGTAGAGAA AAAGAGACAAAGAGATGAAAAATAGGAGAGAAAGTGTAGAAAAATTAGAGGACCATTTCTATACAG TCCAATATTTGAATAATAGTTATTCAAAAAAGAGGCAAGAAAAATGAAGGGAGAAAAATCCAC AAAAATCTC
WI-11222b	136 G A GGCTGG	CATACCACTGC AGTTGIGA		AGCCACAGTGGAAATCATTTACACTACCGAAATCAGCAAATGCTAAAAATGGGCTTTGGATTTTGT TTTTGTTTTTCCATAGACCCACCCTTGAACCTATTGTTAAACATTTACCAGCATACCCTGCGGCTG G[G]AJTCACAACCTTGGCTACCAGGAGAACCTGACACAGACTTCGTAATTTGCTTTACAGGCTACTGG AAAGCC

WI-11222a	25	C T A	GCCACAGTGG AATCATTTAC	TTTAGCATTT GCTGATTCG	AGCCACAGTGGAAATCATTTACACTA/C/TGGAATCAGCAAATGCTAAAATGGGGCTTTGGATTTT TGTTTTGTTTTTTCATAGACCCACCGTTGAACATATTGTTAAACATTTACCAGCATACCACCTGCGG CTGGGTCAACAACCTTGGCTACCAGGAGAACCTGACACAGACTTCGTAATTGCTTTTCACAGGCTACTGGA AAGCC
WI-10775	39	C T CACTC	TTTATGCCATA TTAATTCATTA	CTAGATGTATT TGCTAAGAAA ATATGATG	TTGCAAGTTTGTTTTATGCCATATTAATTCATTACACTC/C/TACATCATATTTTCTTAGCAAAATACA TCTAGACACCTGGCACTCAGTAAGGATATTCCTGGCAGATAATCATTTGTTATCATTTAGACATTGCA GGAACCAACCATATGGATGGATAAATGTGTGTTTAAATGAAGGCAAGCAATTA
WI-11226	165	A C ---		---	TTGCATGCATTTATACGAAAGGAATTAATAATATCTTCCTTATAGTTGAATTTTAAAGTAAAAATAAA GTTATACATATAATACAAAAAGTTGTAAGTATAGTAACAAATGAATTAGAAAAATGTCAGTGGTTGC TAGTACAGGAATCAAAATTTGGACTATGAACA/A/C/GACATAGTTGCTAAGGATATTCACACAAATTA TTCATGA
WI-10778	62	A G G	GCAAGGGAGG AACATTTACA	CTGGTGACATC AGAGATGGAC	CAGTGGCTGGCTACTGACAAAACGTAACATCGTGGCAGGTGGCAAGGGAGGAACATTTACAG/A/G/G TCCATCTCTGATGTCACCGACGAGGGCCAGGAAGGTTGATCTGGAG
WI-10789	21	C T GCTCTAGACC	GGGACACACT GCTCTAGACC	TTGAGGGACCC TGGA	TGGGACACACTGCTCTAGACC/C/TJCCCAGGGTCCCTCAAAGGTGGGTGTAGAGGCCCTACTGCCCT GCCCTGGGACGACAGGACATCAGGGCCTTAGTCTCTCGGGACAGTGAAGGGGCCACCAACC
WI-10810	58	C T GCAGGAATT	CATCTTCATGG GCAGGAATT	CAAAACCCTAAG AAACACAGAA ATG	ACAGAAAATGCCTAGTCTTGTAGCAAGAGAGGAAGCATCTTCATGGCAGGAATTC/TJCATTT CTGTGTTCTTAGGGTTGTGGCTGGCCATCAGTTCACATCAGCCCTGTCCCTGATCCAGCAACATT TCCGTAACCTACCCCTCTAGAAGTCATGCAAGAGAAAATGATGA
WI-10828	23	T C ---		---	GGACCAACACAGAAATTAATCTGGCAT/CJAGGGTTCTTAAACTATTTCTGCAGAACATTAGTAAAGT TTAAATAAGGATCAGGCTACCAGGAATACAGTTAGGGAACATGTGGATGAATATTTCTTTAGTAGAG GACTTCTAAAAGGCTATAATATTGGATACATTAGGCTCATTATGAATCTCAAAGGAGCATGTAGT AGGGCATATCTAA
WI-10832	91	G C AGGCTCTCC	CATTAATCTGC AGGCTCTCC	CCTAACTGCAG GTGACTTAGAA A	TATGCCTTCCCAACGAGCCATCCACGCTGCTTAGCACAAAAAATAGATACATCATCTGAATG GGCACATTAATCTGCAGGCTCTC/CJTTTCTAAGTCACCTGCAGTAGGCTGCAGACACTGTGTA TACCATATAAATCTGATTTCTGAGCAGGAGGGCAGATGAGAGAAGGGCTGCTCCGTGAAATAC TAGTTCCGG
WI-10834	96	C T GTGTTAAT	AGAATTAAC GTTCAAAAGT	TGGCCCTATAA AATTGGTATTA AG	GATTTGAGTATTATCAAAATTTGCCCAAAGACCATTAACAAGATTTAATAGTTAAAGCCAAAACATA AAGAAATTAACGTTCAAAAGTGTGTTAAT/C/TJCTTAATACCAATTTTATAGGGCCACCATTAACCT CTGAAGAAAGGTCAGCATATGCAACTAAATTTCTAAAGTCCAGT
WI-2287	24	T C ---		---	GGATGATGTTCTGTGTCCTTTAT/CJAAAGCCTCTTGATCCCCAAATGTGTAATATTTTATTCT TGGTATTTCTCGCTTACCCATAGTCACCTGTCAAGTGTCCACCCCT

WI-2296	81 A	GA	TGTTACTTTGA TTCTTTGCTGT	GCAATCACAC AGCTAACTGG	TGGAGGGTTAGAAATGACAGTGGCATCTAGAAAGGTCTCAGGCTTTAGAATAAGTTGTTACTTTGA TTCTTTGCTCTGAC[A/G]CCAGTTAGCTGTGTGATTTGCAGAAGGTACATTGTTTGTG
WI-2300	77 G	T	GGCACAGAAG CCAGTCATAC	GGTTGGGTCAA TTTTAAAGCA	TTTCATCATGCTGCTTCCCTGGAAATTTCTTTAATTGAGCGGGGAGGTGGTAGGCACAGAAGC CAGTCATAC[G/T]TGCITTTAAATTTGACCCCAACCATTAAGAAATAGCATTTCA
WI-2371	55 G	T	GTCCTTGTTCTT CCAGCTTCT	CAAAGATTGAC AGCCACCAC	CAATGATCCCCCAACATTTCCAGGAAAGGTCTGGTCTTCTCCAGCTTCT[G/T]GTGGTGGCT GTCAATCTTTGACATTCCTGTCTTGACGCTGTATAATCCATCCTTGCCCTCCAGCTTTACATGATGT TCTCTCCGTGTGTGTG
WI-2395	122 A	C	GAACATATTT GTAGAAAAT	TCACCTTTCTA TTTATTCTGAA	GGGGGCACAAATTTAGCTACAGTGCATATTTAAAGATAACATAGAAATATCATATAACTTGGTTTAC TGAAATCTGAAAACTTAGGATGAGTGAACATATTTGTAGAAAAATTTACTATCCAA[A/C]CTGAATTC AGAAATAATAGAAAGGTGAATCATCTTATATCATTAAGAAAGCTAAATTTATTAGTAACAATCTTTA CATTTACACAAACCCA
WI-2437c	192 G	A	---	---	CACCAGCCACCACCTACAACTCCTGTGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCAATCACAACTTTCTAAATAATAGACACCAAAAAATTTCCCAATGCTCTAA ATAGATGGACTCAACCCCTTCTCCTTCTGCAAGAGGCAATCGACGAACATCACAGTG[G/A]GCTGTG GTGCCAAGGACGCATTATG
WI-2437b	179 G	A	---	---	CACCAGCCACCACCTACAACTCCTGTGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCAATCACAACTTTCTAAATAATAGACACCAAAAAATTTCCCAATGCTCTAA ATAGATGGACTCAACCCCTTCTCCTTCTGCAAGAGGCAATCGAC[G/A]AACATCACAGTGGGCTGTG GTGCCAAGGACGCATTATG
WI-2437a	128 G	A	---	---	CACCAGCCACCACCTACAACTCCTGTGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCAATCACAACTTTCTAAATAATAGACACCAAAAAATTTCCCAAT[G/A]CTC TAAATAGATGGACTCAACCCCTTCTCCTTCTGCAAGAGGCAATCGACGAACATCACAGTGGGCTGTG GTGCCAAGGACGCATTATG
WI-2440	71 G	A	GCAACCTACT GACAAATTA TTTATGTT	AACAACTCTGC TATTGGTCTCA C	CAGTAGGAAACGGGTCTTCTCTAGACCCCTCCAGAAAAATAATGCAACCTACTGACAAATTTAATTTTA GTTG[G/A]GTGAGACCAATAGCAGAGTTGTTACCTGCAGAACT
WI-1356	123 T	C	TGTTTAGGAA ATAATGACAA	TGTTTACAAC GTACCAAAACAT	CTGTAACCTACACACATCCTCCTGTAACTCTAGGTTACTTGTATACAAAACACAATGTAAATGCT ACATAAAATAATTGTACATATATTGTTTAGGAAATAATGACAGAAAAAGCC[T/C]GTACAT GTTTGGTACAGTTGTAACCCAGCCATTTTCCCCCAATAATTTCAATCCACAGTTGGTTTAAATCCACAG AAACCCAGGAATG
WI-2886	46 C	A	CAGAGTCTGG GGGAGAAGA	TTGCCATGCTT TATCTCGTT	ACAGTTAAGAAAAAGGCTGCAGCCGTTGCAGAGTCTGGGGGAGAAGA[C/A]AACGAGATAAAGCATG GCAAGACCACGCTGAAAGTATCCAGGGTCTGTATGTGCACATAGGAAGATCACATTACCTCAGCA TAGGAGGAGGGCTAGGCAAGGAAAGGTGTCAGAGAAACAGAGGAGCGTT

WI-2906b	77 T A ---		---	CCTGAACACCTGGAGCACTCCCTCCCTGGACACCTTCATTCTGCTGGAACCTTTGCTGGAATGCTCTTTCCCTCT/AJGAGCTTTGCTGGCTTACTTTTCTTTTCTTTAGGTTTACAGCTTCAAAGTGACCTCCTTAGAGTTGGTTTGTGCTGACCAACAAA
WI-2906a	50 A C TCTTGCTGG	GACACCTTCAT	AGAGCATTCCA GGCAAAAGT	CCTGAACACCTGGAGCACTCCCTCCCTGGACACCTTCATTCTGCTGG/AJGACTTTGCTGCTGGAATGCTCTTTCCCTCTGAGCTTTGCTGGCTTACTTTTCTTTTCTTTAGGTTTACAGCTTCAAAGTGACCTCCTTAGAGTTGGTTTGTGCTGACCAACAAA
WI-1736	175 C T ---		---	TACTCCTCATTCTCATGTCCCTAGACGCTACTCAGATTTCCATGCCCTGAAACATTTATTTCCCTAAATAGATTTCCACCCCGACACTATTTACACAGAAACAGCATGGAGCAGTTTGGAGTCTGGCTCTTAGAGAACCTTACTTAAGGACAGTGGTTTTCOCATCTGCTTCCA/CJTAGAGATCTAGGGTGTCTTTTGGAAACCACCTTGG
WI-1851	136 G A GTGTTAAGTA	GCATTGAATT AACTATAGAT	CAC TAGCAATG TTAAACTGAAG TTG	AATACCCACGCTCAACACCATCACACTGATCATCAATCAGGTTTTAACATATTATCTGGGGAGGACACAAACATTTAGACCATAGCATTTGAATTAACATATAGATGTGTTAAGTAATTATATAACATGGTACA/GAJACAACCTCAGTTTAACATTGCTAGTGATTCCATGTGGATACCATGTACCTTCTTACATCATGTGA
WI-3000	62 G A AGAGACCCG	CCCAAAACAC	GCCACTATAGG ATTGACTAAGA CTCA	CTGATGTTTGGGAAGCACTGTCTTACATCTCTAAATGTGAGCACCCCAACACAGAGACCCCG/AJTGAGTCTTAGTCAATCCTATAGTGGCAGTACCTGAATCAGTGCCTGGTGCATAGTAGACACT
WI-1754	177 G A TAGTC	TTTTCTCCCTT CTTAAAGAGA	AAAGTCGAATT GCTCTGG	ATGGATCTGCTCAATTATAGTCCCGAGATAAACAGCCCTTCTCCCGCCACCCCGGATTATTTTACTTAAGGGTTTAGCAAAATTCACCTGACAAAGAGTTAGGTTTCAACATTTGACCTCATAAAGTGATTTTTTCTCTTTCTGTTTTGTTTTCTCCCTTCTTAAAGAGATAGTC/GAJCCAGAGGCAATTCGACTTTCTGTAGCCACAAGATT
WI-3167	37 T A TAGATTG	AAATTC AAC ACAGATCTAT	TGTGATAGTTT TGAGATGGTG	ACAACACAGCAAAATCAACCACAGATCTATTAGATTCT/AJACCCCATCTCAAAACTATCACATCAAAGAAGCAAGGAGACATATTACTGGTGAGGAAGCCAAATTCAA
WI-3208	140 G A AGATAAAGA	GTGGAGTGGGC	TCACTCAAACT AGGCTTGG	CAAGCACACATTCAGGCAGTGGGCAGGTAGGGAAGGTGGGCAACTTGGCAGCAGAGAGAGGGAAGAAGTTCAGACCCGTTGGGTAGGATAAGTGGATCCAAACCCCTTTGTAGGCGCAGGTGGTGGAGTGGGCAGATAAAGA/GAJCCAAGCCCTAGTTTGAGTGCACACTGTGGGGATTCAAG
WI-1775	47 C T TTTTCTCTG	OCTGCATGGTC	AGTTGAGATTT ATGACAATGAT GTAAA	ACTCCACCAACAGTTTTGTGAGCCAAACCCCTGCATGGTCTTTTCTCTG/CJTTTTACATCATTTGTGCATAAATCTCAACTGACACATCAGTGTCTCTGCCACCCCA
WI-3402	55 G A ACAT	AGCATATTCA TTGATTTCCCTT	GAGGACTTAAA AAGGAGCAITTT G	CTGCCCTTTACATCCAAAGCCAGTTACTCGAGCATATTCATTGATTTCCCTTACAT/GAJCAAATGCTCTTTTTAAGTCTCAACTTTTAAAGCGGAAGTTGAGACATGCACAAATAGATTTCCCTTAGGA

WI-3416	33 C T	CCAAGTTGTA GCATTGAGAA	ACGAGCACAA CTACCTCTAAG AG	TCTGGTTCTCCAAAGTTGTAGCATTGAGAAAGTC/TCTCTAGAGGTAGTTGTGCTGCGTTAAAA TATGTTTTCAAGATAGTATCTCCCTGTTGTCACTTCTCCAAACAAGTGTACCAACAGCATTTGTTAAG GAAATGTGCAATGCTTGCTACCTCTGACGACAAACATAATTAATCCCATTTGCTTAAAAAGACCAGG
WI-3453	70 C T	TTCTTAGGCCC ATCAGAGAA	TCAATTTCCC CATGACTTC	TCCTATTCTTACAACAACAGAAATTAACAAATTGAAATCAGCTACTCTCTTAGGCCCATCAGAG AATTC/TGAAGTCATGGGAAAAATTGATGCCATGTGAATTGGAGAAACAGACAGGCATATATGGAG AATTACAGTTTACCAGGGACACAATCCCACTTCCAGAGCCATCATCTGTAAAGAC
WI-3474b	109 GA	---	---	CATGCTAGGTAGATCTGATCATGAAGTTTGAACAACCTTAAATCATCAAGTGTGTCAACTGGTTTGA GTCAGTTTCCCTAATTTTAGCACAGTATTTAATGAGGTGGTGTGGAGAAAAATTGATGGTTGCG TAGTTGAGTTTCTGTCCACC
WI-3474a	90 A G	AGTCAGTTTCC CTAATTTTAGC	CAACCATCAAT TTTCTCCCA	CATGCTAGGTAGATCTGATCATGAAGTTTGAACAACCTTAAATCATCAAGTGTGTCAACTGGTTTGA GTCAGTTTCCCTAATTTTAGCACAGTATTTAATGAGGTGGTGTGGAGAAAAATTGATGGTTGCG TAGTTGAGTTTCTGTCCACC
WI-3502	79 C T	CCTGGGTTTCT GGATGCT	GGGTGACCTG TCCTCA	TTTGACCCCATACATGAGAAATAAACCATAGAAATGTGGAAAAATAAACCGGGAGAGACCTGGG TTTCTGGATGCTCTCTGAGGACAGGGTCAACCCAC
WI-3600b	146 G C	GGTTCTAACC TGGATATAAA CATCT	CCAGTGCAGCC TTCCAT	TCACGGCAAGTTCTGCAGCAGTGTCTGACTCTGCTGCTTCCAGAGTCTGATTATCCATGCCCTG ATAGTTCTGTGAGCCACCTAACTGCTTCTGCTTAAAGTTATCCAGAGGTGGTTTCTAACCTGGATA TAAACATCTGCTGATGGAAGGCTGCACCTGGATGAGGTCACAAA
WI-3600a	78 T G	CCATGCCCTG ATAGTTCTG	GGAAACGAGTT TAGGTGGCTC	TCACGGCAAGTTCTGCAGCAGTGTCTGACTCTGCTGCTTCCAGAGTCTGATTATCCATGCCCTG ATAGTTCTGTG/GAGCCACCTAACTGCTTCTGCTTAAAGTTATCCAGAGGTGGTTTCTAACCTGG ATATAACATCTGATGGAAGGCTGCACCTGGATGAGGTCACAAA
WI-3678	125 GT	---	---	TAAATCATGCTTATTTTCACAAGGTAATCCACTCAATAGGCAATTGATGTGATCTCTTTCTGTAA GAAAGCTCTCATGCTCTTCTGAACCTTCTACTTACTGTGCTGTTATGATGCACTG/TCCCTTTTGG ATAGATGGTTGATAGGAGATGGGTTGTTAAAGACACAATTTACCTTGTGTGTTTCAGGCAGAAATAG ACTCTCTGTGTAACTCACTGAATGAGTTCACAAAGCCCTTATGTCTTAC
WI-3687	67 A C	---	---	AAAGCGATGTTGAGATACCACATTCATGAAAAAGTAAAAACACACACAAAAATATGACATAAAA T/A/AAAAAATCTATAGTTTATGAAAAATGACTTCCAAAAATTCAGAGAAAAAGTCACTTAAACAGG ATTCTCAATTCAATCCAGAAATCTCTCTGTCATCTTAACTTTGACTGCACAG
WI-3735	72 T C	CCTCAGTTATG TATCAAAATGA	GGCTCACCAT CATTGTTTT	TCTAAATGTGAAACCAAGAAATCTGACACGACCTAACTGCCAGTCTCAGTTATGTATCAAAATGA AAAACT/CJACACCGGTTCAATGAAAAAACAATGATTGGTGAGCCATGTCCCTTATTTAATGAAAA GATCTTGGGCAATTAACTC

WI-1819	51	C T	---			<p>GA AAAAGCAGGAAGCCAGGCAGGACAAAAC TTTTGAAAAAGTCTTTT CAGCAC/C/TTTCGTGGATCCG</p> <p>AAATTTAGTGTGATTTGGCAGGCAATGCGGGTAACATGTTCCAGTGTTTTAACTTGCACAGAAATTGC</p> <p>CAGATTAGCGATTGTTGACTTGTCCAATTAATGAAATGTGGAAAAAAGGGTGGTAACTGTT</p> <p>AAGCCTGCTGCAATGTTTAGACACGAGGGTGGGGTGGGAGGTGGAATACC</p> <p>GGCCTATTACATGACACTGGGCCAAGATCTTGCTCCCTTTCTTTCAATAGATAGACTAACTAGAAA</p> <p>ACTGCCCTGGCCAGGAAGATGGTTGTCTTCATCATCTCTGCTCTG/C/G/AGGCCCCAGGATAAGCA</p> <p>GGCA</p> <p>AGCAATGAGTTAACTCCTTACATGAACAGTCATTTAGTCTTCCTGACAAT/C/CGGATGTACCTAGT</p> <p>ATGGTTATCTTATCTGACAGACAAGGACACTGTGACACAGAGATTGTTACTTTGAACAAGACACAGT</p> <p>CATTAAGTGGAGAAGCCAGCATTCTAATCAGGCTCAGTGATCTGCCAAACCAACCCCTTCTGCTATAG</p> <p>CATC</p> <p>CAATGACCAATGTCTTTAGAAAGCAG/C/CGGAGAGGACACCCGACGAGACACACAGGAAGGAGTGAG</p> <p>GTGAAGATGAAGCAGTGTGACGCAGCCACAAGGTGAGGAAGAGCAAGGGTGTCTGGCCACT</p> <p>GGACCATTTGCCCTCAGAAGTACATTCAAGCCCTGGACGGTGTCTCTTAACACTGTGAOCTCAGGCA</p> <p>AGTCATGTCTGCTTCCTGAACCTCGGCTTCCTCACCTGACAAGTGG/C/G/TATCATGTGCTACACTGC</p> <p>AGTGTTTATAATGCTGCAT</p> <p>CTGAGGAGATTGATGCTACTTTACCTGAGGAAAC TTTTATTACCTCCCTGAGTTTGTTCCTTGCAA</p> <p>GACATTGCTGATTCTCTCAAGACTCACAGC/C/TAACCATCTTCATTGCTCTAGACCTATAACTAG</p> <p>ACTCAAGTCCCAGCAGGCCCTTAAAGGTAAAGTACAAAGTGTGACCCATGGGAGGTATGTTACGCTA</p> <p>CAAAAGAG</p> <p>CCACTCCCAGGCCAAGAGCGTCTATGAATCAT/C/AGCATTTGTTCTGTTATTGCTGTTACACAGAGT</p> <p>GGCAACTCTTGCAAAGGGAGGGGTACAAAGTGAATTTTAGATGCTGCAGGAGACGAAGGGTC</p> <p>TAATTACAGATTGCTCTTTGTTGTGCAITTTATTGCTCTCTTATGTAAACAATCACCACCAATTGAGG</p> <p>TCTTAGTCATTGCATG/C/TTGTTATAACAATATTGTCACITTAATAGGAAC TCAAGCATAGTTATGTT</p> <p>ACATTTATTGCTAACAGCAG</p> <p>TCCTCTCTGTAATAGGAAGTCTGATTAGATGCC TTTTGAGGTAGGTGGCTCTAAGATGGTAATT</p> <p>ATCTGTCCAAGTTTGTTCCTATAATTTAGCAACAATATCAACAGAA/C/G/GGCTATATTAGAAA</p> <p>ATTCTACCTGCATCCCCCTGGATCTGAACGTTCTTCATGATACT</p>
WI-3746	116	G A	---			<p>AGCAATGAGTTAACTCCTTACATGAACAGTCATTTAGTCTTCCTGACAAT/C/CGGATGTACCTAGT</p> <p>ATGGTTATCTTATCTGACAGACAAGGACACTGTGACACAGAGATTGTTACTTTGAACAAGACACAGT</p> <p>CATTAAGTGGAGAAGCCAGCATTCTAATCAGGCTCAGTGATCTGCCAAACCAACCCCTTCTGCTATAG</p> <p>CATC</p> <p>CAATGACCAATGTCTTTAGAAAGCAG/C/CGGAGAGGACACCCGACGAGACACACAGGAAGGAGTGAG</p> <p>GTGAAGATGAAGCAGTGTGACGCAGCCACAAGGTGAGGAAGAGCAAGGGTGTCTGGCCACT</p> <p>GGACCATTTGCCCTCAGAAGTACATTCAAGCCCTGGACGGTGTCTCTTAACACTGTGAOCTCAGGCA</p> <p>AGTCATGTCTGCTTCCTGAACCTCGGCTTCCTCACCTGACAAGTGG/C/G/TATCATGTGCTACACTGC</p> <p>AGTGTTTATAATGCTGCAT</p> <p>CTGAGGAGATTGATGCTACTTTACCTGAGGAAAC TTTTATTACCTCCCTGAGTTTGTTCCTTGCAA</p> <p>GACATTGCTGATTCTCTCAAGACTCACAGC/C/TAACCATCTTCATTGCTCTAGACCTATAACTAG</p> <p>ACTCAAGTCCCAGCAGGCCCTTAAAGGTAAAGTACAAAGTGTGACCCATGGGAGGTATGTTACGCTA</p> <p>CAAAAGAG</p> <p>CCACTCCCAGGCCAAGAGCGTCTATGAATCAT/C/AGCATTTGTTCTGTTATTGCTGTTACACAGAGT</p> <p>GGCAACTCTTGCAAAGGGAGGGGTACAAAGTGAATTTTAGATGCTGCAGGAGACGAAGGGTC</p> <p>TAATTACAGATTGCTCTTTGTTGTGCAITTTATTGCTCTCTTATGTAAACAATCACCACCAATTGAGG</p> <p>TCTTAGTCATTGCATG/C/TTGTTATAACAATATTGTCACITTAATAGGAAC TCAAGCATAGTTATGTT</p> <p>ACATTTATTGCTAACAGCAG</p> <p>TCCTCTCTGTAATAGGAAGTCTGATTAGATGCC TTTTGAGGTAGGTGGCTCTAAGATGGTAATT</p> <p>ATCTGTCCAAGTTTGTTCCTATAATTTAGCAACAATATCAACAGAA/C/G/GGCTATATTAGAAA</p> <p>ATTCTACCTGCATCCCCCTGGATCTGAACGTTCTTCATGATACT</p>
WI-3867	49	T C	CA A	<p>TGACCAATGTCT</p> <p>TTTAGAAGCA</p>	<p>TAAGATAACC</p> <p>ATACTAGGTAC</p> <p>ATCCG</p>	<p>AGCAATGAGTTAACTCCTTACATGAACAGTCATTTAGTCTTCCTGACAAT/C/CGGATGTACCTAGT</p> <p>ATGGTTATCTTATCTGACAGACAAGGACACTGTGACACAGAGATTGTTACTTTGAACAAGACACAGT</p> <p>CATTAAGTGGAGAAGCCAGCATTCTAATCAGGCTCAGTGATCTGCCAAACCAACCCCTTCTGCTATAG</p> <p>CATC</p> <p>CAATGACCAATGTCTTTAGAAAGCAG/C/CGGAGAGGACACCCGACGAGACACACAGGAAGGAGTGAG</p> <p>GTGAAGATGAAGCAGTGTGACGCAGCCACAAGGTGAGGAAGAGCAAGGGTGTCTGGCCACT</p> <p>GGACCATTTGCCCTCAGAAGTACATTCAAGCCCTGGACGGTGTCTCTTAACACTGTGAOCTCAGGCA</p> <p>AGTCATGTCTGCTTCCTGAACCTCGGCTTCCTCACCTGACAAGTGG/C/G/TATCATGTGCTACACTGC</p> <p>AGTGTTTATAATGCTGCAT</p> <p>CTGAGGAGATTGATGCTACTTTACCTGAGGAAAC TTTTATTACCTCCCTGAGTTTGTTCCTTGCAA</p> <p>GACATTGCTGATTCTCTCAAGACTCACAGC/C/TAACCATCTTCATTGCTCTAGACCTATAACTAG</p> <p>ACTCAAGTCCCAGCAGGCCCTTAAAGGTAAAGTACAAAGTGTGACCCATGGGAGGTATGTTACGCTA</p> <p>CAAAAGAG</p> <p>CCACTCCCAGGCCAAGAGCGTCTATGAATCAT/C/AGCATTTGTTCTGTTATTGCTGTTACACAGAGT</p> <p>GGCAACTCTTGCAAAGGGAGGGGTACAAAGTGAATTTTAGATGCTGCAGGAGACGAAGGGTC</p> <p>TAATTACAGATTGCTCTTTGTTGTGCAITTTATTGCTCTCTTATGTAAACAATCACCACCAATTGAGG</p> <p>TCTTAGTCATTGCATG/C/TTGTTATAACAATATTGTCACITTAATAGGAAC TCAAGCATAGTTATGTT</p> <p>ACATTTATTGCTAACAGCAG</p> <p>TCCTCTCTGTAATAGGAAGTCTGATTAGATGCC TTTTGAGGTAGGTGGCTCTAAGATGGTAATT</p> <p>ATCTGTCCAAGTTTGTTCCTATAATTTAGCAACAATATCAACAGAA/C/G/GGCTATATTAGAAA</p> <p>ATTCTACCTGCATCCCCCTGGATCTGAACGTTCTTCATGATACT</p>
WI-3898	25	A C	G		<p>TCGTGGTGTCT</p> <p>CTCTOC</p>	<p>AGCAATGAGTTAACTCCTTACATGAACAGTCATTTAGTCTTCCTGACAAT/C/CGGATGTACCTAGT</p> <p>ATGGTTATCTTATCTGACAGACAAGGACACTGTGACACAGAGATTGTTACTTTGAACAAGACACAGT</p> <p>CATTAAGTGGAGAAGCCAGCATTCTAATCAGGCTCAGTGATCTGCCAAACCAACCCCTTCTGCTATAG</p> <p>CATC</p> <p>CAATGACCAATGTCTTTAGAAAGCAG/C/CGGAGAGGACACCCGACGAGACACACAGGAAGGAGTGAG</p> <p>GTGAAGATGAAGCAGTGTGACGCAGCCACAAGGTGAGGAAGAGCAAGGGTGTCTGGCCACT</p> <p>GGACCATTTGCCCTCAGAAGTACATTCAAGCCCTGGACGGTGTCTCTTAACACTGTGAOCTCAGGCA</p> <p>AGTCATGTCTGCTTCCTGAACCTCGGCTTCCTCACCTGACAAGTGG/C/G/TATCATGTGCTACACTGC</p> <p>AGTGTTTATAATGCTGCAT</p> <p>CTGAGGAGATTGATGCTACTTTACCTGAGGAAAC TTTTATTACCTCCCTGAGTTTGTTCCTTGCAA</p> <p>GACATTGCTGATTCTCTCAAGACTCACAGC/C/TAACCATCTTCATTGCTCTAGACCTATAACTAG</p> <p>ACTCAAGTCCCAGCAGGCCCTTAAAGGTAAAGTACAAAGTGTGACCCATGGGAGGTATGTTACGCTA</p> <p>CAAAAGAG</p> <p>CCACTCCCAGGCCAAGAGCGTCTATGAATCAT/C/AGCATTTGTTCTGTTATTGCTGTTACACAGAGT</p> <p>GGCAACTCTTGCAAAGGGAGGGGTACAAAGTGAATTTTAGATGCTGCAGGAGACGAAGGGTC</p> <p>TAATTACAGATTGCTCTTTGTTGTGCAITTTATTGCTCTCTTATGTAAACAATCACCACCAATTGAGG</p> <p>TCTTAGTCATTGCATG/C/TTGTTATAACAATATTGTCACITTAATAGGAAC TCAAGCATAGTTATGTT</p> <p>ACATTTATTGCTAACAGCAG</p> <p>TCCTCTCTGTAATAGGAAGTCTGATTAGATGCC TTTTGAGGTAGGTGGCTCTAAGATGGTAATT</p> <p>ATCTGTCCAAGTTTGTTCCTATAATTTAGCAACAATATCAACAGAA/C/G/GGCTATATTAGAAA</p> <p>ATTCTACCTGCATCCCCCTGGATCTGAACGTTCTTCATGATACT</p>
WI-3901	114	A G	---			<p>AGCAATGAGTTAACTCCTTACATGAACAGTCATTTAGTCTTCCTGACAAT/C/CGGATGTACCTAGT</p> <p>ATGGTTATCTTATCTGACAGACAAGGACACTGTGACACAGAGATTGTTACTTTGAACAAGACACAGT</p> <p>CATTAAGTGGAGAAGCCAGCATTCTAATCAGGCTCAGTGATCTGCCAAACCAACCCCTTCTGCTATAG</p> <p>CATC</p> <p>CAATGACCAATGTCTTTAGAAAGCAG/C/CGGAGAGGACACCCGACGAGACACACAGGAAGGAGTGAG</p> <p>GTGAAGATGAAGCAGTGTGACGCAGCCACAAGGTGAGGAAGAGCAAGGGTGTCTGGCCACT</p> <p>GGACCATTTGCCCTCAGAAGTACATTCAAGCCCTGGACGGTGTCTCTTAACACTGTGAOCTCAGGCA</p> <p>AGTCATGTCTGCTTCCTGAACCTCGGCTTCCTCACCTGACAAGTGG/C/G/TATCATGTGCTACACTGC</p> <p>AGTGTTTATAATGCTGCAT</p> <p>CTGAGGAGATTGATGCTACTTTACCTGAGGAAAC TTTTATTACCTCCCTGAGTTTGTTCCTTGCAA</p> <p>GACATTGCTGATTCTCTCAAGACTCACAGC/C/TAACCATCTTCATTGCTCTAGACCTATAACTAG</p> <p>ACTCAAGTCCCAGCAGGCCCTTAAAGGTAAAGTACAAAGTGTGACCCATGGGAGGTATGTTACGCTA</p> <p>CAAAAGAG</p> <p>CCACTCCCAGGCCAAGAGCGTCTATGAATCAT/C/AGCATTTGTTCTGTTATTGCTGTTACACAGAGT</p> <p>GGCAACTCTTGCAAAGGGAGGGGTACAAAGTGAATTTTAGATGCTGCAGGAGACGAAGGGTC</p> <p>TAATTACAGATTGCTCTTTGTTGTGCAITTTATTGCTCTCTTATGTAAACAATCACCACCAATTGAGG</p> <p>TCTTAGTCATTGCATG/C/TTGTTATAACAATATTGTCACITTAATAGGAAC TCAAGCATAGTTATGTT</p> <p>ACATTTATTGCTAACAGCAG</p> <p>TCCTCTCTGTAATAGGAAGTCTGATTAGAT</p>

[illegible]



WI-5204	54 C T ...		...	TAGATTTGATTGATGACATAGGGAAGCCTTTGTAAATTTGGGTTTTGAAGAA[C/T]GAAGAAAA TGGAAAGGGAAGAAATGACAGAAACCAAGAGAGTGTGAGGGGCAGCAAATCCAGTTTGAAGTGA ATATAGAGTGTGACAGGGTGTG
WI-5215	70 A G C T C A A A A A	GGACCTTAAT ATTTAACAGA	AGATAATTTTG TAAAGATAGTT TTGGC	TTTTCCCTTATTTATTTAGGAAGCAAAATGTTTCATACAGGACCTTAATATTTAACAGACTCAAAAA TAT[G/G]CGCAAAACTATCTTTACAAAATTTATCTCCATAGCAAGTAGACATTTTAGCACATTTTCCT GTAGTCAAGGTTTTAAAGGCCAAATGAAGTTGACTAAAGACAAT
WI-4448	112 T G A T A A A	TTGTATCAAA GAGATGGGT	AATTAAGAA ATCTTTACATG GTTCITT	CCCTGAATGTCTTTGCTTCTCTCCCACTCTCTAGGGAACCTTTTCCATGTGAGGTGAAGGTTTGA AGAGTACTTTAATTAACCTTGATCAAAAGAGATGGGGTATATAAT[G/G]AAAGAACCATGTAAAGATTT CTTTAATTAGTGAATTCATCAGGGCTCTTCCACTGTCTATCAGTAAA
WI-4456	49 C T T A T A G T T C C	AGTTGAATTA TTCAGAAAT	TTTCCCTGTTAT GCATGAACITG	ACACATTTTCATTTTGCCTTAAGTTGAATTAATTCAGAAAAATATAGTTCC[C/T]CAAGTTTCATGCATAA CAGGAACACCAAGGTGGGCAATTGATTGAATTGT
WI-4461	49 A G C C T T C C	TCACTGTTATT TTAAAATTAT	TTTGACCTTTC ACCAATTTCA	CTGAAACTAATGAGGTGCTAAATCACTGTTATTTTAAATTTATCCTTCC[A/G]TGAATTTGGTGAAA GGTCAAGAATGAATCCACCTTTAGATTTCTGGAAATTTTATTTGGATGATAATGCAATGGGC CTACTGGATTTTACTTTGCTCAAGCCAGACACACGAAAGTATATAAAGAAACACAGTTAGTAATCTT TCACCTTT[G/A]TATTTCTCTTCTACCTCAGGGAATC
WI-4465a	41 A G A C A C G A A A G T	AAGCCAGACA ACACGAAAGT	GGTGAAGATT ACTAACTGTTT TCTTT	CTACTGGATTTTACTTTGCTCAAGCCAGACACACGAAAGT[G/G]TATAAAGAAACAGTTAGTAAT CTTTCACCTTTGTAATTTCTTCTTCTACCTCAGGGAATC
WI-1949b	160 T C T A A T C	GAGTGAATAA ATGAATGCCA	TGAGAGGTGGG GACAAAA	GGGGTTAGGACCTCGAGATCTTTTCAAGAAAGCACAATTCAAACCATAATGGCAGTGCACAGGTAACCA GTGGTGAGATGCTCTGAGTT[G/G]CAAGGCTGCTGACATGGCTGAATATATATTTGAAGAAATAAA GGAGTGAATAAATGAATGCCATAATC[T/C]CTGTGTTTTTTGTCCCACTCTCAGACCTTTCCCTGG CACA
WI-1949a	86 T G A T G C T G A G T	CAGTGGTGAG ATGCTCTGAGT	CCATGTCAGCA GCCTTG	GGGGTTAGGACCTCGAGATCTTTTCAAGAAAGCACAATTCAAACCATAATGGCAGTGCACAGGTAACCA GTGGTGAGATGCTCTGAGTT[G/G]CAAGGCTGCTGACATGGCTGAATATATATTTGAAGAAAT AAAGGAGTGAATAAATGAATGCCATAATCTCTGTGTTTTTTGTCCCACTCTCAGACCTTTCCCTGG CACA
WI-4529	64 T C A A G A T G	CCAAGTAAGT CTATCAATCTG	TTCTAAAAATA ACACTTCCTGA AAAA	TGAGAGAGTTTTGGATTATTCATCCTCTGCAACACTCCCAAGTAAGTCTATCATTTCTGAAGATG[T/C] GAGTTCTCTTTATATCCTATGATTATTTTTCAGGAAGTGTATTTTGAATATAAACTCCTGGGT CCCATCCAGGCTAGGGTCAATGGCATCCATCCGCTGGACAAGATGGGCCCTAGGATCATTTT

WI-4540	110 A G	GCACCATGTGG CATCC	GACAATGCAGC CATGCA	AGCTTTTCCTTTCTTAAAAATTGGTGCCATAGTACTGGCTTCTGTGTGCATCAGGAAGCAAGCCTAT TGCTCGGTAAACAGTACTTTGCAATAAGCACCATGTGGCATCC[A/G]TGATGGCTGCATTGTCCAGTC AAATGAGACAACCTTCCTAT
WI-4582	226 T C	---	---	AGCAAGCATCTGGCAAGCCTCGGTGACCAGAACATTAATACCAACAAACACCCTGCTCCAAATGT CCATGTTAATGCAATTATAGAAGACTCCAGTAGCATCAAGGCCAGTTTAACTTATTCCTGTACACA AATACTTTATGGGAGACAGCATTTAATCAATCAATAATGACTCGGTTTGGCTGTACAAGCAT AAACAGAACGCTTGCAAAATATGGTT/CJCTCTTGTAGAAACCATTTGAT
WI-1965	105 G C	AG GCCATTGAGG AAGTGTTAA	GAATGGATGGG TCATCTCT	CAAGGTTAGTTTAACCTGGGGGCAACACAAAAGTTATGAGTACTCAATAACCTATGTTCAAGGG TAACCAACACCTTTTGCCATTGAGGAAGTTTAAAG[G/C]JAGAGAGATGACCCATCCATTCTCTGG GCTTCTTATATGACACCATACTATCCACACAGATGTGGAGTCATTTATTTGGTTGGTGTATGACAGT CATGG
WI-5248b	99 C T	TTG CACTGTTTCT ATTGACCGTAC	AGAAAAGAG AAGAAGGAA AAA	TGTTTAAACCACATACAGTTTGTGCTGCTACGTTGTTAGAGCAACCCAGAAAATTAACACGCCCTAG CATTTTCACTGTTTCTATTGACCGTACTTG[C/T]CTTTGCTTTTTTCCCTTCTCTCTTTCTG CCCTCTTTTAACATA
WI-5248a	38 G C	CTACGTTGT AGTTTGTCTG	TTTTAATTTT TGGGGTTGCT	TGTTTAAACCACATACAGTTTGTGCTGCTACGTTGTTA[G/C]JAGCAACCCAGAAAATTAACAGCCC TACCATTTTCACTGTTTCTATTGACCGTACTGCTCTTTGCTTTTTTCCCTTCTCTCTTTTCTG CCCTCTTTTAACATA
WI-4596	69 T A	TGAAGCAGAA AGCACTGTGA	CAGGAGATGGG CCTAATAATG	CATTGGTGGTCCAACTCTCGGTGACATTACTCTGTTGACTTTGCTGTAAGCAGAAAGCACTGTGA CT[A/C]ATTATTAGGCCATCTCCTGCCTGAAGCCTGCTACAGCAATTTGTAAACATATGGCATTTGGG ACATACTCTGAGCCCATCACTATTGACAAGATTCTCCTTTTAAACA
WI-5252	119 A C	---	---	GAAATAGGGCAAAATTAAGACTTCAATAATTAAGAAAGCTTGGGAAAGGATTTGTGATGATCATTG AATCTGTTTAAATACAGAAATTAATACTGAATACCTGTGTGAATCATTTGCTTT[A/C]TACCATGTACA TATTATATGAATTAACAATGTAAATAGTATGACTAAGAAATATTGGGCCCT
WI-4606	61 A G	CT GCAATGCTAG AAAATTATGC	TTAGGTGCTTA AGTTGCTACT TGG	TGCAAAAAAGGAAAATGATAACCAGGACTGTTGTTCAAGCAATGCTAGAAAATTTATGCCTA[A/G]C CAAGTAGACAACCTTAAGCACCTAAGGCAGAAATGAAAGTTTCTCTGTGCTATTAGTCTCTATTCA ATTACCATTTATCGGGTAATTAACACTGGAAAGTAATGCCAGGCTAATTGTTAGATTATGATAAT TACACGCTTTTGCTATGCT
WI-5257	77 C A	GAGGCATGAA GCAAAGAGG	CCAGGGGCAGA TGAAAG	CAATGAGAAGTTACCAGATGGGGCAAAATTAAGCATATGAAAATACCAAGTGTGGCAGAGGCATG AAGCAAGAGAGG[C/A]CTTTCATCTGCCCTGGTGGGTTTTTCACTAAGTCAACATGTCTTTGCCCTCC CGGATGAAAAGATACCCCTTCTATGACTCAGCAATCCACTCTAGGTATGCACCCCTAAACATGGGTG GCAAAAT
WI-4649	50 C T	TTCCGAATG GAGACCATCT	TGTACTAGGTG TACTTACAAGA AATCATC	TCACGTGTTAGAAAATTTCTTCTCCTCAGTGAGACCATCTTTCCGAATG[C/T]GATGATTTCTTGTA AGTACACCTAGTACATCTATGAGCACACAATTAACAAGTACTTGTCTACCTGAATTTGTATTTTTTAA AAATCCTCCCAATATTG

WI-4650	148	A	G	GCACAAAGAA AGTATAAGTT G	CTGAAGTGTTA AACTGGATTG G	AACTGTGGTATGTTGTTGTATTTTCTGGAGAGTCAGTTACTCTCACTAGATCAATAAAGGG GACTTGGGAACCAAGATATCTAAGACATTTAATCCTAGAAGCACAAGAAAGTATAAGTTGTCTC TTATATTGCTTTT[A/G]CCAAATCCAGTTAACACTTCAGTAACGTT
WI-4677	82	T	C	TCCAAAAGTG ATTAGGTGAA AAA	TTTCAACAGTG TCATTATTCAA CTT	AATTCAGATTTTGAACATACGTCGACATTTTGAAAAAATTGTCCAAAAGTGATTAGGTGAAAAAT GAGTTGAAATAAATG[T/C]AAGTTGAATAATGACACTGTTGAAAATGATGAATCTGCTTTCAAATTC CATGGAAAGGAGACTAGAACACAGCAGGTTTATAGGGGAATACTCAT
WI-4698	135	C	G	---	---	ATGATGCTATCATGAGGAATCTGTAGAAAAATTTTCCCTGGCAATGATTCAATAAAGTTTGTCC TCACCTGGGAACCTGTTATCTGTGATGTCAGTGACATTTCTTTTTCACGGAAGAAAACTTCAA C/GTTTCGAGAAGGCTTAGATTATATCGCTGAAGCCCATCTG
WI-4722	88	G	A	TGCACATATGG AACACCACAC G	AATATGGAATC TGCATTTCAGTT G	CTTCCCATTTCTGCCAGTTAGATGACTGCTCTCCACCAGCCTAGAAAAAGATGGGAGATTATTTTC TGCACTATGGAACACCACAC[G/A]CAACTGAATGCAGATTCATATGAACTACTGGGAATCAGTGA AAG
WI-2020	145	C	A	---	---	GCCACAGTAAAGAGGAAAAATGGAGCCATGTAACAGAGGAGAGCTTTCTGAAGATCAGTGTATTGTCA TAAAGGTCAGTAAATCACCTTTGATGGTTGAGATTCAGAAATTCAGAAAAACGTGAAATTTATGAGTAACCATGGG TCAACTATGAT[C/A]CCAAAACAGCAGTGTGTCTAAAAAATATGATAGTTTCTTCTCCTGTCCACC GCAATGAAAAGGAGTT
WI-2028	176	T	C	TGTTACGTTT CCTGTCTCATC GAA	GGTTGGAACCT CAAATTACCTA GAA	GACTACAGCGCACAGACAGGCATTGTGTGGCTTGCACAGGTTTGGTTTGTAGTTAGATT TGAATCCTTTTAAAGAAAGAAAGTGCTCTTCAAGTTTACTACAGACCTCATCATCTCCTGGTTCTCTTG CACCAGTCCACTTCACCTGTTACGTTCCCTGTCTCATC[T/C]TTCTAGGTAATTTGAGTTTCCAACC TGTTGG
WI-2033	183	T	C	GGTGCTAGA ACTAATCCCTC A	CAGTGGTTCCA CGTTCTCC	ATGTGTATGAGCTCCACATTCGCAGATTCACCAACTATGGATAGAAAAATATAGTATCCCAGATGG GCAGCCCCAAGGATCAGAGGGCTAAATTTTAAATTTTCCAAAGTTATACAGGACCGAGTGTGGAAATTT AGCATTTCTGGTTTGGCATCCATCAGGGTGCTAGAACTAATCCCTCA[T/C]GGAGAACGTGGAAACC ACTGATATACCAAT
WI-4745	131	T	C	---	---	TTATGGATACATGTTTCTGGTGAAGGACAAGAGTTGAAGCAAAAGGACAAAGGAGATCAACTGGG TAGAATAACTCATCGATCCACAGGCTCCTCCACCATTCTCCATCTACTTTCTACTCTGA[T/C] AGGCAGACTTATATGGAATAAGGGA
WI-2034	150	T	C	CCACAGTGCA CCAAGGAC	GGGTAAGAT AGAGTGCAGGT CC	CCACGACTATGCTTTCAGAGTCCCTGGTACTGACAGAGAAGGCTTTGAGGACCATGTGGCGCCCAAGA CCTCCTCTGCGGTTTCAGTGAAGAGACGATGAACCTCTCATCTTCTACAGCAGCTGGACTTCACCA CAGTGCACCAAGGAGT[C/G]GGACCTGCACCTATCTTTACCCCTCCGACACCCAGATGCTGAGATGCC ACACTCTGAGTG

WI-2038	155	C T	TGTCCTTTAA GTGTGAAGT ATTAATTAG CA	ATTTCTCTTG AAAGAAACAT CA	TCAGGTGACAAGAAAAAGTCACATTTCTTCAATCACTCACCATTTGCTGTTATTGTCTCTTGCAGTGT ATCCAAAGGATGTCACATTTTGGAACTCTGTAGATCAGAAAAAAGTGTGCTTTAAAGTGTGAAGTATTA ATTAGATTTCTATTTTGATA[C/T]GATGTTTCTTTCAAGAGGAAATTTGTGTAAGAGGATTTCCCAT TGCATTTCCATTGGC
WI-4782	113	C T	GATCAGAAG ATAACTAGAA AATGC	GAATCTTCTG GTTATTTTCT GTTG	TCATTGACTTTTAGAGTTCTTCAGTCTTTATGTCCTTTTCTTTAGAAAAAAGTCTAGGCTAGGAGAA CACAAATTCAGTTCTCTCCAGATGCAGAGATACTAGAAAAATGC[C/T]GAACAGAAAAAATAACCA GAAGAGTTCAATTATGGTTTTTTTCCAGAACGATTAC
WI-4788	65	A G	GCATAGAATC ATCTTGCTAAG TTCC	GGATAAAAT AAAAATTTGGC ATAA	AGGAGAGTTTGGCTCTTTTCCGACTCTTGGAAATTCAGTGCATAGAAATCATCTTGTCTAAGTTCC[C/G] JTGAAGAAAAATATGCCAAAAATTTAAATTTATCCAAACTTTAAGTCGAGATTATAATTGATATTT AAAAAACTATATTGAGTCTTTCTAAAAAGATGGCGTATCACTCTA
WI-5300	38	T C	TCCAGAGAC CACTTCATTC	ATTTCAATC CAAAA	CTTACTTCCAAAGTGTTCCTCAGAGACCACCTTCAATTC[C/T]TTTGGATTATGAAATAGAAAGAGT AGGTGTTATTATCTCTTTTACCAAGGTGAAATTTGAGGCTCAGAGACAAGGTAGATGATGAGCCCA AGGTCAAGTGCAGAGCCA
WI-4818b	121	G T	TGATAATGG GCCCTGTT	CCCTCCTTTA TATGTATGCCA GA	TATAATGTTTTGTTCCATAGTTGCCATAGACTAGGTTATGTCCACACATGAATAAACAAATCTTATATA ATAATTTATCAAGAGGAAATATACATATGGGGTGATAATGGGGCCCTGTT[G/T]CTCTGGCATA CATATAAAGGAAGGCTAA
WI-4818a	43	A G C	TTGCCATAGAC TAGGTTATGTC	CATATGTATAT TTTCCCTCTG ATAAAAT	TATAATGTTTTGTTCCATAGTTGCCATAGACTAGGTTATGTCC[C/G]CACATGAATAAACAAATCTTAT ATAATAATTTATTTCAAGAGGAAATATACATATGGGGTGATAATGGGGCCCTGTTGCTCTGGCATA CATATAAAGGAAGGCTAA
WI-5317	139	T C	TTCCATTTCTG GTAGCAGGT	GATGCAAAGA AGAAATGAGTC C	TTTTTCCATTTGTTTGATCTTTTGTCTGAGCCCTTAGATCTCCTTTAAATTAATAGCAAGGTTAAT AATATAATAATATGATGTTATATTTACAATTTCAACTCAACAGGAAATTCATTTCTGGTAGCAGGT ATAT[C]GGACTCATTTCTTTGCACTATTTCTAGGTTATTTGCAGCCCCGAGATCTACCCAGG
WI-4888	56	G A	GCAAGATATA AAGATTAAAGA AAAGATAACA	CAATCCACTA CCTCATTTATT CA	AAATGAGTAACCCCAAGTTACTCGGCAAGATATAAAGATTAAAGAAAGATAACAAGA[G/A]ATGAAT AAATGAGGTAGTGGAAATGCTTGATAAAGTGGAGTAGTGCCTT
WI-5328	44	A G		---	AACATTTTTTAACCATGCTACATTTACAAACACTGAAAGACAG[G/A]AAAAAAGAAATATTTTG CCTCAAAAAGCTCTTAAGAGATTATGTAATAAAAGAAAAAATATGAATCAGAAAAAGGAAAGAAAT AGAAACACGTGATACTGGAAGGAG
WI-4897	93	A G		---	GCCTTTTGAGTTTAACTCTTTTGAAGTGTCTTTTTTTTCCCCACTAGGTACTCTCGGCCCAAT CCCCAAAAGAAAAAAGCGCTTGG[G/A]GIGATAAACACATCTTC
WI-5345	29	G A		---	CCCTGCTATAGGTCAGTTTAAAAATCCT[G/A]CCTGCTATGGTTGCTTTGTTGAAGCCACATCCACT GAGGTATATCTGTCTGCATTTTCTATATCACTCAGCTTCAGATCCACTCCATCAACTTGCAG

WI-5370	143 T C	AATAAGATGG TACCTTAACTA	CAAAGTTGGTA CAGAGAATTTG AAA	TGCATGTTACTTCTTGGAAATCATAAAGGATCTGAGAGCCTACAGTATATGGCAACATTAAACCAAT CTTTTGAATAATTTACCTGTATCCCATCATGGTTTCATTTGCAAAAAATAAGATGGTACCTTAACTA ATAAAACAATTCJTITGAAATCTCTGTACCAACTTTGCTTTTC
WI-9711b	423 T A		---	GATCTCCTTCATCCCTCTCCAGAAGAGGAGAGGAGAAACACAAGAAAGAAACGCCCTGGTGCAGAGCC CCAAITCCTACTTTCATGGATGTGAATGCCAGGTGAGGAGACGGCTTCTGTAGTGGGAAAGCAC TGGACCTCAACAGTTGGAAATGTTAGTGTAGTGTAGTGTCTCGTATCCTTGAAGCTGTGCAGCAGCTT CAGTTTCTCGCCTGTGGAAATATTTCCCTGATACCTCTTAAATTTGAATG
WI-9711a	390 C A	---	---	GATCTCCTTCATCCCTCTCCAGAAGAGGAGAGGAGAAACACAAGAAAGAAACGCCCTGGTGCAGAGCC CCAAITCCTACTTTCATGGATGTGAATGCCAGGTGAGGAGACGGCTTCTGTAGTGGGAAAGCAC TGGACCTCAACAGTTGGAAATGTTAGTGTAGTGTAGTGTCTCGTATCCTTGAAGCTGTGCAGCAGCTT CAGTTTCTCGCCTGTGGAAATATTTCCCTGATACCTCTTAAATTTGAATG
WI-9702c	345 G A	---	---	GGAGGAATTTACGGGTGAATGGACTGCTCCCGCTCCTGAGTTCAGTCTACTCAGCCTGAGGTTGCAG ACTGGTCTGAAGGTGTACAGGTGCCCTCTGTGCCCTATTAGCAATCCCTACTGGTATGTATCAGGAT AGAGGTGAATCAAGCTGATATTTGCAACTTCTCAGTCTTATTTCTAACTTTAATGATCTCTGTGACTT TTATACTAGCTTTAAGAGGTTTTCATCCAGTGTGCTACAGCATCTGATAG
WI-9702b	344 C T	---	---	GGAGGAATTTACGGGTGAATGGACTGCTCCCGCTCCTGAGTTCAGTCTACTCAGCCTGAGGTTGCAG ACTGGTCTGAAGGTGTACAGGTGCCCTCTGTGCCCTATTAGCAATCCCTACTGGTATGTATCAGGAT AGAGGTGAATCAAGCTGATATTTGCAACTTCTCAGTCTTATTTCTAACTTTAATGATCTCTGTGACTT TTATACTAGCTTTAAGAGGTTTTCATCCAGTGTGCTACAGCATCTGATAG
WI-9702a	179 C T	---	---	GGAGGAATTTACGGGTGAATGGACTGCTCCCGCTCCTGAGTTCAGTCTACTCAGCCTGAGGTTGCAG ACTGGTCTGAAGGTGTACAGGTGCCCTCTGTGCCCTATTAGCAATCCCTACTGGTATGTATCAGGAT AGAGGTGAATCAAGCTGATATTTGCAACTTCTCAGTCTTATTTCTAACTTTAATGATCTCTGTGACTT CTTTTACTAGCTTTAAGAGGTTTTCATCCAGTGTGCTACAGCATCTG
TIGR- A003N21	49 C A	---	---	TATAGTATTTAACGAAGCCTAGAAGCAGCGGCTGTGGGTGGTATTGGTTC/AJAGCATATCTTAGGT ATATAATAACTTTGAAGGCCATAAGCTTTAACTGGAGTGGTTGATTCCTTTTAAITTTTATGGGA GGGTTTGGATTTTAACTTTTAAATGTTGTTAAATATTAAGTTTTTGTAAGAAAAACCATCTCTG TGATTACCTCTCAATCTATTGT
TIGR- A004V30	203 C T	---	---	AGAATGGCTACTTCATAGGCGAGAGCAGCCACTTTTGGCTAATTTTAAACATCCAAAGCTAATAAT AATCAAGAAGAAATAGAGAACAATTAAACAAAATAAATTTATGTTCTATTTGGGAATACCTAATATCAG ATACTAACAAAGTACAGTGATAAGAAATAAAAAAGATAATAATCACACATACCTTCTAGGTTAGTAGA AAAGC/G,TCTTCTAGGTTAGTAGAAAAAGTT

TIGR- A004W22	232 C A ---	---		GGATAATCAGTACAATAATGGGACCTTAAACTGCTGTGATGACAGAGTGAGGGCTGGGCGAGTG CCCGAGGCGAGGGAGGACAGTGGACAGGGATGCTCAGTGGTGGAGCCACAGCCCTGGGCTCTGGA TGGGCGATGGGAATGACCAGGTTCCACATCATGCACAGAGGGCTGTAGCTTGAGTCCAGACAG GCCTGCCACATTTGGTGTGCTGCCCGCCCTAC/ACTGGAGATGCTCTAAAA
TIGR- A005D24 b	138 C T ---	---		CATAGAAAGGAGTCTTTGAGTATTGTACAGTTTGAATACTCTTTGAGATAATTGATTTCATATTC TGTGGCTTTCAACCTCCATTTACCTCTTGTCATCCCAACATCTTTATAGAGAAATAGAAACCCAA CTC/TTTCCACCAATTTAGTTGATTATCATCTGATTTTCACTCAAGATGCAGCTCCTAAGATTATT GTTATGTTAAATTCATAAATCCTTACCTTTAATAATTAAAGGAAACAAT
TIGR- A005D24 a	123 A G ---	---		CATAGAAAGGAGTCTTTGAGTATTGTACAGTTTGAATACTCTTTGAGATAATTGATTTCATATTC TGTGGCTTTCAACCTCCATTTACCTCTTGTCATCCCAACATCTTTATAGAGAAATAGAAACCCAA TTTCTCTTTCAACCAATTTAGTTGATTATCATCTGATTTTCACTCAAGATGCAGCTCCTAAGATTATT TTATGTTAAATTCATAAATCCTTACCTTTAATAATTAAAGGAAACAAT
				TGAGTCTGACGAGGTTGCAGCCAGGGCCAGTGGAGGGGTCTGGGCCAGTGCACCTTCCGGGGCC GCATCC/CTGTAGTTCCACTGCTCTGTGACGTGAGGCCATCTTCACTCTTTGAAGCGAGCAG TCAGCATTTAGTAGTGGGTTCTGTTCTGTTGGATGACTTTGAGATTATCTTTGTTCTGTTGGA GTTGTTCAATGTTCTTTTAA
U03735	74 C G ---	---		GGTTGTCTGGCATAGCCATGCTGGTAGCAAGAGAGAAAAA/TC/CAACAGCAAAACCAACACA CAACCAAAACCGTCAACAGCATAATAAATCCCAACACTATTTTATTTTATTTTATTTTATGCAACCC TTGCCCCAGTGCAAAAGACTGTTACTTTATTATTGATTCAAAATTCATTGTGTATATTACTACAAA GACGGCCCCAAACCAATTTTTC
U39840b	42 T C ---	---		GGTTGTCTGGCATAGCCATGCTGGTAGCAAGAGAGAAAAA/TC/CAACAGCAAAACCAACACA CAACCAAAACCGTCAACAGCATAATAAATCCCAACACTATTTTATTTTATTTTATTTTATGCAACCC TTGCCCCAGTGCAAAAGACTGTTACTTTATTATTGATTCAAAATTCATTGTGTATATTACTACAAA GACGGCCCCAAACCAATTTTTC
U39840	56 A C ---	---		GTGGCATCGATCTGGACCGTCCCTGCCCCACTTGCTCCCC/G/ATGAGCACTGCGTACAAACATCCA AAAGTTCAACAACACCAGAACTGTGTCTCATGGT
WI-8997	41 G A OCCC			TATACCACITCCATTTGATGATGGAATGCTGCTGTTTCATGACCAACTTTATGGCTAGATGGGTCAGAA AGCACCCAGTTTCATGATAGGAGTTCAGGTTCATGAGTGTGAGTGTGATGACCCAGAGTCAACATTTCAG TTTCCACCAAGGCCAGTAACAGGCCAAGAGCTGCTCTCAAAAG/AGAGAGTAGTTATCTGCAGA AGATGGCAGGGCCTTGCTCCGAAAGCCTAGAGACCCGCTGATTACCT
WI-7008	180 A G ---	---		GGTCCCACGAATTTGCTGGGGAATCT/CTGTTTCTTCTTAAGACTTTTGGGACATGGTTTGACTCC CGAACATCACGCGGTCTCCTGTTTCTGGGTGG
WI-9005	26 C T	GGGAATCT	AAA	

WI-7593	46 G A ---	---	TTTTTTGCTCTGGACACCCACTGCTCCAGGATGAAAGGAGAG(G/A)AATGAGATCAGTTTTGGA CACTTCCTCTTGAAATATAAGAAATCAACAAGTTACAGTCATGTTGGGACTTCTTCTCTCTCCAA
WI-6962	78 A G ---	---	AGTGCATCTGGGGAAAGGCTCCAGTGTTATCTGGACCAGTTCCTTCATTTTCAGGTGGGACTCTT GATCCAGAG(A/G)GACAAAGCTCCTCAGTGAGCTGGTGTAATCCAAAGACAGAACCCCAAGTCTCC TGACTCCTGGCCTTCTATGCCCTCTATCCTATCATAGATAACATCTCCACAGCCTCACTTCATTCCAC CTATTCTGAAATATTCCTGAGAGAAACAGAGATTTAGATAAGA
WI-7059	43 C G ---	GCTCCTCGCTG GGTCA	GCAGAGAAGAGAACCATGCCAGGGGAGAGGCCACCCAGCCATC(G)GTGACCCAGCGAGAGCCAA CTATCCCAAATATACCTGGGTGAATATACCAAATCTGCATCTCCAGAGGAAATAGAGAAATAAA GATGAATTGTTGCAACTCTTAAAAAAA
WI-9063	53 A C TT	TCTACTTTCTG CCTTGGGT	AGCAGCCATCACATGATCTGTTTTTACCACCTTCACTGAAAGACACCATTTAT(A/C)TACCCAAAGGG CAGAAAGTAGAACTTACTATTCAATAATGTTTGACACAATTTGGAATTGTC
WI-7079	293 T G ---	---	AAGGGCATTGAGACTATAAAGCAGTAGACAATCCACATACCATCTGTAGAGTTGGAAC TGCAAT CTTTTAAAGTTTATATGCATATATTTAGGGCTGTAGACTTACTTCTCTATTTCTTTCCATTGCT TATCTTGAGCACAAATGATAATCAATTATACATTTATACATCACCTTTTGTGACTTTTCCAAAGCCC TTTTACAGCTCTGGCAATTTCTCGCTAGGCTGTGAGGTAAC TGGGAT
WI-9074	38 A G AAA G	GACAGATTTT GACCTAGTTCC TT	TGGATGCCGAGGTAAAGTTCTTTTGTCTAAAGAA(G/A)AAGAACTAGGTCAAAAATCTGTCC GTGACCTATCAGTTATTAATTTTAAAGGATGTGCCACTGGCAATGTAAC TGT
WI-7104b	249 C T ---	---	GGAGTTGCCCTTCTAAGGAAGGAGATCTTAICTTTCTGGTTGGCTTGACCAGTCACGTTGGGA GAAGAGAGAGAGTGCCAGGAGACCTGAGGGCAGCCGGTTCCTACTTTGGACTGAGAGAAGGGAGCC CCAGGCTGGAGCAGCATGAGGCCACCAAGAGGGCTTGGTTCTGAGGAAGCAGATGTTTCATGCT GTGAGGCTTGCAACAGGTGGGGCCACAGCACCAAGCAGCATCTTTC/T
WI-7104	157 C A ---	---	GGAGTTGCCCTTCTAAGGAAGGAGATCTTTATCTTCTGGTTGGCTTGACCAGTCACGTTGGGA GAAGAGAGAGAGTGCCAGGAGACCTGAGGGCAGCCGGTTCCTACTTTGGACTGAGAGAAGGGAGCC CCAGGCTGGAGCAGCATGAGGC(C/A)CAGCAAGAAAGGCTTGGTTCTGAGGAAGCAGATGTTTCAT GCTGTGAGGCTTGCAACAGGTGGGGCCACAGCACCAAGCAGCATCTTTCCT
WI-8974	34 C T AAGA ACTCA	TGTAGGCTGA GCTGGC	CATACATGAGAGCCCTGAGCCCTCAAGAACTCA(C/T)GCCAGCTCAGCCCTACACCAGTTTCCACC TGGAGTTGATGCAAGGGCAAAAGGCAGTGCCATGCAAGCTGTTAA
WI-9161	61 C T CCTGGC	GCTTACAGGAG AGACTAGACA GGAA	CTGTAGGGTGACGTTAGCATTACCCCAACCTCATTTTAGTTGCCTAAGCATTTGCCTGGC(C/T)TTC CTGTAGTCTCTCTCTGTAAAGCCAAAGAAATGAACATTCCA
WI-9014c	93 T C ---	---	CCCTGTTCCCATGCTGACCTGTGTTTCTCTCCCAAGTCACTTTCTCTGTTCCAGAGAGGTGGGCTGGAT GTCTCCATCTCTGCTCAACTTTAT(T/C)GTGCACTGAGCTGCAACTTCT

WI-9014b	44	C T	---	---	COCTGTTCCCATGCTGACCTGTGTTTCTCTCCCGAGTCATCTTTC/TGTTCCAGAGAGGTGGGGCTG GATGCTCCATCTCTGTCACACTTATGTGCACTGAGCTGCACTTCT
WI-7023b	206	C A	---	---	TCTGAGAGAAATGACTTGTGGAGACACCTGCAGATCCCTATGGGTTTGTGACAGACCCCTGCGTGCT CAGTGCCCTTTAAGTGCATCCGCTGTGCTGACTTTGAGTGGATCAACATCTGTCTACGGGTCCCC TCTTTTGGCCCCAGTATTCATGGCAGGGTTTGTGGACACCTACTAGCTTCCCTTCCCATTCACAC A/C/AJACACACATCTTCTCTACCCAAAGCTCTGGCTGGCAGCACTAA
WI-7023a	56	A C	---	---	TCTGAGAGAAATGACTTGTGGAGACACCTGCAGATCCCTATGGGTTTGTGACAG/A/CJCCCTGGGT GCTCAGTGCCCTTTAAGTGCATCCGCTGTGCTGACTTTGAGTGGATCAACATCTGTCTACGGGTGTC CCCTCTTTTGGCCCCAGTATTCATGGCAGGGTTTGTGGACACCTACTAGCTTCCCTTCCCATTCAA CACACACACATCTTCTCTACCCAAAGCTCTGGCTGGCAGCACTAA
WI-7093	54	C T	---	---	CTGAATCCCCCTCTCTGCCCTGGCTGGATCCGGGACCCCTTGGCCCTTCCCTCTGGCTCCAGCC CTACAGACTTGTGTGACCTCAGGCCAGTGTGCCGACCTCTCTGGGCTCAGTTTCCAGCTATG AAACAGCTATCTCACAAAGTTGTGTGAAGCAGAGAGAAAGCTGGAGGAGCCGTGGGCCAAT GGGAGAGCTCTTGTATTATTAATATTGTGGCGCTGTGTGTGTGTTA
WI-9171	62	G A	---	---	ACATATCTGAAAAATGTTGAAAGCCTAAGCCAGGAATAAAGAAAAAGTAGAGATAATAATCA[G/A] TTCTTTACAACCGATGGTAATTAAAGCTTGTATTCAACAGACTTCATGC
WI-9174	47	T C T	---	---	GTGTGAGACCATCATGTTGCCAGTCTAGGACCCCATCTCTCTATTTAT/CJAGTCCCTGTCTCTATATA CCCTCTAGAAACAGAAAGCAATTTTAGGCAGCTATGGTCAAAATTGAG
WI-7753	52	A G	---	---	AAGCCAGATGCACATCCCTGGAAAGGACATCCATGTTCCGAGAAGAACAGATTA/GJATCCCTGTATT TCAAGACCTCTGTGCACTTATTTATGAACCTGCCCTGCTCCACAGACACAGCAATTCCTCAGGCTA AGCTGCCGGTCTTAAATCCATCCTGCTAAGTTAATGTTGGGTAGAA
WI-9186	76	G A	---	---	AAAGAACTACAGAGGAGGATGTCCAAAACAAAAATGGCATCACCTGTCAAAAATGGAGTTCCACT TCTCCCCGCA[G/A]ACCTAGGTGAGACTTTCCTTTTCATCTT
WI-9193	94	G A	---	---	TTGGACAAACCTAGAAATTTCTCCCTTATGTATCTCTATOGATTGTGTAGCAATTGACAGAGAAATAA CTCAGAAATATTGTCTGCCTTAAAGCA[G/A]TACCCCTTACCACACACACCCCTGTCTC
WI-9015	48	C T	---	---	TTTGGATTGATATCGTGAATCTCAGCCGAGAAATTTGGGCTGGATTG/C/TJGCTTTGGTTATACAT CTTTCCCTAAAGAAGATAAACACAAAATCCATTCAGGTAGCTCGGCACCACTAAGAA
WI-7254	37	A G	---	---	GGAGCCAGGAGACAGCAGGGTCTGAGAGAGGAGCCAC[G]GTCCCTAATGACACCCACTCCTAGCC CTGAGGCTGTGCCCTCAGACTGGGGAAGAGTCCAAAGGAAGGGAGGAGCAGCAGCCACTCCTCAATGC TCAATGGCTCCCTGAAATCAAGACAGG



[illegible]

WI-9281	68	G A	---	---	ACTGGTGGGAGACTGTGAGGATCCAGGATTCAGTATTCCTGGCCAGAGGGCCTTCTGGCTACTGGG [G/A]TGTAGTTTGCAGTCTGTGTGCTCCCTCTCTATGACTGTGCCC
WI-7848	142	A G	CTC	CAATTAATTTG AAAGCTATTCA GACA	TTCTGAAATATAACAGCCATTGAGCTATTTAAACCTTGTAAATTTTAAATTTACAAAAATATAA AATATGAAGACATAAACCCAGTTGCCATCTCGTGACATAAAACATTAATGCTAACACTTTTAA ACCGTCTC[A/G]TGTCTGAATAGCTTCAAAATAAATGTGAATGGT
WI-9304	70	G A	ACTGA	CCACACAGAAC TATTGTAAAC AA	TCACGTTTGGTCTCTCAGATTTCGAGGAAATTCGTTTGTATTGATATTACAATGATCACCGACT GA[G/A]AATATTGTTTACAATAGTTCTGTGGGCTGTTTTTGT
WI-7933b	314	C A	---	---	TTACAGAAACTTCCCTGTGCCTGTGTCCTCCCATGCTAGGGCGGAGGGTCTTTCTCTCTCTTCC TACCTACCCCTTTTCTCTTGGCCAGGGCTGATCTACCTTTCTCTGTCCTGGCTGGCTGCAC AGAGGATTGCCCTTCTCTTTTCAGAGCTGGCCCTCGATGCCAAATTAGCATTTAGTATTTTGCACAA AGTCTAAGGGACCATGGCTGCCTGCCCTTGGGAGGAACCATAGCTCCCT
WI-7933	96	G C	---	---	TTACAGAAACTTCCCTGTGCCTGTGTCCTCCCATGCTAGGGCGGAGGGTCTTTCTCTCTCTTCC TACCTACCCCTTTTCTCTTGGCCAGGG[G/C]CTCGTATCTACCTTTCTCTGTCCTGGCTGGCTG CACAGAGGATTGCCCTTCTCTTTTCAGAGCTGGCCCTCGATGCCAAATTAGCATTTAGTATTTTGA CAAAGTCTAAGGGACCATGGCTGCCTGCCCTTGGGAGGAACCATAGCT
WI-7374	182	T A	---	---	CCAGATGTCCCATCACGTTTTTCTGAGGCTTTTGTACTTTAGTAAATGCTTCCACTAACTGAAA CCATGGTGAGAAAGTTGACTTTGTTAAATATTTGAAATGTAATGAAAGAGTACTGTATATTA AAAGTTGGTTTGAACCAACTTCTAGCTGCTGTGAAGAATATATTG[T/A]CAGAAACACAAAGGCTT GAT
WI-9343	78	C T	CCTGCOA	AAATGAAACTT ACGTTTGTG TG	GGTCTGCTCCTGCTACCTTGACCCCTTCCCTTCTCTGCTTCTCTCTCATCATCATCCCAACACAT CCTCTGCCA[C/T]ACACAAACAAACGTAAGTTTCATTTGGGCAAA
WI-7386b	104	T A	---	---	CTATATGTGAGAGGCGTGATATCTGGATGGAAGTTGGCTGGATGATCTCCAAAGTCGTTTCAACTCT TAAAGACATCTTAATCCTGAATGTAACAAATTGTTA[T/A]GTGTTTAGAATCAGAAATTTGATTTTGA ACTTGAGTAATTCATCCTT
WI-9357	75	A G	---	---	AAGAAGGAGCTCAGTTACGGGGTTTTTAAACCTTCATGAAACCTGAAGAGTTCACTTTGTATTAT GCTCTTA[G/G]GATTACAGACTGATGCCAGACAAACCTTGGGAAGA
WI-9360	79	T C	TGG	CCTTAGAAAA TCTGCTTTAAC A	TGAAGGGGTGTGGCATCTGTGTTTCTGATGCTTACTACAATATGGAACCACTACTTTAGAAAACTGT CTTTAACTTGGT[C/A]TTCCTCTAATTGTGTTCCCTAGGAAATGACTGICCCAAG
WI-7423	107	T C	GTTC	GGTCCAGAAGA GCOOG	TGCTCCCTGTCCCATCTGCAGTGGACCCAGGCCACCCCTTTGAGGAGGTGGGTGAACGTGCTCCTT GGCAGGGATTGTGACACTGCACTGCTGGGTGTTCC[T/C]GGGCTCTTCTGGACCTTGCACCGTG GATACCAGGCCATGTGCCATGGTATTGGGTCTGGGAGGGTGGGTGAAATAAAGGCATCTGTCT



WI-9448	184	G A	---			TGGGGCTGCTTTAGACTTCATTTCTAGAGCAGACACCTAGTGAGAGGAATACCTGGGAGAGAGAC TGCTTGCCCATGGTGTAAACCTACATGAGGGGACTGAAATCTCTTTGGATGCCAGTCCAGATCCC TTTTAAGAAAATGGGCTTGTTCCAAAGGCTGAGAGCTGGCACAC[G/A]CACTGGTTTCTAAA TCCTGCTTGATTTATCCAAAGCGCATGTTCTTAACGTGCCGIGAGCAG
WI-9470	204	G A	---			ATGTCAGAAGAGACACAGACAAGGAGTTTTCCTTTTAAATGCTAAACAAGTGCCACTAATCCACA GATCTGAAAAGTACAGCTCTCCAGGTTGATAAATCAGATCCAGGCTTTTCTTGTCAGTCCGCTTA TGAGATCAGGAATATGATCTCCCTAAAGCCCGAGATTCCTACTAGAGCCGCTGGGACACTGATGAC AA[G/A]GCAATCAACTCATCTCCTCAAGCTCACCGGGCTCACCTTCCCAG
WI-1245b	201	G T	---			GATGATTTCTGAAGTCTCAGCAGCCCTGATTCTAAGCCTCATAAGGAAGAGTAGGTGTTAATGGCA TCCTAGGGCAATGGTAGTGCTGATGCAGATCTGCTGTAGCCATGTGCTGGCATCACAGGGTGGT TTATTAATTTCAATTTATCATCTGACAGCCCTTCTTTAAGGTACATCCTTGCCTCTTCTGAGGC[G/ T]CTAAGATCCCCAAGGTGGCTCCTGTATCCAGAAA
WI-1245a	85	T C	---			GATGATTTCTGAAGTCTCAGCAGCCCTGATTCTAAGCCTCATAAGGAAGAGTAGGTGTTAATGGCA TCCTAGGGCAATGGTAGG[T/C]GCCTGATGCAGATCTGCTGTAGCCATGTGCTGGCATCACAGGGT GGTTTAAATTTCAATTTATCATCTGACAGCCCTTCTTTAAGGTACATCCTTGCCTCTTCTGAGGC GCTAAGATCCCCAAGGTGGCTCCTGTATCCAGAAA
WI-1031	149	G A	---			TTCAAGTAAAGGACAGGCTAGAACAAAGCGTCCCACCCCTGGCACCAATGACAGTTTGACCAAA TAACTCTTTGTTTTCAGGGGACTGTCTTACACATTTGTGGGATTTTACAGCCCTCCGCTTCTACCCA CTAGATGCCAGCA[G/A]CACAAACCCCTCCCCAACAAATCATGACAATGAAAATGTCTTTAGACATT GCCAAATATACCTTGTGGGACAAAATGGCCCTGATTGAGAACCACTGGTT
WI-5385	110	G A	---			AATGAGTCATTGTGGAGTTAGAGGAGGTTACTGAAAATGGTGACTCCAATGGTGGGATTTGAAGAGG GAAGTCCTGATAATTTAACATATGGTTCTTGCCAGGAATCG[G/A]CAATGCTAATCTATTGCTTAA TTCTTTATCAACAGACTCTTTGAATCAATTTAGAGATACTCAGTGACCCCATGGCTAGAGTTCTGTGAC CCCTGCTACGGGAAACATTGAATGCA
WI-5403	199	T G	---			ACCAACCGTTGGCAAGGCTCCCAAGACTCACCAACCTTGGTGTACCCTATGCCGGGTG GGATTGAAGAAATAACCAATAATAATTGCTACAATTTTCCAGTAGTTACAGGCACCGCCTAT TGGAAGAAATCAATAATGTAACCTACAAATGATTTGCTCTGGCTTGGTCCAGGCATAGAGTT/G JGGCTACAACCCATTTTATCATTTGAACCTCAGAAGCATCCAGTTGGGGCT
WI-5801b	157	G A	---			TGGTATTTTCTTTCTTAAATGTTATGATTAATTAGTGCTTTGTAGAAATTTGAAAAATGTAAA TCAGAGAACAGAGAAAATAAAGTATAGTTGAAACCTCTAACAAATTTAGATTTTAAAGGCCTAG GGAAAGAAAGAGAGCCTGGGA[G/A]AGGGAATGAGAAAAGCACCAACCAAGAAAAAGTGTGT GGCTTAAGGGAAGCCCAAGGAAAGTTAAGT

WI-5801a	48 A G ---	---	TGGTATTTTCCCTTAAATGTTATGATTAATTAGTGTCTTTGTA/GJGAATTTGAAAAAATGT AAATCAGAGAACAGAAAAAATAAGTATAGTTGAAACCTCTAAACAATTTTAGATTTTAAAGGCC TAGGGAAAGAAAGAGCCCTGGGAAGAGGGAATGAGAAAAGCACAACCAAGAAAAAAGTGTGT GGCTTAAGGGAAGCCAAAGAAAGTTAAGT
WI-5696	61 C A ---	---	TTCTATTTAAATCCTGTGCCCATTTGCAAGACTGCATTAGTCTGCATGAGCCTTAGTTTC/AJTA AAGCCCCCTCACACCGAGGGACAATGTTCAAGAACTAAATGACTGCGAGGTGAGCAATCTCTGTATTA TACAACTGGGACCAAGATGACTTTATAATAGTGGCAAGAGACAATCAGGCAGACTGGGAGGACC TTATAAATAGATTATAAGGCTGTGTGAGTTTATTTAACTT
WI-7461	153 C T ---	---	TATTACTAGGTTTCATAGAGCCCCGTTGTAATGATAAATAGCCAAATAGTTAAAGAGGCTGCAGGCC AATCTAACGCTCCTCACTCCCTTCGAACCCAGCCTCAGAGATGACACTTAGGCTGCACATTCCTG TGGCAGGGACTGTGTCTC/TJGTTCCCTGTTGGGTCCCGAACCAGTGTGGTGCCTGGCACAGAG GAGGCCCTGAGTAGCAITGTGTGCA
WI-9716	221 G A ---	---	AGAAGACAGGAGCACTGGGATCAAGGACTGATAAATCTGAGGCTTTAATGGTCCCTGTCTCTAAC GCTTTTGGTATACTTTCTCTTCTGAAGACCAACCTTTCAAACCTCTCAGAACACAGGCAAGATGCAT ATTCTGTAGTTTTCAGATGTGTACTCTCTACATTCGAAACACTAGATGAGTAGGCTCTCTTCATCT CAATTGAAAATCTAGAA/GJA/AAACACCTAATTGGCTCATCTTGGATCA
WI-9760	49 C T ---	---	TTTTCGTTAAGTCTTGGAAGCCACACAGAAGTGATCTACTCTTTAC/C/TAAGTGTACTTTGCA TATATTTATGGGATGATTTCTATCCCTACTTAAGATTTCTCTCTCAGGTTAAATATCCATTCTCT TTGTTCAAGGATTTCTATTGTCCTCTTTCTAAACCTTAACCATTCCTGCTTATCTCTGCTTGACA CATGCTATTTAATCAAGGTGACATT
WI-9855	31 A C ---	---	GAAAACCTCGTTGGCTCAAAGGAACTGTAG/A/CJAAATCTTTTTTTTATTTTGTTTTAACTC AAAGAGTGGAGTTTGCATTGACCTTGTGATGGCAGCTGCTCTTTGTTTGGTAAATCCCTCTAGT GGGCACCTTGCAAAAGCAATTTAGAGCAAGGTGGTGGCATGGAGTTGTGTGAGGTTGCTGAAAAG TAGCAATGGAAGAAAGTTAATGGA
WI-10312	41 A G ---	---	AAGGCCAGTGGGAAAAAGCAGACAAAAACACTCCAAGAATAC/A/GJAGATATAAACATCATCATCA GTAGAGATGGGATGACCTAGGAGGTCTGCTGATGAGGGCATGTGAGACCAAAAGACATTTGGGTCT TGAGGGTTGAATAGGAGTTTGTCTGGTGAGTCTTGCCAGTCCCATAGTAGGTGTTCCATAAATAAAC AGTGACTAACTGAGGTAGAGTCACAGAAAGAAATTTCA
WI-11152	179 C T ---	---	GAATCTTTGCGACATGCAGAGCAGATACGGCAAGGCATCTTGGGCATTTGGAAGGAAACGAGCCCTA ATTCTAGAAACACAGACTCTACAAAGGACCAGTTAAAGGTCTGCACCCAGGGGACTGGGTGGCCAAAG TCAGTCAAGGCATAAAGGGGGACAAAGTGGGACAAAAGGCTTGTCA/C/TJCTGTCAGAAAACATTGAA AACAGCCAGTACATGCCACTGATAGA

WI-1968	167 A G ---	---	TGGTGGAGGCTGTAAAGCTGAAAGAATAGTCTCTGCTGCTGCTTTCGGTGGAAATGGATGAGTCCT TTTACAAAATTTTCCCTCTGCCATGGGTGTTATGTTAGAAATCGGAGTTGGAAGACTTAGATTCA ATTTGGGGCTGTACAGTTTACTGGAAGTTGTA/GTGAACCTTGAGCAAGTGCTCTTAATGTCCTCA GCCTCAATGCCCTTCCCTGTAA
WI-4701	198 G A ---	---	GGGTTCATTTAACAGCCTCCCACTGGGTCAGATTGCACGGAGATGTAAAAATAGGAAGAGATAG AAAAATGGTGGCCCACTATTGACTTGATAACACCTACAAACAACACATTAAACCTCCTCCCACTCTA CCCGCAAGTCTACCTTTTGGTCTTTTATTCTGCTAATGACCATACTATTTCCCAATTAGA[G/A] CCATGTCATTTTCAGAAAAGCAGTATA
WI-4823	164 C A ---	---	TTTATCTTTCCAAACCATGTGTGTTTTCTTCACATACITTTACGTAATTTTAAATCATGTCAATTA TGCACCTACTTGTGGCTACAGACATTCCTTCCAAATGTAATCCCTAACACAGCAAGCATAACT GATGTGCCATCTTTGTATTCTCTAAAC[C/A]AAAGAAAAGTGCTTTTGTGCATCTGCCCTCTCTGT CTTCTCTGTTTCACCTCCCTGATTTCCCTATTTCAGCATTCATGATTA
WI-4860	72 A G ---	---	AAAAAACAACCTTCATTGACATCTAAGAAAGATAAAGAAAACAACGATCCACTGTGTTGCTTT GATTTA/GGAGAGATAAACCTGATCTTAAGAAAATTAACCAAAGCAGTACACTAAAATAGCCT TTGTGTGGTTTTTCAGGAAAGAAAGCCAAATCCAACTAAGTTGCTAAGAAAATAATGTTTCATATCA CTCTAACTTCACATAGAGCAATTAATAGCA
WI-9705	111 C A ---	---	TGAAAGGACCAGTTCGAATGCTTACCAAGTAAAGTAATCGGAGGGGCGAGGAGTGGAGTTGCTT CCGGATGTTGCATAAATTCAGGTTCTTTAAGGAGTTCGGCTGCC[C/A]AAAATTTGTTAACACTGATGC TGCTACAAACGACATAGAAATCGGTGGTAGATTGCGGTTCTCTAGTAGCTAATGTTTAGATA TGATTGTTGAATTAATGTTGCTGTGTTCTTGGTG
TIGR- A004Z48	177 A G ---	---	CAATAATCTCTGCTTAGAAGTTGCTCTAGGGCCATGGATTATGTAAGGTGGGCGAGGTGGACTG AAGATCTGTTGGCAGGCTCACAGAGACGGGGGTGAGGGGAGAGATCGTGGTTTCATGAGATCCCAT CTTGGGCAATACGGTTATCCCGTGGTCTTCATACGCCACAGA/GTCCCTCCAATTCAGGGGCTCCC GTGGGATGGTGGAGCCCAATGAAGACCAGGTAGATGATGCCACTAGAGATG
U17579	34 T G ---	---	GGGATTCATGTGTCTGTCTCATCCAATAAGCACT/GJCATGACCTCAGCCCCATACTCTTCTCCC TATGTTCCAGAGACAGATAGACCTGGCCCCCTTCTCTAGGGGATCACATAATTGGAAGGATGAG GACTCCAAACAGCCAGCTCCCATGCCAAATAGAACGATGAGTGTGGGATCAATTTCTATGGGAGCC TGGGGAGAGGGATCCTTCTAGTTGA
WI-7747b	88 T G ---	---	GTGAGAGCGAGGCTGAGCCTACAGATGAACCTTTCTGGCCTGCTTTCGTTAACTGTGTATGACATA TATATATTTTAAATTTGAT/GJAAAGCTGATTACTGTCAATAAACAGCTTCATGCCCTTTGTAAGTT ATTTCTGTTGTTGTTGGTATCCTGCCAGTGTGTTGTTGTAATAAGAGATTTGGAGCACTCTGA GTTTACCATTGTAAAGTATATAATTTTTTATGTTTTGTTCTGA

WI-7747a	44	T C ---	---	GTGAGAGGAGGCTGAGCCTACAGATGAACCTCTTCTGGCCTGGT/CJTTCGTTAACTGIGTATGTAC ATATATATATTTTAAATTTGATTAAAGCTGATTACTGTGCTCAATAAACAGCTTCATGCTTGTAAAGTT ATTCTTGTTGTTGTTGGTATCTGCTGCCAGTGTGTTGTAATAAGAGATTTGGAGCACTCTGA GTTACCATTTGTAATAAGTATATAATTTTATGTTTGTTCCTGA
WI-7189	197	T C ---	---	TCCAGAAATTTCTCTTCAGCTCATTGCTCTCTCACAATTAAGGGAGTAGGTTAAGTGAAAGGT CACATACCATTAATTTCCCTTCAACACAAATAATTTTACAGAAGCAGGAGCAAAATATGGCCTTT CTTCTAAGAGATATAATGTTCACTAAATGTGGTATTTTATATTAAGCCTACAACATTTTTC/JAG TTTGCAATAGAACTAATACTGGTGAAATTTACCTAAACCTTGGTTAAT
WI-7850	57	G A ---	---	AGCCAGCTGGACTCATGGATGTGCACCTTTGCTCCCTGCTCTTCTGCCTCTGG(G)CTCATGTA TCTGCGCAGCTCTGTACCTCTGTGGTGGCATCTCTACCTCTGACACAGACTGCCTGCCTTGAAGCT GAGAAAGCACAGGGCAAGGAGCCAAAGGACACAGAGCCTCAGCCAGCCAGGATCCGTCCTCATTTT ATTGGTGATGATGAATGGGAATGAAATCAGGGGGCTGTCTACTAGAGCC
WI-7907	69	G C ---	---	CTCTCTCTCATCCCATCCCCCTAAATAGGTCAGGTGAGGGAGGCTGGGAAGAGGTGGGAGGAGG G(G)/CJAGAAAGTGAAGGAAGATAGGAAGGATATTACCTCTTCTGTTATTTTAAAGAACATTGTTT GGTGGCAGCAATCTCCCTGTCCTATCAGTGTAGAGGCTTAATTTTATATCTATAAATATATTAAVA AGCAAGTCAAACTTGGATGATCAAGGTAAATATTGTCAAAAGTTAAAT
WI-7919	242	T C ---	---	GAAGCAGCTGGATCACTTCCCGCAGTCCTTGGCAGGCTTTGCTGTGGAACACAGAGCTCCTCCT CAGGGGCTGGCAGCTACCTTCTATTCTGTATGATGATGATTTGTTAAACACACTGTCAATAATAGAGAT GTGCCAGATTTAGATTTCTTACCCTAATCTGTTTAAATTTGTAACCTTATCCCATTTGAAAGTGCA AGCCCATTCAGATAAGCTATAATCTGGTCTTTAAGGAAIT/CJACAACCTT
WI-7928	101	T G ---	---	CTCCCTTCTCTATGCTCTCAGCAGCAGCTTGGGGCACACTTGTTCATCTTCTGACCGTTTGTGGGCTA TTCCCTGCGAGTGCGAGACATCGTCAAAATTCAT/GJACAAGAGGAAATTTTCAATGCAGAAAGCTGTA TGCAGGATGCTCACTGATGTTTGCACCTTTAAACCTGAAATCAACTCTTTATATAGGATTTTCTTTT CTATCTCCATCTCCTCAITTAATAAATACGTACATTTGAGGTAATGGTA
WI-7936	131	T A ---	---	TTTTGAGTCAAGACTTAAAGGGCCCAATGAATATTATATACATACTGCATCTTGGTTATTTCTGAA GGTAGCATCTTTGGAGTTAAATGCACATATAGACACATACCCCAACACTTACACCAAACT/A ACTGAATGAAGAAGTATTTGGTAACCGGCCATTTTGGTGGGAATCCAAGATTGGTCTCCCATATG CAGAAATAGACAAAAGTATATTAAACAAAGTTTCAGAGTATATTGTTGAA
WI-7944	99	T C ---	---	TACAGTTCCAGCCCGTTGCCCACTCATCTGCGGCTTTGCTTTTGGTGGGGGCGAGATTGGGTTGG AATGCTTTCCATCTCCAGGAGACTTTTCATGTC/JAGCCCAAGTACAGCCTGGACCAACCCCTGGTGTG TGAGCTAGTAAGATTACCTGAGCTGCAGCTGAGCCTGAGCCATGGGACAGTTACACTTGACAGA CAAAGATGGTGGAGATTGGCATGCCATTGAACTAAGAGCTCTCAAGTCA

WI-7805	101 A G ---			TTTCTAGGCTGTACAGTCTGATGCATGATTTTTTATAAAATTTTCATACCTCTGTGAATTTGGATCTT TTTACTTTGAGCATATATTTAGAATATGTGT/GJTGTTAAAGGATCTCCACAATGTCTGCAGTGTG AAGCAGGTTTCATTGTGAATAGTTAACAGTCAGGAAGGCTAAACTGGTCAGTATTAATGTGTAGC CCTACCAAAATAGCCAGTAGTATCTGAAATGAAAAATAAATGAAGTAT
WI-7416	137 G T ---			GGCCAGGAGATTAGCAACAAGGATTCTGTACTTACTTGGCCCTTTTATCTTCCCTCTTGGCC CAGTCCCTCTCTCCAGCTTCATGTGAAGCTCTGCACAGACAGACAGTCTGCTCTTGGCAGTGT [G/J]CTACTCCTCAGGTGCAGCATACATAACCAGTAAGAGACTAAATCTGCAATATATAAAGAGCTC CTACAAATCAGTAACATGAAGAACACTCAAAAATTTGGCAAATGTCATCAG
WI-140	252 C T ---			ATTTGAAGATTGGAGGCTTTCAGAGGAAATAGATTCAATTTGGATCCCCCAACTATAATGACA AGTTTTTAATTAGGTGTGATCAAGGCTTCTAAAGTGAAATGCAAGTTGTACCAGTAAAGTTTATA TCTTCCATTCAGCCAGCTCATTTGCCAGAAAATTCAGGTGAGTGGATTGGCCAGACTATCTGGCAAG GATGAAAATTTAGTTTAAATGTGTCATTTGCTGTATTGGCATTCCJ[C/
WI-198	218 C T ---			GAGGTCTTTCAGCAACATGGAGCCCTACTGCTTCAACCCCGAGTTCOCGGATCAAGTCTGGCACC CATGATGGAACCTCTGCCATGGTTTTAGTACCCCTGGACCAAGTAGTATCCATCTGACTTTTAAAA TTCTAAACAGCCCTTGATGGGACAACTCTGCTAAAGACTAACCACTTCTTATCTTATCTTCAGCTA CCTGCTCCCTTTCTC/JTGTTTAAACAAAGCATAGAAATTTCTGAACAAC
WI-205c	146 T C ---			TTTCATGGTCCCAAGACAGATTTTAAAGAAAGAAAATAAGCCTCATCTCCTAACTATGACTTGGTCGG AAGCCAAGAACCTACTTCAACATTTGACCCATAACCTTCTCTTGAGATGATGGCTGACTTTTTCAT GCATGAGTTTG/JCJCCAAAGGCTTGATGGGAAAATCTCAACATTTGTACCTAAGAAAGAGGATGT ATCTTACTTTGTTTAAAAACTGCATAIGCCTTTATTTTGTAGTCCG
WI-205b	146 T C ---			TTTCATGGTCCCAAGACAGATTTTAAAGAAAGAAAATAAGCCTCATCTCCTAACTATGACTTGGTCGG AAGCCAAGAACCTACTTCAACATTTGACCCATAACCTTCTCTTGAGATGATGGCTGACTTTTTCAT GCATGAGTTTG/JCJCCAAAGGCTTGATGGGAAAATCTCAACATTTGTACCTAAGAAAGAGGATGT ATCTTACTTTGTTTAAAAACTGCATAIGCCTTTATTTTGTAGTCCG
WI-234	165 G C ---			GAAGACTGAGTTTCCAGGAGGTGCAGCCGTTTCTCTCGGGCCATATGGCTAATAAGGAGCTTGAGCA GGGATTCAACCTGTTTGCACCCCAAGTNCITTTCCAGAGGCTCAGACTACCTCCTCCATCTCCCT CTCCCCACAACACACAAATACAGAGATTG/CJAATTCAGGAGCCAGTTTCTAGGTGGGCTTTGAGC AATCATACACAGTAATCTCTTGGTCTTAGTTTCTCAATGGGAAATGG
WI-276b	25 A G ---			AGCTTTTGAATCCAAAACACACAT/GJCTTGACTCTCTTATCTCCTCTTGTGTAACTATATCC CTGAGGAGAAAATACAGAACACCCCTGTGGCTGCTGAACGGAGGAGGATGGGGGGGGGAGACAT CGGTCAATGTATCAAAAGCATCTCTCTGCTGAAAGACCTCTCCTGAAAGACATGAGCTATTAGGAGC TCTGGCAAGGGCTTTGCTTATCCTCTTGTCTATCCCTGATGACTGGGCAA



WI-276	25 A G ---	---	AGCTTTGAAATCCAAACCACATAGJCTTGACTCTCTTATCCTCCTCTTGTGTGAACATCTATCC CTGAGGCAGAAAATACAGAACACCCCTGTGGCTGCCTGAACGGAGGAGGATGGGGCGGGGAGACAT CGGTCAATGTATCAAGCATCTCTCGCCTGAAAGACCTCTCCTGAAAGACATGAGCTATTAGGAGC TCTGGCAAGGGCTTGTCTATCCTCTGCTATCCCTGATGACTGGGCAAA
WI-427	59 G A ---	---	TTTCCCAATCCACAGGTAAACTAATAATGGATGTATAGAAITTAGAACTACTTCQIGJGTTTT TTCCCTGGGAAATATTCACAAAACATTTGTGGTCTGCAATCAGGTTAAAGACATAGTGTGCCA TTTGTATCAGACAGGTAGAGGCTGACTCTGGCAGGATTAGCTACCACTAGCTGTGAGACTTTATGT ATTCAITTTATAGAGCCAGGGTCTGCTCTGTCAACCAGCTTTCAGTGCAGT
WI-562c	106 T C ---	---	CTCTCACTCCAACTATATTGCTTACTTAATGGTTACAGATTAGCCCCAGAAAGGAGCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATTTTAAIT/CJAAATGGTCTTTTATTAACAAAAA AAAGNTATCTAAAGAGAAACCATAATAATCTCTCAGGTAATTATGGCCACAGCCAAACCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-562b	106 T C ---	---	CTCTCACTCCAACTATATTGCTTACTTAATGGTTACAGATTAGCCCCAGAAAGGAGCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATTTTAAIT/CJAAATGGTCTTTTATTAACAAAAA AAAGNTATCTAAAGAGAAACCATAATAATCTCTCAGGTAATTATGGCCACAGCCAAACCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-562	103 T C ---	---	CTCTCACTCCAACTATATTGCTTACTTAATGGTTACAGATTAGCCCCAGAAAGGAGCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATTTTAAIT/CJAAATGGTCTTTTATTAACAAAAA AAAGNTATCTAAAGAGAAACCATAATAATCTCTCAGGTAATTATGGCCACAGCCAAACCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-597c	141 A G ---	---	GTGTAATTTGGTGGCTTGGCACTTTCCACAGTAACCTTTAGAAATNNAAGGTGGAAGGTAAGG ATGAGGAAGAAGAGGGNGTAAGAAACAAAGATGTCTATGTTGAAGAGTATCCTTAGGATATTCT GATACATGJAGJTAATGACCCCTCCATGACTCTGTACCTCATCATACCAATGTGAGAATTATTAAC TTGAICTAATATCTTCACAACATAATACCTGAGAGAAATAAGTCTATTTAAT
WI-597b	141 A G ---	---	GTGTAATTTGGTGGCTTGGCACTTTCCACAGTAACCTTTAGAAATNNAAGGTGGAAGGTAAGG ATGAGGAAGAAGAGGGNGTAAGAAACAAAGATGTCTATGTTGAAGAGTATCCTTAGGATATTCT GATACATGJAGJTAATGACCCCTCCATGACTCTGTACCTCATCATACCAATGTGAGAATTATTAAC TTGATCTAATATCTTCACAACATAATACCTGAGAGAAATAAGTCTATTTAAT
WI-597	136 A G ---	---	GTGTAATTTGGTGGCTTGGCACTTTCCACAGTAACCTTTAGAAATNNAAGGTGGAAGGTAAGG ATGAGGAAGAAGAGGGNGTAAGAAACAAAGATGTCTATGTTGAAGAGTATCCTTAGGATATTCT GATAGCATGATAATGACCCCTCCATGACTCTGTACCTCATCATACCAATGTGAGAATTATTAAC TTGATCTAATATCTTCACAACATAATACCTGAGAGAAATAAGTCTATTTAAT

WI-611	66 G C ---	---	---	TTCAAAATTAACACCATTTGGGTATATTAAATTTNGCTCTATCCATAGTTCTAACCCCTCTCTCTG/CJACAGTGAGACACCTGCTCTCTATTGTCTTGACGTATTACGTATTCGATCAGTCACCCATCTGGAACCAAGGTTTCATTTCTGCTGACCCCTCCCTCTCACCCCTACTTTGGGCTCTGACTTCTCTTCTCTGGGCTGAACCTCTCTGTGTGGCTGTCCGCTTCTCTGCTTGGGCTTCCAAATAC
WI-681b	156 A G ---	---	---	TGAAGCCCTCTCTCTATACCCAAAGTGCTTTATCTTAAATGCTGTGGTGAAGTATCTACCCCTTAAGGATATTGTGAGAAATCAATAAGTTCATACAGGGGAAGACTTTGNCCTGGTATGTCATAAGCAA
WI-681	156 A G ---	---	---	TCCATAATTGTTATAGCTATTAGJTATACTATGGACCAATTTGGACACAGATTATATATGTCAGACACCAGNATGTCCTTTAAGATATGCAGCAAGCACAAATCTGTCAATGGTTT
WI-681	156 A G ---	---	---	TGAAGCCCTCTCTCTATACCCAAAGTGCTTTATCTTAAATGCTGTGGTGAAGTATCTACCCCTTAAGGATATTGTGAGAAATCAATAAGTTCATACAGGGGAAGCACTTTGNCCTGGTATGTCATAAGCAA
WI-681	156 A G ---	---	---	TCCATAATTGTTATAGCTATTAGJTATACTATGGACCAATTTGGACACAGATTATATATGTCAGACACCAGNATGTCCTTTAAGATATGCAGCAAGCACAAATCTGTCAATGGTTT
WI-867b	119 G A ---	---	---	AATCTTAACAGCCTTTTGATGCCAAAGCCACTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTGCAACCTCCAAGGCTCCCAAGTATCTGGCACATCTTCCCTTTTCATCTCCG/AJTGTGTGTTGGCCAAATAATATCTCCCCAGGGAGCTCTTTCTAATCCCTGAAACCTGAGAAAATGTTATCTTATGCAAGTCTATGGTTTGAATGTGTCCCCACAAAGCACACATTAGAAACTTA
WI-867	113 A G ---	---	---	AATCTTAACAGCCTTTTGATGCCAAAGCCACTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTGCAACCTCCAAGGCTCCCAAGTATCTGGCACATCTTCCCTTTTCG/AJTCTCCGTTTGTGTGTTGGCCAAATAATATCTCCCCAGGGAGCTCTTTCTAATCCCTGAAACCTGAGAAAATGTTATCTTATGCAAGTCTATGGTTTGAATGTGTCCCCACAAAGCACACATTAGAAACTTA
WI-867	119 G A ---	---	---	AATCTTAACAGCCTTTTGATGCCAAAGCCACTTTCAGTCTTAATCTTTTGGAGCCTAAGATCAGTGCAACCTCCAAGGCTCCCAAGTATCTGGCACATCTTCCCTTTTCATCTCCG/AJTGTGTGTTGGCCAAATAATATCTCCCCAGGGAGCTCTTTCTAATCCCTGAAACCTGAGAAAATGTTATCTTATGCAAGTCTATGGTTTGAATGTGTCCCCACAAAGCACACATTAGAAACTTA
WI-871b	123 C G ---	---	---	TCATCAGACCTGAGATTGAGCATGAAATCTACCAAGGTACCAAAATGTAACCTTGTCCTCAAAACGAAATCTCAGTTTCTGCATATGTAATAATGGGAATGATAAGAGCACCCACCTACCTCATG/C/GJAACCTGTTGAGAGAAATAAATGAGACATTGTAAGTAAAGTTTGTAATGCACTGTTATGGCCTGAATTGTGTACCC
WI-871	123 C G ---	---	---	TAAATTCATATGTTGAAGCCCTAACACCCAAATATGNCCTGATTTGTACATAA

WI-884	198 T C ---	---	AGGTTCTGGACTTGATGCTGGGAAACAATGGGTNCTGGAGAAATCCTATTTTGAGTNTTCACAGAT CAGTAGAGCCAAATGGGAAAGGTATCCTAGTCCATCCCTTTATTAGGAAGTTCTCTGATCTATTGGGA ACTTCCTCCTAATAGATCAGGAAATCCACCTCATTTAATCATGGACAACNNAAAGGAATAIT/CJG ATCCCGCATGCAACATTTATTCACTGAAACATGATGAAAATGAACATAAT
WI-921b	205 G A ---	---	CACCTCCCAAGGCTCTGGGGANGAGCGGTGGGACGCTGCCGGGAAGCAGTTCGACACTGACTGA TGCTTTGCTGCAGGGCTCTGCTCTGAAGCCGGACACTGCCAGGTGCACACAGGACAGTTATACTGG CAGTGATGCCCTCTCACGCCCTGGCCCCCAAGAAAGTCTTGCCAGGAAAAGCAGCATCCATCTAC TCTG/AJGGGAGAGATCTGACAATTTAATCAGGAGGAAGAAATCTTCCGAG
WI-921	205 G A ---	---	CACCTCCCAAGGCTCTGGGGANGAGCGGTGGGACGCTGCCGGGAAGCAGTTCGACACTGACTGA TGCTTTGCTGCAGGGCTCTGCTCTGAAGCCGGACACTGCCAGGTGCACACAGGACAGTTATACTGG CAGTGATGCCCTCTCACGCCCTGGCCCCCAAGAAAGTCTTGCCAGGAAAAGCAGCATCCATCTAC TCTG/AJGGGAGAGATCTGACAATTTAATCAGGAGGAAGAAATCTTCCGAG
WI-945c	90 G C ---	---	GGCTGGGATGAGAGGTCTACTTTGTGTACTGGAGGTTTCACTGGCTTGCTAGAACTAGNAAAAGNA GAAAGAGACAGNGATTGGCTAAC/GC/CJCATGGCAGTAGTGGCCCCCAAGGCTGAGTAATAAGAAA AAATCATTAGATAAATGTCTCATGACCAAAACAAGTTCAAACANTAGGTGCAGCACANNNGGTT TTCTCTGGTCATAGAAATCTCTTAAAGGGAATCATGACAGATTTCTTGGCTTTA
WI-945b	90 G C ---	---	GGCTGGGATGAGAGGTCTACTTTGTGTACTGGAGGTTTCACTGGCTTGCTAGAACTAGNAAAAGNA GAAAGAGACAGNGATTGGCTAAC/GC/CJCATGGCAGTAGTGGCCCCCAAGGCTGAGTAATAAGAAA AAATCATTAGATAAATGTCTCATGACCAAAACAAGTTCAAACANTAGGTGCAGCACANNNGGTT TTCTCTGGTCATAGAAATCTCTTAAAGGGAATCATGACAGATTTCTTGGCTTTA
WI-960b	167 C T ---	---	TTGCTTCAAAGAAAGTCTTGCTCAGGAAGTTATTCATTCAGCAACCTAAAATGTTTTTGGTACAT ATCAAGCACAGGGTTCTGAGCAATGTCTTAGGAAGACCATAAAGGTGAATAATGAGTGTCTTCTACC CTGAGGAATTTATCAAAGATGTTAAGTTATCT/CJCTTAGAGGTATAAGTCATATAGGCATATTCT ATGTATACTAAAGGTGGTATGGCATAAGAGTACATA
WI-960a	155 G A ---	---	TTGCTTCAAAGAAAGTCTTGCTCAGGAAGTTATTCATTCAGCAACCTAAAATGTTTTTGGTACAT ATCAAGCACAGGGTTCTGAGCAATGTCTTAGGAAGACCATAAAGGTGAATAATGAGTGTCTTCTACC CTGAGGAATTTATCAAAGATG/AJTTAAGTTATCTCCTTAGAGGTATAAGTCATATAGGCATATTCT ATGTATACTAAAGGTGGTATGGCATAAGAGTACATA
WI-1121	181 T C ---	---	TCCCACTGAGTATGGCTTTCAGTAGTTTTTATTATGATGTGCCTAGGTACATTTGTTTTATTGTTCTG CGAATTGTTGATTACTTTGGGAGAAATGCTCAACTATAAATATTGCTTGACCCCTTTCTGTGTTTC CTTCTTAAAGATACAAAATAAATGTAACATTAGACCTCTCACTA/CJGCTGTTTTTACTCTCCTCTG ATTTTTTTTCCATTATTTTTATTGCTCTGGCTTCATTTTGTAAATNTG

WI-1147b	204 G A ---	---	---	TTGCCATTATTTGAAGATAACCCACACCTTGGTGTCAGGGTTTTCACAGGATTAGTGGTCAGTCA CATAGGCATATAGTACCTGTATGACTTCTATTCCAGCCACCGCAAACTTCTCCTCCCTGGCTC CTGAGCCAAAACAGGCATTTACCATAAAATCACCTTTGTTAGGATGAATTTATCTGGCCAACTGATA C/GA/GCATGACCCACAGCCTCAGGTATATAAAACACTCTCATCAGGCAGA
WI-1158b	147 C T ---	---	---	GCATTCAGAGGGTTCGTTTATGACATTCACGTAGGCCCTGTCTATGTGAGGCCCTTGGTGTGAAGA CGCAATCATGAACAAAAATGAAATACAAATGTGATGGTCTCCTGAGTGTCTGAATG/C/GGCCAGGT TAAGTCTGGGG/C/TJCTGGGGTCAGGCTGCCTGGGTACATCCTGGCTCCAAACTGCTTTGCTATG GCT
WI-1158a	124 C G ---	---	---	GCATTCAGAGGGTTCGTTTATGACATTCACGTAGGCCCTGTCTATGTGAGGCCCTTGGTGTGAAGA CGCAATCATGAACAAAAATGAAATACAAATGTGATGGTCTCCTGAGTGTCTGAATG/C/GGCCAGGT GGCTAAGTCTGGGGCTCTGGGGTCAGGCTGCCTGGGTACATCCTGGCTCCAAACTGCTTTGCTATG GCT
WI-1304	124 T C ---	---	---	AAGTTACAGAAAAAATACCAGAAAAAGTACCTTCAAGANTCAGCTGAGATAGAAACATATGCCCA TCATCTTCAANGTNCACACAGACACTTATCCCTAGACAGCCATTTCTTTTGAATG/T/C/GNCANT AAAAATGATTTGAAATTTGGGAATAAAGCCCTCCCTCTAATGATTTGACAGTGTAGACCTTTGCCTAG GCT
WI-1305d	202 C T ---	---	---	TTCTCAATTCCTCAATCTGTGTACTTTTATTTCTTTCTTTCCATT/C/TJATGTTGGTAAATATAAAG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCAATTTNCAGAAAGATAAGGTTTTCTCTC TCCACTGCTTTCANTAAATTNACTCCACTNATGCTNACAAAATNACACTGTTTTAANTGNATATG/C /TJAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
WI-1305c	46 C T ---	---	---	TTCTCAATTCCTCAATCTGTGTACTTTTATTTCTTTCTTTCCATT/C/TJATGTTGGTAAATATAAAG ATGATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCAATTTNCAGAAAGATAAGGTTTTCTCTC ACATCCACTGCTTTCANTAAATTNACTCCACTNATGCTNACAAAATNACACTGTTTTAANTGNINATA TGCAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
WI-1305b	153 T C ---	---	---	TTCTCAATTCCTCAATCTGTGTACTTTTATTTCTTTCTTTCCATT/C/TJATGTTGGTAAATATAAAG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCAATTTNCAGAAAGATAAGGTTTTCTCTC TCCACTGCTTTCANTAAATTNACTCCACTNATGCTNACAAAATNACACTGTTTTAANTGNINATA TGCAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
WI-1305	202 C T ---	---	---	TTCTCAATTCCTCAATCTGTGTACTTTTATTTCTTTCTTTCCATT/C/TJATGTTGGTAAATATAAAG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCAATTTNCAGAAAGATAAGGTTTTCTCTC TCCACTGCTTTCANTAAATTNACTCCACTNATGCTNACAAAATNACACTGTTTTAANTGNINATA /TJAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA

WI-1306b	248 A G ---	---	---	TTTCTGCATTGGAATAGTTGACCTTCTATGAGNNNGCAATAATAATGGACAATCTTGNGNNNNTNG GGCTGGGTGACTGTGCTGGGTCAATTTAGAAGCCATAGAGTAGAAGTAGCCTGCAATAAAAGAGGA AAGTGAAGCTAATCTGAAGCTGTGACCTAAGGGNGAGAAAGTGGCCCTNNTTCTGATGGCTTTTCAGT CTGTGAGTACACTCCTTTGTGAAGGCCAGTTGAAATTTATCTCCTTGA/GGC
WI-1306	240 A G ---	---	---	TTTCTGCATTGGAATAGTTGACTTCTATGAGNNNGCAATAATAATGGACAATCTTGNGNNNNTNG GGCTGGGTGACTGTGCTGGGTCAATTTAGAAGCCATAGAGTAGAAGTAGCCTGCAATAAAAGAGGA AAGTGAAGCTAATCTGAAGCTGTGACCTAAGGGNGAGAAAGTGGCCCTNNTTCTGATGGCTTTTCAGT CTGTGAGTACACTCCTTTGTGAAGGCCAGTTGAAATTTGA/JTCTCCTAGC
WI-1307b	118 T C ---	---	---	GACAAGGCTGGTACTAGTTCCAAATCCAAATCTATGTACACTTTCTCTCACATTTCTCAAGTGGACA GATTTCTGCATTATAGTCTGGGGTTGGGGGAGCAGTGGTGTAGGCAAT/CJGTGAGATTGTCTTT CCTACCCCTTAAATGTATCTTNCATAATTATNATGCTAAACCGGTACTGTGATCTATCACTGGTT TCCTTTGGGTGTTGTTGCTGTTGTTTCTCCTGTAAAGNTGTTT
WI-1307	118 T C ---	---	---	GACAAGGCTGGTACTAGTTCCAAATCCAAATCTATGTACACTTTCTCTCACATTTCTCAAGTGGACA GATTTCTGCATTATAGTCTGGGGTTGGGGGAGCAGTGGTGTAGGCAAT/CJGTGAGATTGTCTTT CCTACCCCTTAAATGTATCTTNCATAATTATNATGCTAAACCGGTACTGTGATCTATCACTGGTT TCCTTTGGGTGTTGTTGCTGTTGTTTCTCCTGTAAAGNTGTTT
WI-1325b	169 T C ---	---	---	GAGAGATGGCCAAAGACAAGCAGAGGGAGAGAGAGCAACNTCTGTGGTTTATCGCAGCAAGCN ATGCTGTCTCCATACCCAGAAATGAGCATGTGCTCTCTCTATGTATAGATCAGATGACATGGAGAC ATTCAATTAGGCAACTACAATGTGCTTTGCTCTCTT/CJACCCCTCAGAACTTCTTGAGGGGCAGGC ATTATGATCCCACTTTACATCAGTGGGAATTTGGACTTGGTGAAGTTAGGTT
WI-1325	165 C T ---	---	---	GAGAGATGGCCAAAGACAAGCAGAGGGAGAGAGAGCAACNTCTGTGGTTTATCGCAGCAAGCN ATGCTGTCTCCATACCCAGAAATGAGCATGTGCTCTCTCTATGTATAGATCAGATGACATGGAGAC ATTCAATTAGGCAACTACAATGTGCTTTGCTCTCTT/CJACCCCTCAGAACTTCTTGAGGGGCAGGC ATTATGATCCCACTTTACATCAGTGGGAATTTGGACTTGGTGAAGTTAGGTT
WI-1327b	162 T C ---	---	---	CTACGATAATTAGGTTTGGCAGTGAGGGTATTAAAGCTGTGTAGTGAAGAAGTCTGTATTGTAAA ACACCAAGTGCGGTTTAAATGGAATGCGTATGTGTAGTNCATATTACGACAGGGCTGGGGANGACTC CAGCGACACTATGGAGCTGAGAGTCTGT/CJGAAGTTGGGTAGTACCAGGCTCCCCCAAATGTAGT TCTTNGCTGAAAGTCTCTCCTACTGAAGAGGCAATGGTTCATCTCTAAG
WI-1327	175 C G ---	---	---	CTACGATAATTAGGTTTGGCAGTGAGGGTATTAAAGCTGTGTAGTGAAGAAGTCTGTATTGTAAA ACACCAAGTGCGGTTTAAATGGAATGCGTATGTGTAGTNCATATTACGACAGGGCTGGGGANGACTC CAGCGACACTATGGAGCTGAGAGTCTGTGAAGTTGGGTAGT/CJTACCAGGCTCCCCCAAATGTAGT TCTTNGCTGAAAGTCTCTCCTACTGAAGAGGCAATGGTTCATCTCTAAG

WI-1341b	136 G A ---	---		TATCAGCATGATTGTGGCTGTTGGACACAAAGTCAATTTGTACTTTTGTGCTTNTGCTNNNTCCCTTTCTCTNTTT ACCTGATCCACTATCTTCTCAAGATCANGTTCAAATTTGGCTTNTCTTTGTTNAATTATACCCCAAGC [G/A]GGATTGTGATGGATCTGTTATTTCTCTGTCTTGGAAACAGCAGAGTCGTCTCTGNGAGTNTG GTTTCAGGATTGTCTCTGTTTCCCAGCCCACTTGCACTAGCAAGTGT
WI-1349e	192 G C ---	---		CTGACAAATGTCATATCTCACTCTCTAAACCCACAGGTCATAGAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGGCAGGTGGTAGGTCTGGCTGTGAGTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTCTGAATTTCCATCTCTGA[G/C]TTCAA ATAATTTGAGAAATATGATAGAAATTTGAAGTACTAGATTTCAGAAATA
WI-1349d	264 C A ---	---		CTGACAAATGTCATATCTCACTCTCTAAACCCACAGGTCATAGAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGGCAGGTGGTAGGTCTGGCTGTGAGTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTCTGAATTTCCATCTCTGA[G/C]TTCAA ATTTGAGAAATATGATAGAAATTTGAAGTACTAGATTTCAGAAATATGAT
WI-1349c	192 G C ---	---		CTGACAAATGTCATATCTCACTCTCTAAACCCACAGGTCATAGAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGGCAGGTGGTAGGTCTGGCTGTGAGTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTCTGAATTTCCATCTCTGA[G/C]TTCAA ATAATTTGAGAAATATGATAGAAATTTGAAGTACTAGATTTCAGAAATA
WI-1349b	264 C A ---	---		CTGACAAATGTCATATCTCACTCTCTAAACCCACAGGTCATAGAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGGCAGGTGGTAGGTCTGGCTGTGAGTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTCTGAATTTCCATCTCTGA[G/C]TTCAA ATTTGAGAAATATGATAGAAATTTGAAGTACTAGATTTCAGAAATATGAT
WI-1349	264 C A ---	---		CTGACAAATGTCATATCTCACTCTCTAAACCCACAGGTCATAGAATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGGCAGGTGGTAGGTCTGGCTGTGAGTTGATATATATG GCAGGTGCTCAACAAATGTAGATTCAGTGAAGGATAGTCTGAATTTCCATCTCTGA[G/C]TTCAA ATTTGAGAAATATGATAGAAATTTGAAGTACTAGATTTCAGAAATATGAT
WI-1403b	57 C T ---	---		TGGTATTGGAAATGGGTTCCAGACTCCGGGTTCTGGCTCTGACCTTTGGTAAGTTG[C/T]TCCGAAT GCCACTTTATAAGTTAGAGGTATTACCTTGGAGGGGGGACGTAGAGTAAGCCATAAAATATACGT AAAGTTACATCAACATAATCTTGGCTGTCATGCAATTTGGCAATATGTCACATAGCTGTCTCA TAATCCCCAAGTGCCAAAAGGGTTGATCTGATTGT
WI-1403	58 T C ---	---		TGGTATTGGAAATGGGTTCCAGACTCCGGGTTCTGGCTCTGACCTTTGGTAAGTTG[C/T]TCCGAA TGCCACTTTATAAGTTAGAGGTATTACCTTGGAGGGGGGACGTAGAGTAAGCCATAAAATATACG TAAAGTTACATCAACATAATCTTGGCTGTCATGCAATTTGGCAATATGTCACATAGCTGTCTC ATAATCCCCAAGTGCCAAAAGGGTTGATCTGATTGT

WI-1417c	31 C T ---			CAGGCCGAAGAGATTACGCTGGAGAGATGTC/TTTGGCCAGGGGGGCGAGATGTGAGCCCCACGGG GGTGACAGCATGCCCTGCTGGCAATTTGGAGGGCCCCAGAAAGGAATCCAGTGGCCCTCTCAATGACTTG GGTCTCGACTTCGGAAGTTTAAGGGGCTCGGCTTCAAAAAGCTGGGTCCGGTTTGGAGCGGTTGC AGGCAGGCCCTTAGGTCGGTATTTAATGTTTGGTTGTAGAAAAAGTCGC
WI-1417b	31 C T ---			CAGGCCGAAGAGATTACGCTGGAGAGATGTC/TTTGGCCAGGGGGGCGAGATGTGAGCCCCACGGG GGTGACAGCATGCCCTGCTGGCAATTTGGAGGGCCCCAGAAAGGAATCCAGTGGCCCTCTCAATGACTTG GGTCTCGACTTCGGAAGTTTAAGGGGCTCGGCTTCAAAAAGCTGGGTCCGGTTTGGAGCGGTTGC AGGCAGGCCCTTAGGTCGGTATTTAATGTTTGGTTGTAGAAAAAGTCGC
WI-1729	172 A ---			CCATGAGCAAAACAGCATGTTTCTACTCTGTGATGTGTATGTTAGGGGGCATGTATATCTGTATTTCTT TTTTATTCTCTCCAAAAGAAATTCATATGCAAAACATTATCAGGCAATGCAGCTCGTAATAAAGA TGTTGGAGAACTGAAAAGAGAGACTTACATGCACCCCAATAGCAAAACTCTCCACACATTTCCAGCA GATGATGTGTCCTTCGGTGGTNACCTTCTCCTCCACCACATCACCTGTGTTTTT
WI-1732b	122 T C ---			TGCCCTACTCTTTGTTCAATCCACCATTACATTTTGTAAATTTGGAATTTAGGAGGTAGAAGGA TATGCTGATCAAAAAAGGGGACATATTCAGGAGTNTCCCTGGTCAACCTTTT/CJATTGAGTCT CTGCCACATGTCTAGTAAGTGTGATGGTGCATGATATACTCGAGCCTCCCAAGGTACAGC CTTTCACACTATTTCATATATTGGCTAAGGTATTCATCATATATTGGCTAAG
WI-1732	114 C T ---			TGCCCTACTCTTTGTTCAATCCACCATTACATTTTGTAAATTTGGAATTTAGGAGGTAGAAGGA TATGCTGATCAAAAAAGGGGACATATTCAGGAGTNTCCCTGGTTC/TAACCTTTTATTTCAGTCT CTGCCACATGTCTAGTAAGTGTGATGGTGCATGATATACTCGAGCCTCCCAAGGTACAGC CTTTCACACTATTTCATATATTGGCTAAGGTATTCATCATATATTGGCTAAG
WI-1750	97 A G ---			GCGAATTTAATGACTCCAAAGGTAGTAATTCCTTTCCCCCAAAAAAGGTTTTAAATCTGTGTTGGA CATAATGTTGAATTTGCAGTTACCTTGG/TTTAAAGGTGTGCTTTTCTGGCAAAAGAGTCAG TGGAGTGTCCGGGAAAGGGCTAAGTCTTTGTAGTCAGACAAACCGGCTTGCAGTCCCTGACTGAG CTACATTCACTTTATGATCTCCAGCAGGTTCTTCCA
WI-1780	31 A G ---			GGTACACAAAGAAATGCTTCTGGAAATCTAC/AGTJAGCGCCTTAACATTTTGGCTGAGTATTAATC TGACATGTGTAAATGTGAACCCACCATGAAGCTGGGCAAGAACAAATTCCTAGGAAAGTACAATTAC TGGGAAACTGTAGAACAAATAATCTCATAGTTTACACATAGCTGGGGAATCACTCATGTTCOCATCA ACTGGAGAGACCTTGTGAGTACAGAGGACATTCAGGAATAATCATAAAAAT
WI-1803c	77 A G ---			CCACTCAGTAATAATAGTGTGGAGATAAGTATATGGTAGGCACATAATAATTTTTCAGGCAGAA CCATTATGAT/AGTJAGGTAGGATGAGCATCACACTTGGGAGGACATATCTGGAGTNAGATATCCTG GGTGCTAATTTCAATATATCTACTAAGGATGACTTCTAGAAAATTTACTTATTACTCTTGTCTCTCAA GGAAATGGGAATACCTATAATACAGTCTTATTGAGGAAATAACTGGAATCA

WI-1803b	77 A G ---	---	---	CCACTCAGTAATAAGTGTGGAGATAAGTATATGGTAGGCACATAATAATTATTTTCAGGCAGAA CCATTATGATAGAGTAGGGTAGAGCATCACACTTGGGAGGACATATTCCTGGAGTNAGATATCCTG GGTGCTAATTTCAAATATATCTACTAAAGCATGACTTCTAGAAAATTACTTATTACTCTTGCTCCTCAA GGAAATGGGAATACCTATAATACAGTCTTATTGAGGAAAATAACTGGAATCA
WI-1837b	112 C T ---	---	---	TTTACTGGGATTTTCATAGCTGATCATAATTACCAATTTGATAATTCACCTCTTTTCCAGGGCTCA AGGCTGATAAGCAGTTATCCAGATAGAATAGACCCGTTTATAC[CTGCTGCCAGTTTATTTTT AAGGTTTTTTTTCATTGCACCTGATGCCAAACAAAACCTCAAAGACCTTGAGTGAATTTTGAGCT CGTGTAACTGGGAAGTCTGGGGAACGTTTAGCTTCTGCTGGCT
WI-1837	112 C T ---	---	---	TTTACTGGGATTTTCATAGCTGATCATAATTACCAATTTGATAATTCACCTCTTTTCCAGGGCTCA AGGCTGATAAGCAGTTATCCAGATAGAATAGACCCGTTTATAC[CTGCTGCCAGTTTATTTTT AAGGTTTTTTTTCATTGCACCTGATGCCAAACAAAACCTCAAAGACCTTGAGTGAATTTTGAGCT CGTGTAACTGGGAAGTCTGGGGAACGTTTAGCTTCTGCTGGCT
WI-1840b	79 G T ---	---	---	TCACCTAGGGAGGTGCTAAAATGTAGCTTCATTAAAGACACCTCAGACCTATTGGATCAGGATCTT TCAGGTAGCAGT[G]GAGAATCTGAATATTCAGCACATACAAGTGTGACAACCACTTGTTTAGTAT ATTTATCTCCAGAGTGTTTTGAATTTACTAAAAAGTTCTAAAGAGCCATGAAGAAATTATAAGACT ATCGCA
WI-1840	79 G T ---	---	---	TCACCTAGGGAGGTGCTAAAATGTAGCTTCATTAAAGACACCTCAGACCTATTGGATCAGGATCTT TCAGGTAGCAGT[G]GAGAATCTGAATATTCAGCACATACAAGTGTGACAACCACTTGTTTAGTAT ATTTATCTCCAGAGTGTTTTGAATTTACTAAAAAGTTCTAAAGAGCCATGAAGAAATTATAAGACT ATCGCA
WI-1879b	110 C T ---	---	---	GGGCTCATTTCATCAGAGCACATATCAGTGATAGTCTGTTCTTTTCATAACTTACTCCCGG CACTGTAGGNTTCTTTTGAGGTNAAGGACCTGCCNTTTTAC[CTGCTGCNAAATAAACTCCCAAAA AAGTGGTAGTCCACAGGGTTTAAATAGTCTTGTGAATGAATTTCTGTGCGACCCCTGTGCTTCT CAAGAAAAAAAACATTGAAAAATCTCCACAGAGCCCTTACCCACT
WI-1879	110 C T ---	---	---	GGGCTCATTTCATCAGAGCACATATCAGTGATAGTCTGTTCTTTTCATAACTTACTCCCGG CACTGTAGGNTTCTTTTGAGGTNAAGGACCTGCCNTTTTAC[CTGCTGCNAAATAAACTCCCAAAA AAGTGGTAGTCCACAGGGTTTAAATAGTCTTGTGAATGAATTTCTGTGCGACCCCTGTGCTTCT CAAGAAAAAAAACATTGAAAAATCTCCACAGAGCCCTTACCCACT
WI-1900b	119 C T ---	---	---	TGTTCTGTGTCAGGCACCGGGCTAAGTCTTGTCTGCATAATGGAATAATCAACTGGACAACCCNG CTNAGGTAGNTACCTNGGCAATTAGCCCCCTTACAGCTGCAAAAGAGG[CTGCTCTGAGAGGT AAAGTCCCTGCCCAACGGGCAACTAGAGAGAGCCAAACAGGTTTGAACCCAGCTCTGCCT GACTTCAGATCTGTGTGCTTAAGTGCAATGAGAAACCACTTTCTTTGCTCC



WI-1900	119	C T ---	---	---	TGTTCTGTGTCAGGCACCGGCTAAGTCTTGCTGCATAATGAATAATCAACTGGACAACCCNCNG CTNAGGTAGGNTACCTNNGCAATTAGCCCCATCTTACAGCTGCAAAAGAGG[C/T]GCTCTGAGAGGT AAAGTGCCTGCCCAACCGGCACAACTAGAGAGGACCAACAGGTGTTTGAACCCAGCTCTGCCT GACTTCAGATCTGTGCTTAAGTCCATGAGAAACCACTTCTTGCTCC
WI-1943c	165	C T ---	---	---	ATTCCAGTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGAGGTGGCACCTGTGACCTGGCTAANCATGCTACTTTCAGAGTCAAGC AGCAAGCCAATGGTAGGGAAGACCAAGC[C/T]CTCTGAANCTGGTCCACGTCGAGATAGTGAA TACAGGGCACCGNTGAGCATTCCAGATGACTCCAAAGCCCCGGCTGGAGTAT
WI-1943b	165	C T ---	---	---	ATTCCAGTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGAGGTGGCACCTGTGACCTGGCTAANCATGCTACTTTCAGAGTCAAGC AGCAAGCCAATGGTAGGGAAGACCAAGC[C/T]CTCTGAANCTGGTCCACGTCGAGATAGTGAA TACAGGGCACCGNTGAGCATTCCAGATGACTCCAAAGCCCCGGCTGGAGTAT
WI-1943	164	C T ---	---	---	ATTCCAGTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGAGGTGGCACCTGTGACCTGGCTAANCATGCTACTTTCAGAGTCAAGC AGCAAGCCAATGGTAGGGAAGACCAAGC[C/T]CTCTGAANCTGGTCCACGTCGAGATAGTGAA TACAGGGCACCGNTGAGCATTCCAGATGACTCCAAAGCCCCGGCTGGAGTAT
WI-1960c	270	A T ---	---	---	CCAGGTGAGGCTGAAAGAAAGGAGGCAATTGCTGTTGGAGTGAGGATTCGGAGAAGCACCCCT GCAGAGCTTCATTCTGTTTCAAAAGTGTGCCATGCANGGTCNTCTGGTTGTGAGCTCATNGCTGAG TTATCACAGCTCCTGATGACAGATCATGAAAAATAGGTACTTCCCAAGCTCTGACTAGACCTTGGCA GTTGCAATTAAATCCGTGGTGTCTGAAAACTTAAAAATGCACCTCCCAACTTT
WI-1960b	270	A T ---	---	---	CCAGGTGAGGCTGAAAGAAAGGAGGCAATTGCTGTTGGAGTGAGGATTCGGAGAAGCACCCCT GCAGAGCTTCATTCTGTTTCAAAAGTGTGCCATGCANGGTCNTCTGGTTGTGAGCTCATNGCTGAG TTATCACAGCTCCTGATGACAGATCATGAAAAATAGGTACTTCCCAAGCTCTGACTAGACCTTGGCA GTTGCAATTAAATCCGTGGTGTCTGAAAACTTAAAAATGCACCTCCCAACTTT
WI-1977	203	T C ---	---	---	CTGATGCCAAGTGCAGCTTAGAGTNAGGAATCCAGAGAAAGTNTTGGATCTGGTAAGTAGGATCA TTCTGGGCATTCTTCATAGAGTNTGTTTTTAGTCTCGTAATAACTGTGTCCTAGGAAGGTTGTT TTTCTACTGCGTCTGTGAAAGCCTTCCCATCGAGTGATACAGTACTTCCAGTTATGGAGATTTT /C]TAACAATCAAACTGAGGCTGAGGCTGTTGG
WI-2012	102	T C ---	---	---	AAATTCAGAAGCCAGAAGTCAGCTCAGGATTTATAAGTTGAAGTAAATGCATTGTAGTTTCATGT TTTCTCTTAATCTGCACAAAACCTAGCTAAAAATC[T/C]TTTAAATCAGTTACCAGAGGCAATACCT GGGTTAATGTAGCACTCAAAAGTTATGTAGAGTAGCTGTCTGAGTCACTTTTTCTACTCTCATT GGCTTACCAATGCTTCCACTGGATC

WI-2013	127 C T	---	---	CTTTAGAGGTGGTCATTTGGTTCCTTCGGAAAGTGATTCGGTTAAGAAAAATAGATGCAACG TTGCTAAGTAGACAGCTAACATTTAAACAGTCTCCAGCAGATAAATGCTGATACTGACACTTC/TTCTCA CCAGAAAAAGAGAAATACCCATCATGAGGAAGAGAAATGACITTTTTCAGTTATGCTCCCGGGTCC CCTTTCACTGGAGGATATCTCAGCTTTCTGAGCCCTGGTTACTGCAATCC
WI-2032c	166 G A	---	---	ACCAGACATCCCATCAGGAGTTAGTCCCTCTGGCAAGCCAGCCCTGCCCTTCTGATTTCCCAAAACC TCAATTTTCTTNACTTACTCATATAATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAACCC ACATCACCCAACTGGTTTCTAGATGTACAC/GAJTGTTGGACCTCTGTCTCAACCTCCGACTTTTCAC AGATCATTTGGTTAGGCTCACCTTCTCTGTAATTGCTCTCTGTTTTCAAAGGG
WI-2032b	219 C G	---	---	ACCAGACATCCCATCAGGAGTTAGTCCCTCTGGCAAGCCAGCCCTGCCCTTCTGATTTCCCAAAACC TCAATTTTCTTNACTTACTCATATAATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAACCC ACATCACCCAACTGGTTTCTAGATGTACACGTGTTGGACCTCTGTCTCAACCTCCGACTTTTCACAGA TCATTTGGTTAGGCTCA/C/GTCTTCTCTGTAATTGCTCTCTGTTTTCAAAGGG
WI-2032	219 C G	---	---	ACCAGACATCCCATCAGGAGTTAGTCCCTCTGGCAAGCCAGCCCTGCCCTTCTGATTTCCCAAAACC TCAATTTTCTTNACTTACTCATATAATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAACCC ACATCACCCAACTGGTTTCTAGATGTACACGTGTTGGACCTCTGTCTCAACCTCCGACTTTTCACAGA TCATTTGGTTAGGCTCA/C/GTCTTCTCTGTAATTGCTCTCTGTTTTCAAAGGG
WI-2054b	188 C T	---	---	CGTTTTCTTCTACATCTTTGGGNACATAAAGANGAAAGAGNAGCTGCTTTTGTGGTAGTTTGTCT CAGAGCTGCCTAGAGCNAGGACAAGACAGGTGACCTTTCAAAATACCTTACAGACTTAGGATTTGGA TTTTCAATGGTGGTTGGCACAGCCAGGCTCAACAGAACTAATACCTGCTTC/TTCTGCTCCAC CAGCCCTATCTCTTAGGCTCAAGGAGAAATTTTACTGGATGGGCTGCTTT
WI-2054	183 T C	---	---	CGTTTTCTTCTACATCTTTGGGNACATAAAGANGAAAGAGNAGCTGCTTTTGTGGTAGTTTGTCT CAGAGCTGCCTAGAGCNAGGACAAGACAGGTGACCTTTCAAAATACCTTACAGACTTAGGATTTGGA TTTTCAATGGTGGTTGGCACAGCCAGGCTCAACAGAACTAATACCTGCTTC/TTCTGCTCCAC CAGCCCTATCTCTTAGGCTCAAGGAGAAATTTTACTGGATGGGCTGCTTT
WI-2573d	129 T C	---	---	TGGGATTAACACCCGTTTTCTTCTCTCCAGTTCCAGTTCAGTGGCTTAATGTTTGTGTAGAAATTAACA TTAACAGCAGTAAAAATAGCTCTTAAATGCACCTGCCGTTCAAGGTTTCCGTCCTTT/CJ/GA TATCATCTGATCTTCCCAACAGGCTTATTTATGCTAGGTAGGGGTAGCAACAGAGGCTGTGT GAAGTGAATGATTTGCTTGCACAGGTCAATGCTGGGCTTGGACGAG
WI-2573c	165 A C	---	---	TGGGATTAACACCCGTTTTCTTCTCTCCAGTTCCAGTTCAGTGGCTTAATGTTTGTGTAGAAATTAACA TTAACAGCAGTAAAAATAGCTCTTAAATGCACCTGCCGTTCAAGGTTTCCGTCCTTTTGTATAT CATCTGATCTTCCCAACAGGCTTATTT/CJ/GCTAGGTAGGGGTAGCAACAGAGGCTGTGT TGAAGTGAATGATTTGCTTGCACAGGTCAATGCTGGGCTTGGACGAG

WI-2573d	129	T C ---	---	TGGGATTAAACCCCTGTTTCTTCCCTCCAGTTCAGTGGCCTTAATGTTGTGCTAGAAATTAACA TTAACAGCAGTAAATAGCTCTTAAATGCACCTTCCGTTTCAAGGTTTCCGTTGCTTT/CJTGA TATCATCTGATCTCCCAACCCAGGGCTTATTTATGCTAGGTAGGGTAAGCAACAGAGGCTGTGT GAAGTGAATGATTGCTTGCACAGGTCATATGGCTGGCTTGGACGAG
WI-2573c	165	A C ---	---	TGGGATTAAACCCCTGTTTCTTCCCTCCAGTTCAGTGGCCTTAATGTTGTGCTAGAAATTAACA TTAACAGCAGTAAATAGCTCTTAAATGCACCTTCCGTTTCAAGGTTTCCGTTGCTTTTATGATAT CATCTGATCTTCCCAACCCAGGGCTTATTT/CJTGCCTAGGTAGGGTAAGCAACAGAGGCTGTG TGAAGTGAATGATTGCTTGCACAGGTCATATGGCTGGCTTGGACGAG
WI-2573b	165	A C ---	---	TGGGATTAAACCCCTGTTTCTTCCCTCCAGTTCAGTGGCCTTAATGTTGTGCTAGAAATTAACA TTAACAGCAGTAAATAGCTCTTAAATGCACCTTCCGTTTCAAGGTTTCCGTTGCTTTTATGATAT CATCTGATCTTCCCAACCCAGGGCTTATTT/CJTGCCTAGGTAGGGTAAGCAACAGAGGCTGTG TGAAGTGAATGATTGCTTGCACAGGTCATATGGCTGGCTTGGACGAG
WI-2573a	129	T C ---	---	TGGGATTAAACCCCTGTTTCTTCCCTCCAGTTCAGTGGCCTTAATGTTGTGCTAGAAATTAACA TTAACAGCAGTAAATAGCTCTTAAATGCACCTTCCGTTTCAAGGTTTCCGTTGCTTT/CJTGA TATCATCTGATCTCCCAACCCAGGGCTTATTTATGCTAGGTAGGGTAAGCAACAGAGGCTGTGT GAAGTGAATGATTGCTTGCACAGGTCATATGGCTGGCTTGGACGAG
WI-2868b	60	A G ---	---	GACTTCATGCTCATGAACAAGCATTGTCTTAATTTACAGACATTAGAACAAGCTTTCC/A/GJCTC CCACTTCCCTCCCACTACCTCAACCTCTTCAATCCACTTTAAAGAGGTTTCTTTAGGTCCTCTGCAT ATCATGGAAGCCCACTACTCTATTAAACGCTTCCCAATGATGCAGCCCAAGTTCTGCATACAGTTTGT CAGAAATGCTATATTTATGGAACACAGCTGAAAAATGAAATATCGATATAC
WI-2868	60	A G ---	---	GACTTCATGCTCATGAACAAGCATTGTCTTAATTTACAGACATTAGAACAAGCTTTCC/A/GJCTC CCACTTCCCTCCCACTACCTCAACCTCTTCAATCCACTTTAAAGAGGTTTCTTTAGGTCCTCTGCAT ATCATGGAAGCCCACTACTCTATTAAACGCTTCCCAATGATGCAGCCCAAGTTCTGCATACAGTTTGT CAGAAATGCTATATTTATGGAACACAGCTGAAAAATGAAATATCGATATAC
WI-2870b	131	T C ---	---	CATGCTGTGTAACTCTGTGCTGCTTGTGCTCGGGGAAATTAGAGCAAGGAATTGTATATCCTAGGC TTCAAGGAGCTTCTCATCTCATTTGAGGAGACAAAGATGAACATCAGGAAATGACTGGATAATGAIT/CJ AGAAATGAATAGAGCCCACTTTAAATTTATATCACAGCTTTATGTCCACTTCTGTTCTGCTGCCATCAC TGGGCTTTTACAAAGGAGGGCTTT
WI-2870	131	T C ---	---	CATGCTGTGTAACTCTGTGCTGCTTGTGCTCGGGGAAATTAGAGCAAGGAATTGTATATCCTAGGC TTCAAGGAGCTTCTCATCTCATTTGAGGAGACAAAGATGAACATCAGGAAATGACTGGATAATGAIT/CJ AGAAATGAATAGAGCCCACTTTAAATTTATATCACAGCTTTATGTCCACTTCTGTTCTGCTGCCATCAC TGGGCTTTTACAAAGGAGGGCTTT

WI-2954c	49 T A ---	---	TTAGCACATATCTGTGTGGGACTTAACCTGAGACAAAGGATAAAAAAT/AJAGCACCTCTGGGGCA CAGAGGGAGCTCTATGCATTNAATTCCTCATACCTACCCCTCCTCTCATTCATCAATGAGTCCTTTGAGT CCTTGGAAAGACTCTATCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTCGACAAATAAGTCCA GAG
WI-2954b	41 A G ---	---	TTAGCACATATCTGTGTGGGACTTAACCTGAGACAAAGGCA/GJTAATAAAATCAGCACCTGGGGCA CAGAGGGAGCTCTATGCATTNAATTCCTCATACCTACCCCTCCTCTCATTCATCAATGAGTCCTTTGAGT CCTTGGAAAGACTCTATCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTCGACAAATAAGTCCA GAG
WI-2954a	38 G T ---	---	TTAGCACATATCTGTGTGGGACTTAACCTGAGACAA/GJTGATATAAAATCAGCACCTGGGGCA CAGAGGGAGCTCTATGCATTNAATTCCTCATACCTACCCCTCCTCTCATTCATCAATGAGTCCTTTGAGT CCTTGGAAAGACTCTATCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTCGACAAATAAGTCCA GAG
WI-2971b	62 T C ---	---	ATTACAAATCCTACCTAGCAACTGCTGACACTTCCAGTTAGACTCACCAGCATTTCTAAGA/T/CJG CTGCCAGCACCAATAAGCTTTCTTCAAACAATTTGTGAACCTCCTCTCTTAAATAAACCTAAG ATTTCCCTTTGTTCCCTGACATCTGAAGGCCACGCTGGTCTAGATGTATGCCAGATTGCAATCCT AGTCTTTAATGTTATCTGAAAGAAACCTTTTACTTAGGGATTGGCT
WI-2971	62 T C ---	---	ATTACAAATCCTACCTAGCAACTGCTGACACTTCCAGTTAGACTCACCAGCATTTCTAAGA/T/CJG CTGCCAGCACCAATAAGCTTTCTTCAAACAATTTGTGAACCTCCTCTCTTAAATAAACCTAAG ATTTCCCTTTGTTCCCTGACATCTGAAGGCCACGCTGGTCTAGATGTATGCCAGATTGCAATCCT AGTCTTTAATGTTATCTGAAAGAAACCTTTTACTTAGGGATTGGCT
WI-2995d	133 A T ---	---	TTCTGGGAAAGAAAGATGGGGGTTTTNTGTTCTCTGACTACATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAGGAGCTGGANTTTTTTIA /TAAATCTTTCTTTCTGGTGTAAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAA GAATGAGACAGAACTAGCAGAAAGTGT
WI-2995c	151 G C ---	---	TTCTGGGAAAGAAAGATGGGGGTTTTNTGTTCTCTGACTACATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAGGAGCTGGANTTTTTTIA AATCTTTCTTTCTGGTGTG/CJTAAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGT
WI-2995d	133 A T ---	---	TTCTGGGAAAGAAAGATGGGGGTTTTNTGTTCTCTGACTACATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAGGAGCTGGANTTTTTTIA /TAAATCTTTCTTTCTGGTGTAAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAA GAATGAGACAGAACTAGCAGAAAGTGT

WI-2995c	151	G C ---	---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTNTATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTNA AATCTTTCTTTCTGGT[G/C]TTAAGGAAGTTATCTGAAACCCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAAGTAGCAGAAAGTGTT
WI-2995d	133	A T ---	---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTNTATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTNA AATCTTTCTTTCTGGT[G/C]TTAAGGAAGTTATCTGAAACCCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAAGTAGCAGAAAGTGTT
WI-2995c	151	G C ---	---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTNTATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTNA AATCTTTCTTTCTGGT[G/C]TTAAGGAAGTTATCTGAAACCCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAAGTAGCAGAAAGTGTT
WI-2995b	151	G C ---	---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTNTATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTNA AATCTTTCTTTCTGGT[G/C]TTAAGGAAGTTATCTGAAACCCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAAGTAGCAGAAAGTGTT
WI-2995a	133	A T ---	---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTGTTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTNTATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTNA AATCTTTCTTTCTGGT[G/C]TTAAGGAAGTTATCTGAAACCCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAAGTAGCAGAAAGTGTT
WI-3147	85	C T ---	---	---	GTGGTGCAGTTTCATCCTCTGGAGCTCCCTGTGAGATCAGACTGGAGCCAGTCTCCAGCTTGAGACCCAC ATCTCACTTAGCTCCTTC/TCTGCCCATATCCTGTTTCCCTTACTCTCTATCTCTGAGACTTCTCCT GAATGAATTACATGCACCTCAATCCCTGCCTCAGTCTCTGCTTTNAGGGAACCTTGACCTAAGACAGAA ATCTTAGTACCATAATACITTTGCAAGG
WI-3234b	68	T C ---	---	---	ATTCTGAATGTTTTCAGTCTCCAGTAAATTCITTTATTGAGGTCCATGTCCATTACCTCTACTTA T/C]GACAAGCAAGAAACAACAACAGAAAGCCCTGTTTGCAATCTGGCCCTCTTATAAATACITTTCTG TATATTTAAACAAGTACTGTAGAGTNATGAATCATTACATCCTTAATAAGCATATCAAAATTTTAC TCAGTAATTCAGAAGAAAGGACAAATGGAATGTACTTATTTTATCTTAT
WI-3234	68	T C ---	---	---	ATTCTGAATGTTTTCAGTCTCCAGTAAATTCITTTATTGAGGTCCATGTCCATTACCTCTACTTA T/C]GACAAGCAAGAAACAACAACAGAAAGCCCTGTTTGCAATCTGGCCCTCTTATAAATACITTTCTG TATATTTAAACAAGTACTGTAGAGTNATGAATCATTACATCCTTAATAAGCATATCAAAATTTTAC TCAGTAATTCAGAAGAAAGGACAAATGGAATGTACTTATTTTATCTTAT

WI-3292b	106	G A ---	---	---	GTTTGTAGACTAGGAGTTTCAGCTTCATCCAAATCCCTTTAAGGATANTTAGCTCTGCACATCC TCCCTGTCCTCCGTCACAGCCTATGTTACTGGTATGCTGATGGTATGGATGGGATGATTACTT GCCATGAATATTTCCATTGTTCTCATTAAATGATTAATTAATTAAGTAAATATATTNNCCATGA GACAAATGGAAAAATGGAAACATTCATGGAAAAAACCCATTCAATC
WI-3292	106	G A ---	---	---	GTTTGTAGACTAGGAGTTTCAGCTTCATCCAAATCCCTTTAAGGATANTTAGCTCTGCACATCC TCCCTGTCCTCCGTCACAGCCTATGTTACTGGTATGCTGATGGTATGGATGGGATGATTACTT GCCATGAATATTTCCATTGTTCTCATTAAATGATTAATTAATTAAGTAAATATATTNNCCATGA GACAAATGGAAAAATGGAAACATTCATGGAAAAAACCCATTCAATC
WI-3355	19	G C ---	---	---	CCATGAACCATGGGCTACA/GCJATATTCCTAACTCAGAGTCCCTTACTGGAGAGGGATCCA CTTTTAAATATGATTTCTGAAGTGGCTGCATATTCCTCCAGCACCTTAAACTCATCAGAA AAAAAATCATCAAAAGTCGAAGTTAGTTTATACCTTACCCTTTCAATGGAAAACTTTATAA ACTGGGATCAATTTATTTACTTTTGGATCAGTTTAGATGACTTINAGTTG
WI-3408	194	G A ---	---	---	CCATGAAGAATGAGTTCCCTCCCTCCCTGGGTGCTAGCTAAGAAATAGCACACCCCTTGAGAAATTTNACT TAGCACGTGGCATTGTAATGGCTGGATTTCTCCGCTCTAAGACACACCTTTATGCTTTTCAAGCTTT CTGGAATGGGATGAATCINACATTCATGTCACCTTCGTGGGATCACTTCTCC[G/A]TGCCCC ATCTGAGNAGAACCCACTGGGAAGTCGAAGGAGTCAATCAATCAGG
WI-3505b	131	G A ---	---	---	TAACTTATGCCTCATCTGGCTTACTGCTTAGTCCCATTTGTCATCAGTGCACCTTAAAAATTTT GAAAAATGGCATTATTAATATCTTTGGAAGTTCTTAACACATTACCTATTTTNAACCAAAC[G/A] AGGTATTCCTTATGGGAAATATATACAGCAAGAAAAAANANGGAAAAATGTTGATGATACCT GTTTAAATGGGAAATATGTTTGCATAT
WI-3505	131	G A ---	---	---	TAACTTATGCCTCATCTGGCTTACTGCTTAGTCCCATTTGTCATCAGTGCACCTTAAAAATTTT GAAAAATGGCATTATTAATATCTTTGGAAGTTCTTAACACATTACCTATTTTNAACCAAAC[G/A] AGGTATTCCTTATGGGAAATATATACAGCAAGAAAAAANANGGAAAAATGTTGATGATACCT GTTTAAATGGGAAATATGTTTGCATAT
WI-3564b	177	C T ---	---	---	GCTAGTAAGGTTCCACCTAAATGGTTCCAAAGTCAGGAGAGTCACTAAATGTTTGGAAAAATAAAGT GAAATCAATGTCTTCCAGTGTATTCACATGGCAGAGTGCACAGAGGCTTGAGCGCTGAGCG TGGGACTTCACTGGTTGACTAACGTTAACATGCATGCTGTTCTTACAAGTGTGTTGTTGTTGTCATC AGTGTACACATGCTACCTTCTTACAAAAACAAA
WI-3564	177	C T ---	---	---	GCTAGTAAGGTTCCACCTAAATGGTTCCAAAGTCAGGAGAGTCACTAAATGTTTGGAAAAATAAAGT GAAATCAATGTCTTCCAGTGTATTCACATGGCAGAGTGCACAGAGGCTTGAGCGCTGAGCG TGGGACTTCACTGGTTGACTAACGTTAACATGCATGCTGTTCTTACAAGTGTGTTGTTGTTGTCATC AGTGTACACATGCTACCTTCTTACAAAAACAAA



WI-4110	130	T C	---			GAAATGATGTTTTGATTTCCCTTCTCTATCTTCAGATTATTGGAGTGTCAATTAGAAAACTGATAGT AACCTTTATTTGATGAACTCTGTCTATAATTAAACCTTCTCTCTCTCTTTATTTTGGCTTCJACA GTTTAGGTAAATAAAGATGCCAAGAAATTCAGTATTTCAAGTACAGTAAAAAGTAGCAACCATGGG GTAGGCAAGTNCAGAAAAAGGAGGAGGTTGGGGGTTTCTGGGAAGA
WI-4119b	168	G A	---			ACCTCTATGCCTGAAAGCCCTCATGAGTGTCCAGCAAGGCTTGGGTGGAAAAAGTAAATAATAG AATGGAAGGATAAATAAAGGTAACTACGGGGAAGAACAGAGCAAGAACAGACAGAAAGGGGTT AGAGGAAGGAATCAGTTGTGTGCCATTCAAAGTTAA[G/A]CAAGGTACCAAATTTGTTTTCTTTCA TGAGACCGTCTGCATCTTTTGTTTTAAAGGGCTCTGTTGATCATCATCTTCA
WI-4119	168	G A	---			ACCTCTATGCCTGAAAGCCCTCATGAGTGTCCAGCAAGGCTTGGGTGGAAAAAGTAAATAATAG AATGGAAGGATAAATAAAGGTAACTACGGGGAAGAACAGAGCAAGAACAGACAGAAAGGGGTT AGAGGAAGGAATCAGTTGTGTGCCATTCAAAGTTAA[G/A]CAAGGTACCAAATTTGTTTTCTTTCA TGAGACCGTCTGCATCTTTTGTTTTAAAGGGCTCTGTTGATCATCATCTTCA
WI-4123b	51	T G	---			CAAAGTCAGATTTTGATTATTCAGGATAACAATTTTGAAAAATAGAAAAAGTG[T/G]TTAAACTATTT CAAATAACAATAAAGAAAAACATGATGAAATTTCTCGTTACATAATTGTATAGAAATTTAGTGGGG TTCTTCCATGACATTGGCTTGTCTTCTCAACAGTGGGTGGTTGGATGTTTTCCTATGCTTTCTC AGGCACAAACAACAGTGAAGAAACCTTTAGCAACATTTCTGCTGAATGTGTG
WI-4123	51	T G	---			CAAAGTCAGATTTTGATTATTCAGGATAACAATTTTGAAAAATAGAAAAAGTG[T/G]TTAAACTATTT CAAATAACAATAAAGAAAAACATGATGAAATTTCTCGTTACATAATTGTATAGAAATTTAGTGGGG TTCTTCCATGACATTGGCTTGTCTTCTCAACAGTGGGTGGTTGGATGTTTTCCTATGCTTTCTC AGGCACAAACAACAGTGAAGAAACCTTTAGCAACATTTCTGCTGAATGTGTG
WI-4149b	145	G C	---			TTGTACATGTTCAATTCATCCCTCCCATTTCTTTCTGTCTTATAAGAACCTCGCTTCTTCTCCAAGT CTTACTTCTCCACCTGAGCCACAGATCTCTTTATTTCCATCAAAGCTTCTCAGCATCTTCTATATACT GTGCTGT[G/C]CCTTGTGAAGAGCCAGAGCCGAGCATACCAACATGATCTTTTGTGTTGAAGTGTAGT AGGAGAGACAAGACAGATGTGCGGGTCCCATGATATAAGGTAATG
WI-4149a	137	T C	---			TTGTACATGTTCAATTCATCCCTCCCATTTCTTTCTGTCTTATAAGAACCTCGCTTCTTCTCCAAGT CTTACTTCTCCACCTGAGCCACAGATCTCTTTATTTCCATCAAAGCTTCTCAGCATCTTCTATATACI T/CJGTGCTGTGCTTGTGAAGAGCCAGAGCCGAGCATACCAACATGATCTTTTGTGTTGAAGTGTAG TAGGAGAGACAAGACAGATGTGCGGGTCCCATGATATAAGGTAATG
WI-4182	188	G A	---			TAACACACTTTTCATTTGGTTTCTTACTGACAGTTAAAGGACCATCCATTATATTACAATTCCTC AGTTCTATGCTTTAGAGTNCATTTATAGGACTACTGTAAAATTTTCAGAGGGAATTAATCTCTGGAGTA GGGGAATGAGTTAAATAATCTACCACATGCCAATTCAGGGGACTGTGGTTAA[G/A]ATGTCCTCTCT TGCCCCCTTCCCAAGTTCTTAAATTCCTAG



WI-4230	93 T	---			AGAGACGTTGAATGGGGACATCTTTCTATTTCGATTTTAGTTTAAACATTTGATAAGAATTGATGAAA GTTTGTACATCCAGATTATCTTTATAGCAGCAGAAGTCTGGCAAATAATAACAGCACACTGACT TTTCCATGGTAAAGAAAGTTAGAGAAAAACAGCCTATTTTCTTAATGTTAAATGTAATCTGAAT ACATTTAAATGGAGGAGATGAATAGTGACCTTTGAAATTTTGAATTTATGG
WI-4241	118 CT	---			GAAATTCATTGAAGTTTGAACCTTGAACCTGATCTCATTAATACCTTTTCTGAGTGTGATTT CATTTTGACAACAGAACAGACGAAAAATTTCCACTTAAATTAATCTC[CT]AAGTATCTATGAT TTAGCACTGTTAGCACCAGAACTGTGAAATTAATCTCTAGATATCTTCAGAACTCTAGGATGGAAG AA
WI-4271b	151 A	---			CAGGGCTTTTGGGAAGATCAGTTAAAGCAGANCTGGACCTAAAAAGACTAAGCACATTTTCAGCAT CAACAAAAGGTGACATGTTACCCATGAAGTCCCTGGAGGATTAAGATCAAAATAAGAGCCTCAGG GGACTGAATCCAAACGGGGAATATTAGAGTACTACAGGAGCCCCCAACCTCCCCCTTTGTCTCAGG CTCTAGAAGGTCCAGTCAGGGGC
WI-4271	151 A	---			CAGGGCTTTTGGGAAGATCAGTTAAAGCAGANCTGGACCTAAAAAGACTAAGCACATTTTCAGCAT CAACAAAAGGTGACATGTTACCCATGAAGTCCCTGGAGGATTAAGATCAAAATAAGAGCCTCAGG GGACTGAATCCAAACGGGGAATATTAGAGTACTACAGGAGCCCCCAACCTCCCCCTTTGTCTCAGG CTCTAGAAGGTCCAGTCAGGGGC
WI-4389b	156 GA	---			AATCGAAACATGATTTTGTAAAGGAACCATTTATGATATTTGTGCCAGTTTAGCATAT GAAATTTGAAAGGGATGAACCTGGAGGAAGAGAGATAGAAAGGATATTATGCTAACCTTTTGGGA AGGTAAGATGTGAACCTATACA[G/A]TNGCAAGGAAAGTAGAAATGGAACAGACATGATTGACTTA AGAGGTATTGTAGGAAGTGAAGCGGTAA
WI-4389	156 GA	---			AATCGAAACATGATTTTGTAAAGGAACCATTTATGATATTTGTGCCAGTTTAGCATAT GAAATTTGAAAGGGATGAACCTGGAGGAAGAGAGATAGAAAGGATATTATGCTAACCTTTTGGGA AGGTAAGATGTGAACCTATACA[G/A]TNGCAAGGAAAGTAGAAATGGAACAGACATGATTGACTTA AGAGGTATTGTAGGAAGTGAAGCGGTAA
WI-4488	31 A G	---			GATGACAATTATTGTGATTGGCATTTTAA[G/G]GTACCATTCATTTCTTCTGGCTTTTCGTGTGTT TGTTGTTGAGAAGTCAGGGGTTAGTCGATTGCTCTTTCTAGTCTTCTCAGTAGGAAGACTGATC CTAAACAACCTTAATTACCCATGCCAAAGTACGTCCAAACTGATCTTTAAAGAACAATAAATCAAATTG TATTATCCTATGCTTAAATGCTCAG
WI-4491	145 GC	---			ACCATCAATGTATCACCTTCTAAATTTATTAGATGATTAACTGGCTCTGTTAAAAATAAAAACCT GTCTTGACATTTGAAAAATAAACATTACTATTGGTCATTTTCTGCTACTTACAAAGGTACTGCACCTA AACAAGTTAAG[G/C]GTTTGTGGAGGGGAAAAATCATAAAAATGCATAAAAAATTTCTACCACCTGTCA TTTCTTGTCCCATAAATAAAATTTTACATGCCT

WI-4584	144	A G ---	---	TTGGTTGGCAATTTAGCCTCATAACAACATTTTACAATCATAAATGTTTACTCTTATTTTACAAACAAG AAAAATGAGGCTTAACATCACACTTCTGCTTAGTCGAGAGCCCAAGATTTGAACCCAGGAATCCATT CACCGGTACAGJTGCTACCTGGTAAAAAATGTTTAAATAAAATCTATGGCATTAGATTTCAAAGA GTCCTAATGGTTTGAATAAGGTGCTTTAATTTTATCAGTATGC
WI-4639	185	C T ---	---	TTTCTGCAATTTGAATGTATGGTCAGACTTCAGAGAACCCAGGAATCTCATTTATTCAGTACAATA TGGTGGCCAGGTGCTCAGGCCCTATTATCAGAGAGATCTCAGTTTAACTTTCCAAATCCACCATTTAC TGACCATATGACTTGGGGAACATTTATCTCACCTATCTGAGTGTGTATCC[7]CATCTTTAAATTTGTA AATTTTAAGGACACCTATCATAGTAATAATTGTGAGGATAAAATGAAATAA
WI-5327	63	A ---	---	AAATGAATCCGCTTTAGAGCAAAATACCAGTAAGGGCTGGTGCAGGATGGTGGCTGAGAGAJV-- JGATTACTCATAAAAGCATATTAAATTTATAAAATATGAAAAATTTAACTAGATAATTAATGTGAAT TGAGTTGAAGGTTGCATGAGAGTAGGGAGGAGGTAGTTTCTACTTATAGGGTTTATATAAGTNTGCT TCAATAGAAATGGCTCTTTCGGATGACAATGATGAACCTGTTCTAAGCAGACAG
WI-5390	87	C T ---	---	GCCTTGAGAAATGAAAAGGGAGCCTGGACCATTCAGGGCTTCTCACTCTGATATTTTGTGTAT TTATTGTTCACTTATTAT[7]GTCTGTCTCCCTTCTGGTATGCTTGTCATGAACAATGAATTC CCAGTGGCTGGCCCGAATTCGTGGCTCCTAGAGGTGCCAGAAAAAAGTTTCGGTGAATAGAAATTG ACGAATGGGTTCAGAAATGAAACCTGTGAATCTATGGAAGACAAACGAAT
WI-5404b	87	G A ---	---	CCTTGCCTGCTTTATGCATAATGAGAATAGAGTTGACTCTCCTGTCAAGAAATCAATTTAAGCAGT GCAACATTTATTTAAATTT[G/A]AAAGAAACTTGTCTGAAACTTTGTACTCTTGTAGTNAATTTG AATCTTCTCTCAGCAGTTTCCATGGTGTGAATCCACCCCATCTCTTTTACCAGTAGCAAGATT GCTACTTATATGGAAGGGTTTATAGAGTTTATAACAA
WI-5404	87	G A ---	---	CCTTGCCTGCTTTATGCATAATGAGAATAGAGTTGACTCTCCTGTCAAGAAATCAATTTAAGCAGT GCAACATTTATTTAAATTT[G/A]AAAGAAACTTGTCTGAAACTTTGTACTCTTGTAGTNAATTTG AATCTTCTCTCAGCAGTTTCCATGGTGTGAATCCACCCCATCTCTTTTACCAGTAGCAAGATT GCTACTTATATGGAAGGGTTTATAGAGTTTATAACAA
WI-5545b	77	A C ---	---	TAGGAAAGGGGATGGTATGGCCTCTGAGACATTTAAATCTATCTTTACCACCTCACACTGCCGCCA TATCTCCTC[A/C]CCAACACCTCTGTTTCTGACAGCCCAAGTTTCCATCAGTTGATGGGACTATTT GTTGCAAAACAATTTGTTAAAGATTGGCTGACTTTGGCTGAATTTGCTACAACTCCAAAAAGANTC GAGATACACCATGAATTTTATTTTCAATTTCA
WI-5545	77	A C ---	---	TAGGAAAGGGGATGGTATGGCCTCTGAGACATTTAAATCTATCTTTACCACCTCACACTGCCGCCA TATCTCCTC[A/C]CCAACACCTCTGTTTCTGACAGCCCAAGTTTCCATCAGTTGATGGGACTATTT GTTGCAAAACAATTTGTTAAAGATTGGCTGACTTTGGCTGAATTTGCTACAACTCCAAAAAGANTC GAGATACACCATGAATTTTATTTTCAATTTCA

WI-5860b	134	A G ---	---	ACTCAAGTTGGGGATAAAATCAGAAGTTTCTATGTACAACTTAAATTTTCTGTAAGATTTTATTTGTTCTTTTATATAAAATTAAGGATTTGTTTACCTCCCTAACCAACCTTCTAACTGAGGAACAC/A/GJTATACTGGAATCATGTGAAGACATTTCTAAAGGGTACCCAGGTGCACATAGTTTTAAGGGAATCAATTTCCAAATCATCAACTTCTGTAT
WI-5860	134	A G ---	---	ACTCAAGTTGGGGATAAAATCAGAAGTTTCTATGTACAACTTAAATTTTCTGTAAGATTTTATTTGTTCTTTTATATAAAATTAAGGATTTGTTTACCTCCCTAACCAACCTTCTAACTGAGGAACAC/A/GJTATACTGGAATCATGTGAAGACATTTCTAAAGGGTACCCAGGTGCACATAGTTTTAAGGGAATCAATTTCCAAATCATCAACTTCTGTAT
WI-6106	208	C G ---	---	GCAACAACCTATTATACCTGATTCOAACCCAGGTCTACTAATTAATCAACCCTAACCAATACATATATTGTCCTGTTCTGAATTAATTTTCAATTTAGAACTGATGAGATTTAGCATGGGATAAGTGCAGTGCAGAGATAGTAAACACTGCTCTTTTGGCTCCAGGAGTCTCAATGTGAAGTATAATTTCTTACAGAGTAATT[C/G]ATAGTAGGTCAACCAAAAGTCTATATTGTATGTGAAGGAAAG
WI-6109d	129	T C ---	---	AAGATAGACAAACATATGCCAGACCAACAAACACAGACCTGTCATATTTCTGAGAGAAATGTACATTGAGTCTTCCTTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAAAGGAAAAAACCTT[C/]AAACCCCTATATTNCTGTCCTTGTGCATACCTTTAAATGTATAATGTGGGAGAGAAAGGAATTTTGATGTGNAAAATTATCCCTGAAAAATTTTATACCA
WI-6109c	147	T C ---	---	AAGATAGACAAACATATGCCAGACCAACAAACACAGACCTGTCATATTTCTGAGAGAAATGTACATTGAGTCTTCCTTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAAAGGAAAAAACCTTAAACCCCTATATTNCTGTCCTTGTGCATACCTTTAAATGTATAATGTGGGAGAGAAAGGAATTTTGATGTGNAAAATTATCCCTGAAAAATTTTATACCA
WI-6109b	147	T C ---	---	AAGATAGACAAACATATGCCAGACCAACAAACACAGACCTGTCATATTTCTGAGAGAAATGTACATTGAGTCTTCCTTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGAAAGGAAAAAACCTTAAACCCCTATATTNCTGTCCTTGTGCATACCTTTAAATGTATAATGTGGGAGAGAAAGGAATTTTGATGTGNAAAATTATCCCTGAAAAATTTTATACCA
WI-6109a	129	T C ---	---	AATGCCATACACCTTCATCATGCTGCATACTGATGATTCATTAATGCTTATTGTTAGCACCTGTC TTCCAACACATGCTGTTTGTTCATGAT[C/]GCATATCCCAAGTGCCTTAGACAATGCCTCCCATACAGTGAACAGTATTGACTAAACATACCTTGTAAATCAATAAAATTAATCAACTTGGCATATGCAGGGAAC
WI-6112	96	T C ---	---	GAAC

WI-6244	103	C T	---	---	---	TAATTGCACAACTTACATATCAGGGTTCTGATTGAAAGGAGAGAAATATTCCTTTCTTTTAGTGATT GCTTAATATTAAATCAATAAAGTGACCAATCTCTTCGCTCCTTATAAATGTGTTTGAAGAAGG AAATTGAGTGTGGGAATTAAACAACAGGAGACATTTTATATCTCTACAGTGGGGGAAGACTT CCTATTTCTTTCCCAAGGATGGATACATTTCTAC
WI-6268	124	C T	---	---	---	CTGGCCTTATAATCCAAGTTTAGGATTAACTTACCCCACTTAATAGACTCCAGACAGTTGCAGTT GTCTACAAGATTTCTCTCTAGTAGGGCTTTGGGTGTGGCACCCTTTGGCTCAATTC/TAATCTCCCT GGGTCTTATTGACTTTTCAGGGAGCCTAGAAGAGCTGGACAAAACCTGCTCTTTGCAGAAAGAGTCG GGGTCCAAAAGATTTCGTACGATTTTATA
WI-6336b	234	C T	---	---	---	AGGTGCCATTAAATCCATTCAAATTTGGAAGCTACATCTCAAGGGTCTGAGAGAGCTCACTCCCCCC ATATATCCCCCTTACATGTTTCTTATAAGACATACAGTTTAAATCAATTAAACAATAAACAGCTT ATATACTGGCAATATATTACAGATGGGTTTATGTGACAGTAATAGATCACATGAATGGACCATGTG GTACCCCAAGTGCATTATGCTTGGTAGAGCC/CTTGGAGACACTGACAGT
WI-6336	234	C T	---	---	---	AGGTGCCATTAAATCCATTCAAATTTGGAAGCTACATCTCAAGGGTCTGAGAGAGCTCACTCCCCCC ATATATCCCCCTTACATGTTTCTTATAAGACATACAGTTTAAATCAATTAAACAATAAACAGCTT ATATACTGGCAATATATTACAGATGGGTTTATGTGACAGTAATAGATCACATGAATGGACCATGTG GTACCCCAAGTGCATTATGCTTGGTAGAGCC/CTTGGAGACACTGACAGT
WI-6381	92	C A	---	---	---	TTGGATACAAAATTCAAGTACACAATCAGTAGCATTCAAAATTAGTTATGAGTATTTATACAAATTA CAAAAATGNNTCATGTTTAAACA/C/AGTATTTTAAAGCTCAAAACATTTTAAACACAGGCACAAT ATTCTAANGGCATATGCATTCACCATGGCTTTTGAATGTCTCACTCCCAACTTCACAATCAAAATC TACAGANGCGGCAAAAGATCAGAGTTTCAG
WI-6436	198	C G	---	---	---	GGTTGAGGCATTGGGAAAGGCAGAAATTGAGGCAGTAGAAAATGGACATTTTAGGAAAAGAGAAGT TCAGAGGCAAAAGTCATGACAGACAGGAAATACAAGGCTTAGGAAGACAGTAGTCTCTGTGGTTGAA ATTTTGGTGTCAATAAAGAAAGTTTAGACTTTTGGTGTGTAGTAGTTGTAGTAGGAGTAGCGTT/C/TA GJATTGGGTGTATCCACAGACAAGGTGATGTTCTAAGATTTGATATTTATTGT
WI-6449	186	C T	---	---	---	GAGGCCTCTTTGCTTTCTCAGTCAAGGCTGTATCCAGGGTTGATATCTAGCCTATATGCCATATGT GTATGGCTAGTGTGTTGCTGATTGGTGGTGTGCTCAGACTGCCAGATTGTTAAATATTTTGAAAATC GTATCTGGTCTATTCACTGCACTCTCTGATCTATGCTGGCTCTATT/C/TAATCCCTATTCTCTGA TCTTATGTCAGACCTGAAGTCCCTAAATTTTCTGTGGTGTATTATA
WI-6449	186	C T	---	---	---	GAGGCCTCTTTGCTTTCTCAGTCAAGGCTGTATCCAGGGTTGATATCTAGCCTATATGCCATATGT GTATGGCTAGTGTGTTGCTGATTGGTGGTGTGCTCAGACTGCCAGATTGTTAAATATTTTGAAAATC GTATCTGGTCTATTCACTGCACTCTCTGATCTATGCTGGCTCTATT/C/TAATCCCTATTCTCTGA TCTTATGTCAGACCTGAAGTCCCTAAATTTTCTGTGGTGTATTATA

WI-6463	72 T C ---	---	GCTGGAGAGAAAAGACCTCCAAAAGAAAGAACTAAATCAGAGTCTCTTGAGCAAGAGGAATTGAAA AGAACATTC/TGAAAAAAATTAAGTAGAACTCAAGAGAGCCAAAAGTCCCAATTGTGTCATTAA TAAGAAATATTTGAATGGAAATCTTAAGAAATGATTTTATGATCAGTTAAATGTTCTTCCTCCTCCTC CAGTCCCATTTATATGACATTCGGCATGCTG
WI-6474b	76 C T ---	---	AAGCAGTAAATCTTCCATCGCATGGATGCCAGTGGGTAATGTTATAGAACTTCAGAGGANAC AGAGGCAAA/C/TGTTGGTTATAGCAGTCAACGACATCATCAATGAAGACATGACTTGCTTAGAGCC AAGAAAAAGTAGGATTTTGAAGGCACAGAGAAAAGGGGTACTAGAGGAGAACTATGTAAGCAG AGGTATAGAGGAACCTAAAGTATAAAAGAGTGAGCCATAACTTAGGGTACCATAA
WI-6474	76 C T ---	---	AAGCAGTAAATCTTCCATCGCATGGATGCCAGTGGGTAATGTTATAGAACTTCAGAGGANAC AGAGGCAAA/C/TGTTGGTTATAGCAGTCAACGACATCATCAATGAAGACATGACTTGCTTAGAGCC AAGAAAAAGTAGGATTTTGAAGGCACAGAGAAAAGGGGTACTAGAGGAGAACTATGTAAGCAG AGGTATAGAGGAACCTAAAGTATAAAAGAGTGAGCCATAACTTAGGGTACCATAA
WI-6478b	175 T A ---	---	GAACTCAATTAACCTTGGCAACACTGAGAAATCGGATTTGGAGATCTGCAAGCTGAGGTTGAGATT TTGGACCTTGGTGATCCAAATGGGGAATGCCAGCTTCGAGGCCGTCTATATGCTTTATTTTGTGA CACTGTCTATTTACCTCCCAATAGTGAGAAATCAGAGTTA/GCTCCTTGTCAGTGTGCTACAGA GAAGATATACAGGATGGAAGGACAGCTCCTGTAGGACCTAGACACAACCTG
WI-6478	175 T A ---	---	GAACTCAATTAACCTTGGCAACACTGAGAAATCGGATTTGGAGATCTGCAAGCTGAGGTTGAGATT TTGGACCTTGGTGATCCAAATGGGGAATGCCAGCTTCGAGGCCGTCTATATGCTTTATTTTGTGA CACTGTCTATTTACCTCCCAATAGTGAGAAATCAGAGTTA/GCTCCTTGTCAGTGTGCTACAGA GAAGATATACAGGATGGAAGGACAGCTCCTGTAGGACCTAGACACAACCTG
WI-6559	149 G A ---	---	CACATTTGAATGCAACTGAGAAANTGGTTTNTAGGCCCTACCTTTTATTAAGAGTACATCTGGCTC CAATGTTACCCCAACATGCAAAACATAAGGCAACAATCTGATCATTTTATAGNTCCCAAGCCCA TTAGCAATATCTTA/GA/ITCAAATTTTAAAAAGAGAGAACAGGAAATAAGGAAGGCCTAACAGAGGAG TTAAATAATTGTGCAAAACTTATCAGTTCTTC
WI-6564b	54 G A ---	---	TTCTTTATTGGTCTACCAATGTGACTCTTTACCCAGGCCACTGTTCCCTATGC/GA/CACCTGGCTTTG TAGGCATTCACATCATATGCTGTGCTCCTGAAATCTCAATTAATTTCTCCTNCCTATTCCTTTCCAT GCTCTGCCCTCATTTNCTCAGAAATGAAGGCATTGATTATNATTTTTTTGGTCTGTGTAAAG GTTCC/TGGCAGGAGAACATGCATATGACTTTTAAATAAGACCAACA
WI-6564	54 G A ---	---	TTCTTTATTGGTCTACCAATGTGACTCTTTACCCAGGCCACTGTTCCCTATGC/GA/CACCTGGCTTTG TAGGCATTCACATCATATGCTGTGCTCCTGAAATCTCAATTAATTTCTCCTNCCTATTCCTTTCCAT GCTCTGCCCTCATTTNCTCAGAAATGAAGGCATTGATTATNATTTTTTTGGTCTGTGTAAAG GTTCC/TGGCAGGAGAACATGCATATGACTTTTAAATAAGACCAACA

WI-6608b	46 C ---	---	CTAATCAGTAGCACTGAACATGGCTCTAGTGGGCTCAGT[C/- JAGTTAGGCAGCTAAGGAGGGGATTTCTCTAGCTCTCTCCCTAGAGCTAAATATGCATCTGG GAAAAATTAGGCTCTGGAGCACAGAGGATTTTCTAGAGGAAAAAGAACTCCAGCACTAG GTAAACTGCAAAAGAAAAACACCTGTGCCAGGCCTAGCTACAAGGCCACACCAGAAAAAGGAA AGC
WI-6608	46 C ---	---	CTAATCAGTAGCACTGAACATGGCTCTAGTGGGCTCAGT[C/- JAGTTAGGCAGCTAAGGAGGGGATTTCTCTAGCTCTCCCTAGAGCTAAATATGCATCTGG GAAAAATTAGGCTCTGGAGCACAGAGGATTTTCTAGAGGAAAAAGAACTCCAGCACTAG GTAAACTGCAAAAGAAAAACACCTGTGCCAGGCCTAGCTACAAGGCCACACCAGAAAAAGGAA AGC
WI-6666	68 C A ---	---	GTTAGACAGTATCCAGCAAAAAAGGTTATTTATACCTCTACTTTCCAAAACGAGGAAACCTCCCC A/C/AJAAATCCCATCAACACACAGTCATGCTGGAAGGCATTCTGTCTACTCTGTTGGTTTCATGTAA ATGTTGGGGTGAAGTCAATTCGGCTCTTCTNITCTCAAGTCCAGGCTCTTGGGTAGACCAAAAACTA ATACACAATGTTAGAGCACACAAGAGA
WI-6670b	120 A G ---	---	AGATTACATAATTACTGGGGCCATTGTAGGGTNGGGAGGAGTGTCTTCTATCTGCAGCCAAA CAGAAATACGTAGTACAGCAAAACCGTCTCAACAGTAAGCACACAATGAAC/A/GJTTGTAGCCA GCATTGCCATTAGGGCCGAGTCAGGGTTGTGGGCCAGAACTTAGACAATTTGGGGAATTTCTGA AAAAAAAGAAATACAGAAATTGTAAACACAGACACAGAAATCTTAGAAGGGAT
WI-6670	120 A G ---	---	AGATTACATAATTACTGGGGCCATTGTAGGGTNGGGAGGAGTGTCTTCTATCTGCAGCCAAA CAGAAATACGTAGTACAGCAAAACCGTCTCAACAGTAAGCACACAATGAAC/A/GJTTGTAGCCA GCATTGCCATTAGGGCCGAGTCAGGGTTGTGGGCCAGAACTTAGACAATTTGGGGAATTTCTGA AAAAAAAGAAATACAGAAATTGTAAACACAGACACAGAAATCTTAGAAGGGAT
WI-6704c	33 T C ---	---	TTTGAATAAATTCATGCACCAATGTTTAACT/CJACATATATCATACAGTGCAGGATTTATGA ACATACATAAATCAAAATCATACCATATAAACGTTTACAATAAGTTTTTCATGACACACGGNCA CTATTGCTCTTAAATATGGTTGACATGTCATCATTAATCGATTCAATGTTCTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG
WI-6704b	33 T C ---	---	TTTGAATAAATTCATGCACCAATGTTTAACT/CJACATATATCATACAGTGCAGGATTTATGA ACATACATAAATCAAAATCATACCATATAAACGTTTACAATAAGTTTTTCATGACACACGGNCA CTATTGCTCTTAAATATGGTTGACATGTCATCATTAATCGATTCAATGTTCTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG
WI-6704	28 T C ---	---	TTTGAATAAATTCATGCACCAATGTTTAACT/CJACATATATCATACAGTGCAGGATTTATGA ACATACATAAATCAAAATCATACCATATAAACGTTTACAATAAGTTTTTCATGACACACGGNCA CTATTGCTCTTAAATATGGTTGACATGTCATCATTAATCGATTCAATGTTCTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG

WI-6710	106 GA ---	---	CCATGGACAGTTAATTAGGAAGCTTCGACCTGTTAGTAATAACAGAGGAAGTCCAGTTATCTACCT ATTCCTTAAACACACATTTGTGAGGCTGGAATGATCCCG[G]ATAGTAAACACTCAACATCCACACCT GCATAACATCGCTCCCAAGTACTATTTACTGAGTCGACACAGGATGTCACCAGTGAGCCTC ATCTCAGTCCATGGAGGAGTTGACTTAGACCTTCCTGGACAGGAAGGGTC
WI-6766b	148 GC ---	---	AAAACAAATGGTGCAATGCATAATATTTGTGGTCACAGTATAAACAAATACAATAGTTTCATATAAC ATTGGATATGGACAAAAATACACANGATCCTTCTTTGTCTACGGAAAAATNCTGCAGATCCTTATGT GCCACACTTAAAAAN[G]C/JAAAGTCAACGTTTTCTCTCTAGGNTCTGCACACATATTTATCACTGA GAATTTGGTCAACACAGTGGAGGGAACCTACCCAAATCCAGTCCCTCTTC
WI-6766	148 GC ---	---	AAAACAAATGGTGCAATGCATAATATTTGTGGTCACAGTATAAACAAATACAATAGTTTCATATAAC ATTGGATATGGACAAAAATACACANGATCCTTCTTTGTCTACGGAAAAATNCTGCAGATCCTTATGT GCCACACTTAAAAAN[G]C/JAAAGTCAACGTTTTCTCTCTAGGNTCTGCACACATATTTATCACTGA GAATTTGGTCAACACAGTGGAGGGAACCTACCCAAATCCAGTCCCTCTTC
WI-6787b	97 A G ---	---	ACAGATAAAAGTCTTTATCCCTGTATGTTTACATAAGAAAGTTCTTTACAGACTTTTTTTTATACA ATACCTGTGCAGCAATGTTCAAATTTTACAC[G]GTTTTACTGCATAAGATATCTTCATGTACAACTGT ATGCTTTGTCTCTTGGGAAGGACGCGTTAAAGACCTATGATAAACACACATCCACATGACAAAAGGA GAGTGAATAGGGCAGAGTAGANTACTCACAGGAAAGAGTAAATTCAGGT
WI-6793	105 C G ---	---	GAACCCACAGGTCCTGTTATTTTAAAGGAGCATTTACATTATGATAGCAAGTTTCAACACATTCA TCAACAAGGCGGCTCTCAATCAATCAGTCAACCCCG[G]GAGTTAGAAAGTAGAGTCATGAGGAA GAGCTGCTTGGCTGAGGAAGTAGGTTAATGCCCTCTAATCCCGGAAAGGGCAGACTGAAGCCA GAGCCAGANTCCTGGCAATTCACAGTTTCTCATCACAGGTAAAAAGGCAAC
WI-6810b	37 T C ---	---	CACAATAATAAAATCACTCCCTACCTTGAAACCTTTA[T]C/JAGAAAGCATTTTAAATTTACAACACA AAGCTCAACGNAACCTACAATAAGTCTAGTAGTCTGTTACGNGCCCAAGGATAAGGCTGAACAATA AATTAACCTTTAAAAATGCTATGNACAAAGTACAATTTCTTTTGGTTCTGCAGAGCAATGACC ACTAAGNAATATTTTAAAGGCTGAACAGAAATCCAGCGGCAATGAAGTTAAT
WI-6810	37 T C ---	---	CACAATAATAAAATCACTCCCTACCTTGAAACCTTTA[T]C/JAGAAAGCATTTTAAATTTACAACACA AAGCTCAACGNAACCTACAATAAGTCTAGTAGTCTGTTACGNGCCCAAGGATAAGGCTGAACAATA AATTAACCTTTAAAAATGCTATGNACAAAGTACAATTTCTTTTGGTTCTGCAGAGCAATGACC ACTAAGNAATATTTTAAAGGCTGAACAGAAATCCAGCGGCAATGAAGTTAAT
WI-6817b	145 C A ---	---	GCATGATTAAACAGTGCAGAAAAATACCAAGTACATTTGGTGAACGATGAGCTAGCTGTTCTAGTA TTTGCTTTTGTAAATCCAGTTAAGACCATCAGCATATACAACATCATCACTAACTCAACATGTAGCT GCAGGGTAAC[G]A/JGTGGATACCCCTGTGTGCTCTACTNGCCCTCCAAAGGCATTCAGGGGATCATCA AAGATGTTGGACACCTTGTGTCAAATCTTGGTTCAAGTGGGCTGTGCAG

WI-6817	145 C A ---	---	GCATGATTAAACCAGTGCAGAAATACCAAGTACATTGGGTGAACGATGAGCTAGCTGTTCTAGTA TTTGCTTTTGTAAATCCAGTTAAGACCATCAGCATATACACATCATCACTAACTCAACAATGTAGCT GCAGGGTAAC[C/A]TGTGGATACCCTGTGTGCTTACTNGCCTCCAAAGGCATTCAGGGGATCATCA AAGATGTTGGACACCTTGTGTTCAAATCTTGGTTCAGGTGCGGCCTGTGCAG
WI-6819b	221 C ---	---	GATGGAAGCCATTTTATTTCTCTAAATTTTAAATAGAAGACTTTAATGGAAACATTTAGTAC CATCATGTCAACCTGAATGCCAGCAATACCTCGACTTTTACACACGCGAGGAGCCCTAGTAAAGCCC CGTCAGTAGTACACATTTCTATGTGCTCTCAACAGTTTTCATATACAAAATTTTCTGCTATTTTG CTTTAGCAACAGCAATAACTTTTGTGTTCCCTATATGACACCTAATATCCAG
WI-6819a	175 G T ---	---	GATGGAAGCCATTTTATTTCTCTAAATTTTAAATAGAAGACTTTAATGGAAACATTTAGTAC CATCATGTCAACCTGAATGCCAGCAATACCTCGACTTTTACACACGCGAGGAGCCCTAGTAAAGCCC CGTCAGTAGTACACATTTCTATGTGCTCTCAACAGTTT[G/T]CATATACAAAATTTTCTGCTATT TTGCTTTAGCAACAGCAATAACTTTTGTGTTCCCTATATGACACCTAATAT
WI-6826b	154 A G ---	---	GCAAAAGCTTTATGGCTCCAACAAATATCCCTTTTAAACTCCTCTCTCTCTGCTCAGTG GAACAACACATTTGAATTCAGATTTGCAGTTTATAGCATTTTTCCTAAGAACCATATAAATAC ATGCAAAACCTTGACAT[G/G]GAGCTTAAATAATATCAAAATGCAAAATATAGATTGGGTGCACTGT TAAGCTGAATTCGAAATATGGCAACACACACTGGAGTGGGTATACGTTG
WI-6826	154 A G ---	---	GCAAAAGCTTTATGGCTCCAACAAATATCCCTTTTAAACTCCTCTCTCTCTGCTCAGTG GAACAACACATTTGAATTCAGATTTGCAGTTTATAGCATTTTTCCTAAGAACCATATAAATAC ATGCAAAACCTTGACAT[G/G]GAGCTTAAATAATATCAAAATGCAAAATATAGATTGGGTGCACTGT TAAGCTGAATTCGAAATATGGCAACACACACTGGAGTGGGTATACGTTG
WI-6857a	122 T C ---	---	AGTGCAAACTATTTTGAACAAAAGTAAACTATGAGTCACAGCATTCAGCAAGACATCAGACACGGA AGAGTGAACAATAATTCACATAAGTAAATAACAGCAGATGAGATGTCTCACATGTAT[C/A]TTTAAAT TATTCATGCTTTTCAATAGTCTCTTAGTCAACTTTTCAAGTAAATTTCCACAAATATATAGCAGCTCA AACACAAATGCAGGAGCACAAATGGCAAAAGTTTGGCAACTGTTTGGGCTAATT
WI-6865	153 G A ---	---	TTATAGAATACTTATGGGCGATACGNGTAAATGAACGTGCAACCTTAAATCTAAACAAACAGCTTG TTTGTTGCTGCTGAAATCCTCCTGCTCACAACAGCCAGCTACTNGGTTTTCTAAAGACGTA ATTTGCAGGCAAACTT[C/G]ATGAGCCATTTCTGTCAGAAGAGGGAAGGAGCTGTTTGT TTACCTGTAGTAGAATATCTTTGCGCTGTAGAACTGAGCTCATTA
WI-6909	73 C T ---	---	ATTGAAAACTGGTTAGCAACAGATAAAATACAATAGAGCCTGGATATAAAATGAGAGAAGAAATGC AGACTTA[C/T]AAGCTTATAGAGAAAGTCAAAAGGAGCAAGTTTGAATCAGATTTTATGATAC GGAAAAAAATTTCCCTTTTGGCCAAACAGGATTATTCGAATAATAAATCTGCCAGTGCCCAATCAG AAACACCATTTCCACAATATTTGCATGCCCTAGTTGCTTATTTATACATATC



WI-6910b	163 G T ---			---	CACTCAAAACCTTTATTCAATTGATTTACAAACCTGTACAATAATTTACAAAGTTTTAGGCATTAAATCCCA TATTGACATGAATGCTGTGGAGAGTCTAAAAATAAATATGTGGCACATAGCTTAATATATACACATCAT GGCTCTTTACACTTAAGCCATTACCAATA[G/T]TGAGATGTAATGGAGAATTTAATGTGGTAGAAAA GTCAGAGTGGCTGACCAGTCCGGACCTTCCATGTGAATGACTCTTCCTTGGC
WI-6915	144 A ---			---	GCTGTTTTTTTTGTTTTTTTTTAAGTGACACCTTGGCCTTGTGGCAATTTCTTCACCTTATCTTACCC AAAAGTCCCTTTGGGCCAGCCACTGACTGATTTAAAACCCAGAAATGTGGTTTTAAACAATGTGGT CGTGTGAATCAGGTGATTTTNNATTTTCTATTTGGTAGTATTTTCAGATTTCCACAAAGAACATG TATTGCTTTGTAATTTGAAAAAAAATCAACACAGGATAGTAAAGATAT
WI-6928b	175 T C ---			---	CAATCAAAAAGTTTCCAAAGTTTCAAGCTGGGATGAAAGCCAGGTCTTCTGACTTGCACCTGTCTCAC ACTGGATTTTNCCTCTGATCCAGCTGCAGCTCCCATAGAAAGTTTCACTCTTAATTCATGTCCCATG CTTTGTCTGGTCCCTGTGAGGAAAGGGTCAAGCTAAAGGT/CJAACTGTTCTATAAGGATGGTAGG TATCCTGGCAAGATATTTCTCTGAAATAGTAAACGTGACCTTAGAAGTTA
WI-6928	175 T C ---			---	CAATCAAAAAGTTTCCAAAGTTTCAAGCTGGGATGAAAGCCAGGTCTTCTGACTTGCACCTGTCTCAC ACTGGATTTTNCCTCTGATCCAGCTGCAGCTCCCATAGAAAGTTTCACTCTTAATTCATGTCCCATG CTTTGTCTGGTCCCTGTGAGGAAAGGGTCAAGCTAAAGGT/CJAACTGTTCTATAAGGATGGTAGG TATCCTGGCAAGATATTTCTCTGAAATAGTAAACGTGACCTTAGAAGTTA
WI-6955b	79 G A ---			---	TTTTATGAACATTTCAAGTCCCTCATATCACAGCACATCAATAAGCAGTATGTACATAGACTGA CTTTATAGTAC[G/A]NGTCATGTCCCAAATTTCCCAATCCTAGGTAAAGATATCAAGTTACAAANTAC AAGTCCGNTAATTAACATATAGGTAGTATATTAAACAAAAATGNGTTTTTNGCAAATTTATGTGAAAT AAGGCTTTAACCAAAGC
WI-6955	79 G A ---			---	TTTTATGAACATTTCAAGTCCCTCATATCACAGCACATCAATAAGCAGTATGTACATAGACTGA CTTTATAGTAC[G/A]NGTCATGTCCCAAATTTCCCAATCCTAGGTAAAGATATCAAGTTACAAANTAC AAGTCCGNTAATTAACATATAGGTAGTATATTAAACAAAAATGNGTTTTTNGCAAATTTATGTGAAAT AAGGCTTTAACCAAAGC
WI-6957	47 C G ---			---	AACTAAAAACCCCTATTGTCTCCAAGTGTGGCAAAAATAGAAAAAT[C/G]TTTCAATTACATTAGG AAATCGGGTGGATAACGGAGTATAGTTATTCACCTTAAGAAGCATTCAGTCAAAATAATCACAAAA ACAAATTCAGATTGCTTGGATCTTGGTCATTTATGGCTTGAAGAACTGGATTTGAAACCACTTTAGG CTAAATAAATGTATGTAATAATGCATAGACTGTGTATCTAGAAAAATCATGC
WI-6996c	242 G T ---			---	ACTTCTAGTGCCTGTGTTACCACACTCTAATGCCCTGTGGTCCCGCACTTCTGTATGTCCTGAGGCCT TAAATCTGCCTGGCTGCCCTCCCTCTGTCTTCAGCACCCAGAGGAGAGCCGGCAGTTCCTCTG CAGGAGAGAGGGGCTGTGGAOCCAGGCTCAGTCCCTCTCTCAGGACCCCTGTCTCTGACT CTCTCCTGATGGTGGCCCTCTGTGCTCTCTCTCTCCG[G/T]GTCGGATC

WI-6996b	242	G T	---	---	ACTTCTAGTGCCCTGTGTACCAACCTCTAATGCCTCTGGTCGCCGACCTTCTGATGTCCGTAGGCCT TAAATCTGCCTGGCGTCCCTCCCTCTGTCTCAGCACCCAGAGGAGAGAGCCGGCAGTTCCCTG CAGGAGAGAGGAGGGCTGTGACCCAAAGCTCAGTCCCTCTCAGGACCCCTGTCCTGACT CTCTCCTGATGGTGGCCCTCTGTGCTCTCTCTCCG/GTGTCCGATC
WI-6996	228	T G	---	---	ACTTCTAGTGCCCTGTGTACCAACCTCTAATGCCTCTGGTCGCCGACCTTCTGATGTCCGTAGGCCT TAAATCTGCCTGGCGTCCCTCCCTCTGTCTCAGCACCCAGAGGAGAGAGCCGGCAGTTCCCTG CAGGAGAGAGGAGGGCTGTGACCCAAAGCTCAGTCCCTCTCAGGACCCCTGTCCTGACT CTCTCCTGATGGTGGCCCTCTGTGTCTCTCTCCGTCGGGATC
WI-7021b	112	G A	---	---	TGGGAGGACAGGGAGATGCTGCAGTTCCAAAGAGAGGTTCTTCCAGAGTCATCTACCTGAGTC CTGAAGCTCCCTGTCTGAAAGCCACAGACAATATGGTCCCAAT/GA/CCCGACTGCACCTTCTGTG CTTCAGCTCTCTTGACATCAAGGCTCTCCGTTCCACATCCACACAGCCAATCCAAATTAATCAAACC ACTGTTATTAAACAGATAATAGCAACTTGGGAATGCTTATGTTACAGGTTA
WI-7021	108	A G	---	---	TGGGAGGACAGGGAGATGCTGCAGTTCCAAAGAGAGGTTCTTCCAGAGTCATCTACCTGAGTC CTGAAGCTCCCTGTCTGAAAGCCACAGACAATATGGTCCCAAT/GA/CCCGACTGCACCTTCTGTG CTTCAGCTCTCTTGACATCAAGGCTCTCCGTTCCACATCCACACAGCCAATCCAAATTAATCAAACC ACTGTTATTAAACAGATAATAGCAACTTGGGAATGCTTATGTTACAGGTTA
WI-7056c	118	C T	---	---	GGCAGTAGGACCACAGTGTGGGTTCTGCTGGGACCTTGGAGAGCCTGCATCCAGGATCGGGTGG CCCTGCAGCCTCTCCACCTCACCTCCATGACAGCGCTAAACGTTGGTGA/C/TTGGTTGGGAGCCTCT GGGGCTGTTGAAGTCACCTTGTGTGTTCCAAAGTTTCCAAACAACAGAAAGTCATTCCTCTTTTAAA ATGGTGCTTAAGTTCCAGCAGATGCCACATAAGGGGTTTGCCATTTGATA
WI-7056b	118	C T	---	---	GGCAGTAGGACCACAGTGTGGGTTCTGCTGGGACCTTGGAGAGCCTGCATCCAGGATCGGGTGG CCCTGCAGCCTCTCCACCTCACCTCCATGACAGCGCTAAACGTTGGTGA/C/TTGGTTGGGAGCCTCT GGGGCTGTTGAAGTCACCTTGTGTGTTCCAAAGTTTCCAAACAACAGAAAGTCATTCCTCTTTTAAA ATGGTGCTTAAGTTCCAGCAGATGCCACATAAGGGGTTTGCCATTTGATA
WI-7091b	153	A C	---	---	AATTGCGTGAAGGAACTACCTATCCTTACATTTACCTACTAATGTCTCTTCTAACATCTTAGAG GTCCATGGAGAGGCATATGGAGAACATGTTTATCTGCTCTATAAATAGTATCCAAATCACTGTG CTTAAATTAATAGCATTTA/C/TTCTTATCATTTATCAGCCTTTTATGTTATTTCCAAAGTAAATATTA ACATATTATTTCATTGGTCTCTTTTATCTGTTCTATATGAATGCTAT
WI-7091	153	A C	---	---	AATTGCGTGAAGGAACTACCTATCCTTACATTTACCTACTAATGTCTCTTCTAACATCTTAGAG GTCCATGGAGAGGCATATGGAGAACATGTTTATCTGCTCTATAAATAGTATCCAAATCACTGTG CTTAAATTAATAGCATTTA/C/TTCTTATCATTTATCAGCCTTTTATGTTATTTCCAAAGTAAATATTA ACATATTATTTCATTGGTCTCTTTTATCTGTTCTATATGAATGCTAT



WI-7175	194 C T ---	---	---	CTCTAGACTAGTGCTTTACCTTTATTAATGAACGTGTACAGGAAGCCCAAGGAGTGTTCTCTACCA ATACTTCAGAGAGTCAAGTGGAGAAATGAAGAAAGGCTGGTGAATCACTATAACCATC AGTTACTGGTTTCAGTTGACAAAATATAATGGTTTACTGCTGTCATTGCTCATGCTTACCTA AATTTATTTGTTATTTTGAATAAAAAACATTTGTACATTCCTGATACTGGG
WI-7178b	273 G A ---	---	---	TGTACAGGTCAGGGACTTGGACAGGAGTCAGTGTCTGGCTTTTCTCTGAGCCAGCTGCTGGAG AGGGTCTCGCTGTCAGTGGCTGGCTCCTAGGGGAACAGACCAGTGACCCAGAAAGCATAACACCA ATCCAGGGCTGGCTCTGCCTAGAGAAAATTCGACTAAATGAATCTGTTCCCAAAGAACTACCC CCTTTTCAGCTGAGCCCTGGGACTGTTCCAAAGCCAGTGAATGTGAAGGAA
WI-7178	273 G A ---	---	---	TGTACAGGTCAGGGACTTGGACAGGAGTCAGTGTCTGGCTTTTCTCTGAGCCAGCTGCTGGAG AGGGTCTCGCTGTCAGTGGCTGGCTCCTAGGGGAACAGACCAGTGACCCAGAAAGCATAACACCA ATCCAGGGCTGGCTCTGCCTAGAGAAAATTCGACTAAATGAATCTGTTCCCAAAGAACTACCC CCTTTTCAGCTGAGCCCTGGGACTGTTCCAAAGCCAGTGAATGTGAAGGAA
WI-7182b	116 A C ---	---	---	GCATATTTGGCAGCTTATGCTTCGAAACCCAGCTGGTCAACAAAAGCTTGATATACAGAGAAG AAGGCTCAAGAAATTTATCACCAGTTCTCTGCAACCCACTCTGAGCCTTACCTCTCTCTCTCT TACTGAGGCTGCCAATACAGCCCCACGTTTCAGCTCAAGAGATGCTTAAAGATAATATGTGAGG CCACTTGGTAGCAAGATGGCAGCTATTTCTGAGCCTAGTACCCCAAT
WI-7182	106 C A ---	---	---	GCATATTTGGCAGCTTATGCTTCGAAACCCAGCTGGTCAACAAAAGCTTGATATACAGAGAAG AAGGCTCAAGAAATTTATCACCAGTTCTCTGCAACCCCACTGAGCCTTACCTCTCTCTCTCT TACTGAGGCTGCCAATACAGCCCCACGTTTCAGCTCAAGAGATGCTTAAAGATAATATGTGAGG CCACTTGGTAGCAAGATGGCAGCTATTTCTGAGCCTAGTACCCCAAT
WI-7191b	273 T A ---	---	---	ATAATTGCTTGTCTAGCCTGGCAAGATATTTTCATAAAAGAGGATAACAATGCTGATTACTAC CTTTTAAATATTTAGATAAATGCACAGCACCACAGCACCACATCTAAGCATTAGTGATGGTAGC TGATGTCAGCTTCATGTGGATTTAAGCACTCTAGAAACAATGAAGCTTCTGGCATAATTTAAGGAG CTCCCAAAATGTTACCTATTAAATTTGTAACCTCAGCAAGTAGAAGACCATTT
WI-7199c	112 T C ---	---	---	CCAGTGGTGAACAGAACCTCCAAATTTGAGTTGCACCCCTTCCCTGTGGCCTTATGAGCTCAGCCTC GCTTTGAGGTACCCACCGTCTGTCAGCTCCTTGACCTATGAGCTTCTGGGCGCTGACTAGGAAAGT TGGGAGTTAAGGAGGAAATAGCATTCCTTAATGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTTAT AGTCTATAGTTTACTCTCTCAGTTCTCACCACATCATCTTGTCTAA
WI-7199b	112 T C ---	---	---	CCAGTGGTGAACAGAACCTCCAAATTTGAGTTGCACCCCTTCCCTGTGGCCTTATGAGCTCAGCCTC GCTTTGAGGTACCCACCGTCTGTCAGCTCCTTGACCTATGAGCTTCTGGGCGCTGACTAGGAAAGT TGGGAGTTAAGGAGGAAATAGCATTCCTTAATGTTTGTGTTGTTGTTGTTGTTGTTGTTTAT AGTCTATAGTTTACTCTCTCAGTTCTCACCACATCATCTTGTCTAA

WI-7216c	237	T C ---				TGACACTAACACTCTAATCAAGCGAATGTTGGAACACCATGACCTCCTCTGTGTGCTCTCTCCCTCTCCCTCCAGAAAAATACGTATGT AAGGACAAAATGTAGAAAGATGTGAGATAACTTACTCAAGATTCCCTCCAGAAAAATACGTATGT TTAAAAACCCCTCCTGCTATACATAGGAAAGACACACATCCACCTAAAAATTGACTGTACTGTTTAA CTGTCAATTCTCCTGAGGCTAAACACAGTTTGTITTTTTCCTTGTAAATCACTT
WI-7216b	237	T C ---				TGACACTAACACTCTAATCAAGCGAATGTTGGAACACCATGACCTCCTCTGTGTGCTCTCTCCCTCTCCCTCCAGAAAAATACGTATGT AAGGACAAAATGTAGAAAGATGTGAGATAACTTACTCAAGATTCCCTCCAGAAAAATACGTATGT TTAAAAACCCCTCCTGCTATACATAGGAAAGACACACATCCACCTAAAAATTGACTGTACTGTTTAA CTGTCAATTCTCCTGAGGCTAAACACAGTTTGTITTTTTCCTTGTAAATCACTT
WI-7220b	147	A T ---				AGGATGATGCTCCAAAGGGGACCTTGAACCTATTACCACTATTGCTCTTTAAGCTGGCAACCCCA TCATTAAATAGCACATAAAATAGCAATCATATGGGATAAGTAGTACAGCTTCAGTAATCAATGGGCA GTGGCACTAGAAATTAATCTTGAGCACAGTGAATGACCTATCCTGCAACATCTAATGGATCTCTA AAGGTAACAAACCCCTATAAATCTGGCTTACTGCACATATTAGTGTIT
WI-7220	140	A T ---				AGGATGATGCTCCAAAGGGGACCTTGAACCTATTACCACTATTGCTCTTTAAGCTGGCAACCCCA TCATTAAATAGCACATAAAATAGCAATCATATGGGATAAGTAGTACAGCTTCAGTAATCAATGGGCA GTGGCACTAGAAATCTTGAGCACAGTGAATGACCTATCCTGCAACATCTAATGGATCTCTA AAGGTAACAAACCCCTATAAATCTGGCTTACTGCACATATTAGTGTIT
WI-7226	232	C ---				GATCGAATTTTCAGATGATTCGGAAATTTTCATTACGGTATTGTAATAGTGACATATATATGTATA TACATATCACCTCTATTCTTAAATTTTGTAAATGTTAACTGGCAGTAAGTCTTTTGTGATCATTT CCCTTTTCCATATAGGAACATAATTTGAAGTGGCCAGATGAGTTTATCATGTGAGTGAAAAATAA TTACCCACAAATGCCACCAGTAACCTTACGATTCTTCACTTCTGGGGTTT
WI-7228b	254	G A ---				ATAGCTTCCAGATTACAAAGGCCAAGGTAATAGAAATGCATACCAGTAATTGGCTCCAATTCATAA TATGTTCCACGAGGATTACAATTTTGTCTCTTGTCTTTGTATCTATTAGTTGATTTTAAATTA CTTCTGAATAACGGAAGGATCAGAAGATATCTTTGTGCTAGATTGCAAAATCTCCAATCCACA CATATTGTTTAAATAAGAAATGTTATCCAACATTAAGATATCTCAATGT
WI-7228a	163	G A ---				ATAGCTTCCAGATTACAAAGGCCAAGGTAATAGAAATGCATACCAGTAATTGGCTCCAATTCATAA TATGTTCCACGAGGATTACAATTTTGTCTCTTGTCTTTGTATCTATTAGTTGATTTTAAATTA CTTCTGAATAACGGAAGGATCAGAAGATATCTTTGTGCTAGATTGCAAAATCTCCAATCC ACACATATTGTTTAAATAAGAAATGTTATCCAACATTAAGATATCTCAA
WI-7233c	213	C T ---				CGATCGTACTGCCAGTAGCATTTGCTGTCTGCTCCGGCTTGTGTTGTACATTCATTTCAATTGTTACA GATGTGAACCTTATTCCCTTGTCACTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA TAAAGGGTTGAGCCCTCTACTTCTTCTTCCACCTTTTGTGGCAATTAATTAAGTGAACCTGCTAATA GTGTAAGTATCTGTGCAACAAACCACTGCCAGATAACGAGGGGCTG

WI-7233b	213	C T	---	CGATCGTACTGCCAGTAGCATTGCTGTGTCTCCGGTCTTGTTGTACATTCACATTTCAATTGTTACA GATGTGAACTTATTCCTTGTCACTAATTATATTAAAAATTATTCTAGGAAGTCAAAAAATATAA TAAAGGGTTAGCCCTCTACTTCTCTTGGCCACCTTTTGTGGCAATATTAAAGTGAACCTGCTAATA GTGTAAAGTAC/JGTGCACAAAACCACTGCCAGATAACCCAGAGGGGCGCTG
WI-7233	211	T C	---	CGATCGTACTGCCAGTAGCATTGCTGTGTCTCCGGTCTTGTTGTACATTCACATTTCAATTGTTACA GATGTGAACTTATTCCTTGTCACTAATTATATTAAAAATTATTCTAGGAAGTCAAAAAATATAA TAAAGGGTTAGCCCTCTACTTCTCTTGGCCACCTTTTGTGGCAATATTAAAGTGAACCTGCTAATA GTGTAAAGT/CJACGTGCACAAAACCACTGCCAGATAACCCAGAGGGGCGCTG
WI-7238	128	T C	---	GCCTACAGACAGCTCACCATTTTGTCTGTATCTGTAACACTTTTGTCTTAGTCTTCTAGTCTTTCTTG TAAAAATTGATGTTCTTTAAATCGTTAATGTATAACAGGGCTTATGTTTCAGTTTGTTT/CJCCGTT CTGTTTAAACAGAAAAATAAAGGAGTGAAGTCTCTTCTCATTTCAAAGTTGCTACCAAGTGTAT GCAGTAATTAGAACAAAGAAGAAACATTCAGTAGAACATTTTATGCCTA
WI-7252f	520	T C	---	CCACAGGATCCAGCCAAAGCGGGCCCTCCGGCCCTCCACTCGCAGCAGACGCCGGGACAGAG GCCTGCCCCGGCGCCAGCCCCGGCCCTGGCTGGAGGCTGCCCCGGCCCTGGTCTCTGCTGCTGCTG GACACTCTAGAGAACGCAGCCCTAGAGCCCTGAGAGCTGCTGGAGCGTTTCTAGCAAGTGAGAGATGGGAG CTCCTCTCTGGAGGATGCAGGTGGAACTCAGTCAATTAGACTCTCTCTCCA
WI-7252e	552	T C	---	CCACAGGATCCAGCCAAAGCGGGCCCTCCGGCCCTCCACTCGCAGCAGACGCCGGGACAGAG GCCTGCCCCGGCGCCAGCCCCGGCCCTGGCTGGAGGCTGCCCCGGCCCTGGTCTCTGCTGCTGCTG GACACTCTAGAGAACGCAGCCCTAGAGCCCTGAGAGCGTTTCTAGCAAGTGAGAGATGGGAG CTCCTCTCTGGAGGATGCAGGTGGAACTCAGTCAATTAGACTCTCTCTCCA
WI-7252d	540	T C	---	CCACAGGATCCAGCCAAAGCGGGCCCTCCGGCCCTCCACTCGCAGCAGACGCCGGGACAGAG GCCTGCCCCGGCGCCAGCCCCGGCCCTGGCTGGAGGCTGCCCCGGCCCTGGTCTCTGCTGCTGCTG GACACTCTAGAGAACGCAGCCCTAGAGCCCTGAGAGCGTTTCTAGCAAGTGAGAGATGGGAG CTCCTCTCTGGAGGATGCAGGTGGAACTCAGTCAATTAGACTCTCTCTCCA
WI-7252c	552	T C	---	CCACAGGATCCAGCCAAAGCGGGCCCTCCGGCCCTCCACTCGCAGCAGACGCCGGGACAGAG GCCTGCCCCGGCGCCAGCCCCGGCCCTGGCTGGAGGCTGCCCCGGCCCTGGTCTCTGCTGCTGCTG GACACTCTAGAGAACGCAGCCCTAGAGCCCTGAGAGCGTTTCTAGCAAGTGAGAGATGGGAG CTCCTCTCTGGAGGATGCAGGTGGAACTCAGTCAATTAGACTCTCTCTCCA
WI-7252b	540	T C	---	CTCCTCTCTGGAGGATGCAGGTGGAACTCAGTCAATTAGACTCTCTCTCCA

WI-7252a	520	T C	---	---	CCACAGGATCCAGCCCAAGCGGCCCTCCGCCCCCTCCACTGCGAGCAGCGCGGGACAGAG GCCTGCCCGGGCGCCAGCCCCGGCCCTGGCTGGAGGCTGCCCCGGCCCCCTGTCTCTGTCCG GACACTCCTAGAGAACGCGCCTAGAGCCTGCCTGGAGCGTTCTAGCAAGTGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACTCAGTCATTAGACTCCTCCTCCA
WI-7265m	252	T A	---	---	AACCTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTTACCCCATCTGTGGTTCAATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATATGTAATAAATAACGATCTCTT AAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCTTT
WI-7265l	231	T A	---	---	AACCTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTTACCCCATCTGTGGTTCAATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATATGTAATAAATAACGATCTCTT AAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265k	121	T G	---	---	AACCTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTTACCCCATCTGTGGTTCAATTGTAGTT GTTTAAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATATGTAATAAATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265j	174	T A	---	---	AACCTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTTACCCCATCTGTGGTTCAATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATATGTAATAAATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265i	227	T C	---	---	AACCTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTTACCCCATCTGTGGTTCAATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATATGTAATAAATAACGATCTCTT AAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265h	80	T A	---	---	AACCTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTTACCCCATCTGTGGTTCAATTGTAGTT GTTTAAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATATGTAATAAATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCT
WI-7265g	170	T G	---	---	AACCTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTT TTTCCAGTATGTTTATTTGCCACCAAAAAGTAAATGCATTTTACCCCATCTGTGGTTCAATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATATGTAATAAATAACGATCT CTTAAAAATACCACAGTTTGTATTTTCTTTAAGGAGTAAAGATTGCGCT

WI-7265f	231	T A ---	---	AACTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCATTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATTATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGATTTTCTTTT/AAGGAGTAAAGATTGGCT
WI-7265e	227	T C ---	---	AACTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCATTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATTATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGATTTT/CJTAAAGGAGTAAAGATTGGCT
WI-7265d	174	T A ---	---	AACTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCATTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGT/ATATATTATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGGCT
WI-7265c	170	T G ---	---	AACTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCATTCTGTGGTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGT/ATATATTATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGGCT
WI-7265b	121	T G ---	---	AACTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCATTCTGTGGTTCATTGTAGTT GTTTAAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATTATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGGCT
WI-7265a	80	T A ---	---	AACTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTTT TTTCAGTATGTT/ATATTTGCCACCAAAAGTAATGCATTTTACCCATTCTGTGGTTCATTGTAGTT GTTTAAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATTATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGGCT
WI-7281b	183	C ---	---	GATCACCCAGCCACAAAGCCCTTCGAGGGCCCTATACCATGGCCACCTTGGAGCAGAGAGCCAAAGC ATCTTCCTGGGAAGCTTTCTGGCCAAAGTCTGCCAGCTGGCCCTGCAGGTCTCCCATGAAGGCCA CCCCATGGTCTGATGGGCATGAAGCATCTCAGACTCTTGCAAAAACGGAGTCCGAGGCCGCGAG GTGTTGTGAAGACCACTCTGTTGTGGTGGGTCTGCAAGAAGGCCTCTC
WI-7281	171	C A ---	---	GATCACCCAGCCACAAAGCCCTTCGAGGGCCCTATACCATGGCCACCTTGGAGCAGAGAGCCAAAGC ATCTTCCTGGGAAGCTTTCTGGCCAAAGTCTGCCAGCTGGCCCTGCAGGTCTCCCATGAAGGCCA CCCCATGGTCTGATGGGCATGAAGCATCTCAGACTC/CATTTGGCAAAAACGGAGTCCGAGGCCGCG CAGGTGTTGTGAAGACCACTCTGTTGTGGTGGGTCTGCAAGAAGGCCT



WI-7282b	159	G C ---	---	TGTCACCTGGCACATTCATTTCTCAGTTGAAGAAGAGAAAAATTTGAAAAATGTCCCTTATGCTTTTAGA GTTGCAACTAAGTATATTTGGTAGGGTGAAGTGTTCACACTCAAAATATGTCAACTTNNNNNNNNNT AGGCCCTTTTCATAAAAACCAAACTG/CJGTAGCAAGATGCAAAATGCATGGCAAAATCTGTGGGTCTCCA GTTGGTTATCTGAATAGTGTACCAATTCACCAAGACAGTGTGAGATTGG
WI-7292	92	T C ---	---	CTTGATTACTTCCACTGAGGTGGGAGCATCTCCAGTGTCCCAATATATCTCCCCACTCCACTAC TCTCTTCCCTCCACTTTCATTTTCCG/CJGTGCTCTTCTCTAATTCAGTGTTTTGGAGGCCCTGACTTG GGGACAACGTATTATGATATTATGCTGTTTCCCTTCTCCCAATAGAAGATAAGTGCATGGAGCC TGAAGGGTGCCTAGTTGACTTACTGACAAAAAGGCTCTAGTTGGGCTGA
WI-7301f	133	A G ---	---	AACTATGGCAGTGGTCTGGTTATAGTAGAGAGCGGGTATGGTGGTGGGACCAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTGTTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTG A/GJCGGTAGTAACATATGGTGGTGGGAACTATAATGATTTGGAAATTACAGTGGACAACAGCA ATCAAAATTATGGACACATGAAAGGGGCGAGTTTGGTGAAGAAGCTCGGGCAG
WI-7301e	94	T G ---	---	AACTATGGCAGTGGTCTGGTTATAGTAGAGAGCGGGTATGGTGGTGGGACCAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTG/CJGTGGAGGATATGATGGTTACAATGAAGGAGGAAATTT TGACGGTAGTAACATATGGTGGTGGGAACTATAATGATTTGGAAATTACAGTGGACAACAGCAA TCAAAATTATGGACACATGAAAGGGGCGAGTTTGGTGAAGAAGCTCGGGCAG
WI-7301d	138	A G ---	---	AACTATGGCAGTGGTCTGGTTATAGTAGAGAGCGGGTATGGTGGTGGGACCAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTGTTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTGA CGGT/A/GJTAACATATGGTGGTGGGAACTATAATGATTTGGAAATTACAGTGGACAACAGCAA TCAAAATTATGGACACATGAAAGGGGCGAGTTTGGTGAAGAAGCTCGGGCAG
WI-7301c	211	A C ---	---	AACTATGGCAGTGGTCTGGTTATAGTAGAGAGCGGGTATGGTGGTGGGACCAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTGTTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTGA CGGTAGTAACATATGGTGGTGGGAACTATAATGATTTGGAAATTACAGTGGACAACAGCAATCA AATTATGGAC/A/CJCATGAAAGGGGCGAGTTTGGTGAAGAAGCTCGGGCAG
WI-7301b	182	C T ---	---	AACTATGGCAGTGGTCTGGTTATAGTAGAGAGCGGGTATGGTGGTGGGACCAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTGTTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTGA CGGTAGTAACATATGGTGGTGGGAACTATAATGATTTGGAAATTACAGTGGACAACAGCAA TCAAAATTATGGACACATGAAAGGGGCGAGTTTGGTGAAGAAGCTCGGGCAG
WI-7301	88	G T ---	---	AACTATGGCAGTGGTCTGGTTATAGTAGAGAGCGGGTATGGTGGTGGGACCAGGATATGGAA ACCAAGGTGGTGGATATGGTGGCGGTG/CJCGGTGTTGGAGGATATGATGGTTACAATGAAGGAGGAAATTT TGACGGTAGTAACATATGGTGGTGGGAACTATAATGATTTGGAAATTACAGTGGACAACAGCAA TCAAAATTATGGACACATGAAAGGGGCGAGTTTGGTGAAGAAGCTCGGGCAG

WI-7301	205 A C ---	---	---	A A C T A T G G C A G T G G T T A T A G T A G T A G A G G C G G T A T G G T G G T G G C A C C A G G A T A T G G A A A C C A A G G T G G T G G A T A T G G T G G C G G T T G G A G G A T A T A T G G T T A C A A T G A A G A G G A A T T T T G A C G G T A G T A A C T A T G G T G G T G G G A A C T A T A T G A T T T G G A A T T A C A G T G G A C A C A G C A A T C A A A T T A C T G G A C A C A T G A A A G G G C A G T T T G G T G G A A G A A G C T C G G G C A G
WI-7314c	49 G A ---	---	---	C T C T C C T T T T T C T C A G A T C T G C T C T G G T T T A A T T G G G A G G T C A G A T T G T T C T A C C T C A C T G A G A G G G A A C A G A A G G A T A T G C T T C C T T T G C A G C A G T A T A A A G T C A A T T A A A A C T T C C C A G G A T T C T T T G A C C C A G G A A C A G C C A T G T G G G T C C T T C T G T G C A C T A T A A C G C T T C T T T C C C A G G A C A G A A A T G T A G T A C C T T A T T T T A T T A A C A A A C T T G T T T T
WI-7314b	49 G A ---	---	---	C T C T C C T T T T T C T C A G A T C T G C T C T G G T T T A A G T T G G A G G T C A G A T T G T T C T A C C T C A C T G A G A G G A A C A G A A G G A T A T G C T T C C T T T G C A G C A G T A T A A A G T C A A T T A A A A C T T C C C A G G A T T C T T T G A C C C A G G A A C A G C C A T G T G G G T C C T T C T G T G C A C T A T A A C G C T T C T T T C C C A G G A C A G A A A T G T A G T A C C T T A T T T T A T T A A C A A A C T T G T T T T
WI-7314	36 A G ---	---	---	C T C T C C T T T T T C T C A G A T C T G C T C T G G T T T A A G T T G G A G G T C A G A T T G T T C T A C C T C A C T G A G A G G A A C A G A A G G A T A T G C T T C C T T T G C A G C A G T A T A A A G T C A A T T A A A A C T T C C C A G G A T T C T T T G A C C C A G G A A C A G C C A T G T G G G T C C T T C T G T G C A C T A T A A C G C T T C T T T C C C A G G A C A G A A A T G T A G T A C C T T A T T T T A T T A A C A A A C T T G T T T T
WI-7321b	199 C T ---	---	---	A C T A G G A A G G G A T G C C C A T T A A A G T G A C A A A A G G G T G G G T G G G C A C C A T G G C A T G A G A A G A A C A A G G T C C C T G A G C A G G C A C A A G T C T G A C A G T A A G G G A C T G C T T T G G C A T C C A G G C C T C C A G T C A C C T C A C T G C C A T A C A T T A G A A A T G A G A C A A T C A A A G N N N N N N N N A G G G T G G C A C A C C C A T C C T T G T T G C T G G G G T G T G G C A G C C A C A T C C A A G A C T G G A G C A G C A G G C T G G C C A
WI-7321	199 C T ---	---	---	A C T A G G G A A G G G A T G C C C A T T A A A G T G A C A A A A G G G T G G G T G G G C A C C A T G G C A T G A G A A G A A C A A G G T C C C T G A G C A G G C A C A A G T C T G A C A G T A A G G G A C T G C T T T G G C A T C C A G G G C C T C C A G T C A C C T C A C T G C C A T A C A T T A G A A A T G A G A C A A T C A A A G N N N N N N N A G G G T G G C A C A C C C A T C C T T G T T G C T G G G G T G T G G C A G C C A C A T C C A A G A C T G G A G C A G C A G G C T G G C C A
WI-7336b	248 A C ---	---	---	A G A C A T T C T G C T C C C T G A A A G A C T G A A G A A A G T A G T A G T G C A T G G A C C C A C G A A A C T G C C C T G G C T C C A G T G A A A C T T G G G C A C A T G C T C A G G C T A C T A T A G T G C C A A G A G T C T T A T G T T A G C C C T G G C A G G C A G G T G T T A T A A A A T T C T G A A T T T G G G A T T T C A A A A G A T A T A T T T A C A T A C A C T G T A T G T T A T A G A A C T T C A T G G A T C A G A T C T G G G C A G C A A C C T A T A A A T C A A C A
WI-7338c	221 A G ---	---	---	C T C T T T C T C A G C A C A T T G A T G G C A A C T A G A A T T A C A G C A G T T T C A A A C T C T A C C A T G G A T A A T G C A A A C A A C C G A A G C T A C A T G C C A A T G A T A G T G C A A A G A A T A T T G C A A A A G G T G C T T A C C T T G A G C C A T T A T T T G T G C A G A G A A C A A A A G A A C A G A A T C A A T A T A A A T T C A A A G A C T A T C T G C A G C T A G T G T G T T C T C T T A C A C A C A G A T A T A T A C A C A C A G A C A T C A G A A A A T T C T G T T

WI-7338b	125	A C ---	---	---	CTCTTCTCAGCACATTGATGGGCAACTAGAAATACAGCAGTTTCAAACCTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAATATTGGCAAAAGGTGCTTTT[A/C]CCTTG AGCCATTATTTGTGTGTCAGAGAACAAAGAAAGAAATCAATATATAAATTCAAAGACTATCTGCAG CTAGTGTGTTCTCTTTACACACATATACACAGACATCAGAAAATTCGT
WI-7338	125	A C ---	---	---	CTCTTCTCAGCACATTGATGGGCAACTAGAAATACAGCAGTTTCAAACCTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAATATTGGCAAAAGGTGCTTTT[A/C]CCTTG AGCCATTATTTGTGTGTCAGAGAACAAAGAAAGAAATCAATATATAAATTCAAAGACTATCTGCAG CTAGTGTGTTCTCTTTACACACATATACACAGACATCAGAAAATTCGT
WI-7338	221	A G ---	---	---	CTCTTCTCAGCACATTGATGGGCAACTAGAAATACAGCAGTTTCAAACCTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAATATTGGCAAAAGGTGCTTTTACCTTGAGC CATTATTTGTGTGTCAGAGAACAAAGAAAGAAATCAATATATAAATTCAAAGACTATCTGCAGCTA GTGTGTTCTCTTTACACACATATACACAGACATCAGAAAATTCGT
WI-7384c	146	T A ---	---	---	CCTATGTCATGAATGCTAGGGGGCCAGGGAACAAAATTTTAAAAATAAATAAATTCACCATAG CAATACAGAAATACTTTAAATACCATTAATACATTTGATTTTCAATGTGAACAGGATTTCTTCA CAGATCTCATTTT[A/J]AAAAATCTTAATGATTATTTTATTACTACTGTGTTTAAAGGGATGTTA TTTTAAAGCATATACCATACACTTAAGAAAATTTGAGCAGAAATTTAAAAAGAA
WI-7384b	146	T A ---	---	---	CCTATGTCATGAATGCTAGGGGGCCAGGGAACAAAATTTTAAAAATAAATAAATTCACCATAG CAATACAGAAATACTTTAAATACCATTAATACATTTGATTTTCAATGTGAACAGGATTTCTTCA CAGATCTCATTTT[A/J]AAAAATCTTAATGATTATTTTATTACTACTGTGTTTAAAGGGATGTTA TTTTAAAGCATATACCATACACTTAAGAAAATTTGAGCAGAAATTTAAAAAGAA
WI-7384	145	T A ---	---	---	CCTATGTCATGAATGCTAGGGGGCCAGGGAACAAAATTTTAAAAATAAATAAATTCACCATAG CAATACAGAAATACTTTAAATACCATTAATACATTTGATTTTCAATGTGAACAGGATTTCTTCA CAGATCTCATTTT[A/J]AAAAATCTTAATGATTATTTTATTACTACTGTGTTTAAAGGGATGTTA TTTTAAAGCATATACCATACACTTAAGAAAATTTGAGCAGAAATTTAAAAAGAA
WI-7388c	106	A T ---	---	---	TGAAATCCTGGGTCTCTGGCCTGCTGTAGCTGGTTATTTTACTTTGCCCTCCCTCCCTTTT TGAGATCCATCCTTTTATCAAGAGTCTGAAGCGACT[A/J]TAAAGGTTTTTGAATTCAGATTTAAAA ACCAACTTATAAGCATTGCAACAGGTTACCTCTATTTGCCACAAGCGTCTCGGGATTGTGTTTGA CTGTGCTGTCTCAAGAACTTTTCCCCCAAGATGIGTATAGTTATGG
WI-7388b	106	A T ---	---	---	TGAAATCCTGGGTCTCTGGCCTGCTGTAGCTGGTTATTTTACTTTGCCCTCCCTCCCTTTT TGAGATCCATCCTTTTATCAAGAGTCTGAAGCGACT[A/J]TAAAGGTTTTTGAATTCAGATTTAAAA ACCAACTTATAAGCATTGCAACAGGTTACCTCTATTTGCCACAAGCGTCTCGGGATTGTGTTTGA CTGTGCTGTCTCAAGAACTTTTCCCCCAAGATGIGTATAGTTATGG

WI-7388	94	T A ---	---		TGAAATCCTGGGCTCTGGCCTGCTGTAGCTGGTTATTTTACTTTGCCCTCCCTCCCTTTT TGAGATCCATCCTTTATCAAGAAAGT/AJCTGAAGCGACTATAAAGGTTTTTGAATTCAGATTTAAAA ACCAACTTATAAGCATTCGAACAAGGTTACCTCTATTTTGCCACAAGCGTCTCGGATTTGTGTTGA CTTGCTGTCTCCAAAGAACTTTTCCCAAGATGTGTATAGTTATGG
WI-7438	64	A G ---	---		TTAGATTTTAATTGGCAACCAGCAACTCACTGCCACCATCCACTGCAGATCTNCTATTCTCTGG[A/G] GTTGATATGACAAGGAACCTATTGGAACCAAGTCTTCAGATTGTCAGATGTCAGACAGGCTCCT TGCTGTAGGTGTAGTGCATGTACACTGTACTGTTCACCTGTACATAGTTTGTCNCTGGTATTGTTA TTGGAATGAATATCGCTTCCACTGACTTTTACCA
WI-7454b	152	T C ---	---		CCATGATCCCCTCCTCTTGCCAAATGGAGGAAGCCTGTGGATGGTACCAACAACAGCCCCAAACC CAGTACAACTGAGAAATGAGAGAACCTCTGATAGCACTGTCTGAATGCCAGGAGCCTCCAAGGCTAA TCCTACCCCTGGATTCTT/CJGTGTTGTTAAAGTTATTTAGCCACCACAAAGAGGGTACTGCCCAA CAGACTCATCCTTAAAAATCCCATTTGTCTACTTCTCAAAATGTTTTGACA
WI-7454	152	T C ---	---		CCATGATCCCCTCCTCTTGCCAAATGGAGGAAGCCTGTGGATGGTACCAACAACAGCCCCAAACC CAGTACAACTGAGAAATGAGAGAACCTCTGATAGCACTGTCTGAATGCCAGGAGCCTCCAAGGCTAA TCCTACCCCTGGATTCTT/CJGTGTTGTTAAAGTTATTTAGCCACCACAAAGAGGGTACTGCCCAA CAGACTCATCCTTAAAAATCCCATTTGTCTACTTCTCAAAATGTTTTGACA
WI-7464c	177	G C ---	---		AATTTGAAAATCTGAAAAAAGTGTCATAAGCAGAGAAATGACACTTATCCAAATAAATAAATGT CCATTTTTCAGTCAGTCCATCTTAACCATGTACAATGCACATAAATCTATTATTAATTCCTATGTA CAACAGAGCCACAGCACAAAGAGGGTGGGCATAAGCAGTTGCCA[G/C]CCAGAAAGAGCTTTCACAT GAAAGAAAGCCCTACAAATAGGCCCAGGAGGAAGCAACGTTCCACCAACAATTAT
WI-7464b	168	C A ---	---		AATTTGAAAATCTGAAAAAAGTGTCATAAGCAGAGAAATGACACTTATCCAAATAAATAAATGT CCATTTTTCAGTCAGTCCATCTTAACCATGTACAATGCACATAAATCTATTATTAATTCCTATGTA CAACAGAGCCACAGCACAAAGAGGGTGGGCATAAGCAGTTGCCA[G/C]CCAGAAAGAGCTTTCACAT GAAAGAAAGCCCTACAAATAGGCCCAGGAGGAAGCAACGTTCCACCAACAATTAT
WI-7464a	103	C A ---	---		AATTTGAAAATCTGAAAAAAGTGTCATAAGCAGAGAAATGACACTTATCCAAATAAATAAATGT CCATTTTTCAGTCAGTCCATCTTAACCATGTACAATGCACATAAATCTATTATTAATTCCTAT GTACAACAGAGCCACAGCACAAAGAGGGTGGGCATAAGCAGTTGCCAGCCAGAGAGCTTTCACAT GAAAGAAAGCCCTACAAATAGGCCCAGGAGGAAGCAACGTTCCACCAACAATTAT
WI-7499b	134	T G ---	---		CAATTCCTCAATCCAACTAGTCTGNTGCCTAAACCATCCAGACAAACTCCACTTCGAAGGTTTAA AATGCATAAGTCAGATAGCAATCCTTCAGTTGCCCCAGAGGCACATCAGCTTCTTTGAATGCTTCAIT /GJTATAGTCCTTTCATTTAGCAATCAGTGAGGCAATACACTGGCATCATGATCCCTTTTTTAGGA ACTCTGTACAAAATTCCTTTGAAAATATAAATTTTGGAAATGAGTGATGA

WI-7499a	33 A G ---	---	---	CAATTCTCAATCCAAACCTAGTCTGINTGCCTAA/JGICCATCCAGACAAACCTCCACTTCGAAGGTT TTAAATGCATAAGTCAGATAGCAATCCTTCAGTTCCTCCAGAGGCACATCAGTTCCTTTGAATGCTTC ATTATAGTCCCTCTTCATTTAGCAATCAGTGAGGCAATACACTGGCATCATGATCCCTTTTTTAGGAA CTCTGTACAAAATTCCTTTGAAAATATAAATTTGGAAATGAGTGATGA
WI-7506b	118 A C ---	---	---	TGGGAATAGTAAGAGAAAGATGGGAAAGGTGACCAAAAACAATATAGAGGCAGAGGCCAAAGTGAAT GCATCCAGCAGCAGACCACTTNAAGTAGTCTGGTGGCTGATTGCCTAGC/A/CJGGAGAGTTGAG TGCCACAGGTAAAGATGAGTGAAGAGGAAAAAATCATGATGTCATGTATGCAGTAATTACTATGTCA GAAGAAAATATTTTAAATATTGGACCACTCTTGTTCTACCATCCCTACCCACT
WI-7506	118 A C ---	---	---	TGGGAATAGTAAGAGAAAGATGGGAAAGGTGACCAAAAACAATATAGAGGCAGAGGCCAAAGTGAAT GCATCCAGCAGCAGACCACTTNAAGTAGTCTGGTGGCTGATTGCCTAGC/A/CJGGAGAGTTGAG TGCCACAGGTAAAGATGAGTGAAGAGGAAAAAATCATGATGTCATGTATGCAGTAATTACTATGTCA GAAGAAAATATTTTAAATATTGGACCACTCTTGTTCTACCATCCCTACCCACT
WI-7534b	143 C T ---	---	---	TGTGAATCTTAGCTCTGGAAGGTGTTTATGCCCTTTGCGGGTTCTTGATGTGTCGCAGTGTACCCCA AGAGTCAGAACTGTACACATCCCAAAATTTGGTGGCGTGGAACACATTCOCGGTGATAGAAATGCT AAATTGT/C/JTGTGAATAGGTAGAAATTTCTTTAAATATGTTTCTTATTCGTGAAAAATTCGG AGAGTGTGCTAAAATTTGGATTGGTGTGATCTTTTGGTAGTTGTAATTT
WI-7534	135 T C ---	---	---	TGTGAATCTTAGCTCTGGAAGGTGTTTATGCCCTTTGCGGGTTCTTGATGTGTCGCAGTGTACCCCA AGAGTCAGAACTGTACACATCCCAAAATTTGGTGGCGTGGAACACATTCOCGGTGATAGAAATGCT /CJAAATTGCTGAAATAGGTAGAAATTTCTTTAAATATGTTTCTTATTCGTGAAAAATTCGG AGAGTGTGCTAAAATTTGGATTGGTGTGATCTTTTGGTAGTTGTAATTT
WI-7543b	162 G A ---	---	---	GGGAAAGAATAAAATTAGCTTGAGCAACCTGGCTAAGATAGAGGGGCTCTGGAGACTTTGAAGACC AGTCCTGTTTGAGGGAAGCCCCACTTGAAGGAAGAGTCTAAGAGTGAAGTAGGTGACTTTGAAC TAGATTGCATGCTTCCTCCTTTGCTCTT/GA/JGGAAGACCAGCTTTGCAGTGACAGCTTGAGTGGGT CTCTGCAGCCCTCAGATTATTTTCTCTGGCTCCTTGGATGTAGTCAGTTA
WI-7543	162 G A ---	---	---	GGGAAAGAATAAAATTAGCTTGAGCAACCTGGCTAAGATAGAGGGGCTCTGGAGACTTTGAAGACC AGTCCTGTTTGAGGGAAGCCCCACTTGAAGGAAGAGTCTAAGAGTGAAGTAGGTGACTTTGAAC TAGATTGCATGCTTCCTCCTTTGCTCTT/GA/JGGAAGACCAGCTTTGCAGTGACAGCTTGAGTGGGT CTCTGCAGCCCTCAGATTATTTTCTCTGGCTCCTTGGATGTAGTCAGTTA
WI-7555c	60 T C ---	---	---	GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCTCAAAATTTGTAGAGGTC/JCTA AAAAGAAAGTGTGATGTTGTGTGATGATCAGCACTAAGTCTGCATCTCTGTTAAAGCCACTTGGGTC ATAAGAAGGGAAGTAAAAATGAAGTCTGACTAGAAATCTATTGCAGAGGCCAAAGTACATTTAGT ATGGCAATTGAGTTGTGATATAGTTTTCATTTGATGTGCAATTTTGAATTCAG

WI-7555b	60	T C ---	---	GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCTCAAAATTTGTAGAGGTC/TCTCTA AAAAGAAAGTGGTATGTTGTGTGATGATCAGCACTAAGTCTGCATTCCTGTTAAAGCCACTTGGGTC ATAAGAAGGGAAAGTAAAAATGAAGTCTGACTAGAAATCTATTGCAGAGGCCAAGTACATTTAGT ATGGCATTGAGTTGTGATATAGTTTTCATTTGATGTGCATTTGAATTCAG
WI-7555	60	T C ---	---	GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCTCAAAATTTGTAGAGGTC/TCTCTA AAAAGAAAGTGGTATGTTGTGTGATGATCAGCACTAAGTCTGCATTCCTGTTAAAGCCACTTGGGTC ATAAGAAGGGAAAGTAAAAATGAAGTCTGACTAGAAATCTATTGCAGAGGCCAAGTACATTTAGT ATGGCATTGAGTTGTGATATAGTTTTCATTTGATGTGCATTTGAATTCAG
WI-7567b	290	G T ---	---	TGAGCCATCACTAGAAAGAAAGCCATTTTCAACTGCTTTGAAACTTGCCTGGGGTCTGAGCATGAT GGGAATAGGGAGACAGGGTAGAAAGGGCGCCTACTCTCAGGGTCTAAAGATCAAGTGGGCGCTGG ATCGCTAAGCTGGCTGTTTGATGCTATTTATGCAAGTTAGGGTCTATGATTTAGGATGCGCTAC TCTTCAGGGTCTAAAGATCAAGTGGGCTTGGATCGCTAAGCTGGCTGTTT
WI-7569b	63	T C ---	---	AATGTATCCCTTTCGGTCCAACAACAGGAAACCTGACTGGGCAGTGAAGGAAGGATGGCATTC/C AGCGTTATGTGTAAAAACAAGTATCTGTATGACAACCCGGGATCGTTTGCAGTAAGTAACTGAATCCAT TGCGACATTTGTAAGGCTTAAATGAGTTTAGATGGGAAATAGCGTTGTTATCGCCTTGGGTTTAAAT ATTGTAGATTCCACTTGTATCATGGCCTACCCGAGGAGAAGAGGAGTTTG
WI-7574c	216	A G ---	---	GCCACAGCAATGGAGCGGTGTAGGAAGTCCCTTTCTCTGTTTGTGTTGCCAAGGCCAAAC TCCCACTCTGCCCCCTTTAATCCCTTTCTACAGTGAGTCCACTACCCCTCACTGAAAATCATTTTG TACCACCTACATTTTAGGCTGGGCAAGCAGCCCTGACCTAAGGGAGAATGAGTTGGACAGTCTTG ATAGCCAGGGC/A/GTCTGCTGGCTGACCAGCTTACTCATCCCGTTA
WI-7574b	216	A G ---	---	GCCACAGCAATGGAGCGGTGTAGGAAGTCCCTTTCTCTGTTTGTGTTGCCAAGGCCAAAC TCCCACTCTGCCCCCTTTAATCCCTTTCTACAGTGAGTCCACTACCCCTCACTGAAAATCATTTTG TACCACCTACATTTTAGGCTGGGCAAGCAGCCCTGACCTAAGGGAGAATGAGTTGGACAGTCTTG ATAGCCAGGGC/A/GTCTGCTGGCTGACCAGCTTACTCATCCCGTTA
WI-7574	216	A G ---	---	GCCACAGCAATGGAGCGGTGTAGGAAGTCCCTTTCTCTGTTTGTGTTGCCAAGGCCAAAC TCCCACTCTGCCCCCTTTAATCCCTTTCTACAGTGAGTCCACTACCCCTCACTGAAAATCATTTTG TACCACCTACATTTTAGGCTGGGCAAGCAGCCCTGACCTAAGGGAGAATGAGTTGGACAGTCTTG ATAGCCAGGGC/A/GTCTGCTGGCTGACCAGCTTACTCATCCCGTTA
WI-7576c	168	A T ---	---	AATGATGATGATAATGATGATGACGACGACAAACGATGATGCTTGTACAAGAAAACATAAGAGAGC CTTGGTTCATCAGTGTAAAAAATTTTGAAGGCGGTACTAGTTTCAGACACTTTGGAAGTTTGTGT TCTGTTTGTAAAACTGGCATCTGACACAAAAAA/A/TGTTGAAGGCCCTTATTCTACATTTACACCTAC TTTGTAGTGAGAGAGACAAGCAAGCAANNNNNNNNNNAAGAAAAAATAAAC



WI-7577j	117	A G ---	---		AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCAAACATAAGTGTTCCTTTAA AAATATGCATCAAAATCGTCTCTCACTTTCTCTGAGGGTTTAGTA/GJACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577i	77	T C ---	---		AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCAAACATAAGTGTTCCTTTAA AAATATGCATCAAAATCGTCTCTCACTTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577h	50	G C ---	---		AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCAAACATAAGTGTTCCTTTAA AAATATGCATCAAAATCGTCTCTCACTTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577g	157	G A ---	---		AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCAAACATAAGTGTTCCTTTAA AAATATGCATCAAAATCGTCTCTCACTTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577f	48	A G ---	---		AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCAAACATAAGTGTTCCTTTAA AAATATGCATCAAAATCGTCTCTCACTTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577e	84	G A ---	---		AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCAAACATAAGTGTTCCTTTAA AAATATGCATCAAAATCGTCTCTCACTTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577d	93	T C ---	---		AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCAAACATAAGTGTTCCTTTAA AAATATGCATCAAAATCGTCTCTCACTTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577c	154	C A ---	---		AACCATGTTCCCTTCTCTTAGCACCACAAATAATCAAAACCCAAACATAAGTGTTCCTTTAA AAATATGCATCAAAATCGTCTCTCACTTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTACACGTAGGAAAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC



WI-7577b	117 A G ---				AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTA/GJACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTTACACGTAGGAAGAGAGACATCAAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTATACATGACACTCTCTGAATTGACTGTATTTC
WI-7577	107 G A ---				AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCCAACATAAGTGTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTTCTCTGAG/GA/GJTTTGTAGTAACAGTAGGAGTTAAT AAAGAAGTTCAATTTGGTTTACACGTAGGAAGAGAGACATCAAAAGTGGAGATATGTTAACTAT TGATAATGTGGCCTGTATACATGACACTCTCTGAATTGACTGTATTTC
WI-7619q	106 C G ---				ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGACACAAGAC AGAGAAGGGCCAAATGGGTCATCCCTCCCTAACGAGACTC/GJCTGTGCTGGGGTGTAAATTAC ATGGCAGGAAGAAATGGGCCCTTAAGGGAGTGTGGGTCTGTCTCTCCCTTTTTCATCTTTTCTCT CTCTCGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619p	150 T C ---				ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGACACAAGAC AGAGAAGGGCCAAATGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGTAAATTACATGG CAGGAAGAAATGGGGCTT/CJTAAGGGAGTGTGGGTCTGTCTCTCCCTTTTTCATCTTTTCTCT TCTCGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619o	228 A G ---				ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGACACAAGAC AGAGAAGGGCCAAATGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGTAAATTACATGG CAGGAAGAAATGGGGCTTAAAGGGAGTGTGGGTCTGTCTCTCCCTTTTTCATCTTTTCTCTCT CGCTTCTTCTTACACAGAAACAT/A/GJACATACCGAGAAACCTATTTC
WI-7619n	237 G C ---				ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGACACAAGAC AGAGAAGGGCCAAATGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGTAAATTACATGG CAGGAAGAAATGGGGCTTAAAGGGAGTGTGGGTCTGTCTCTCCCTTTTTCATCTTTTCTCTCT CGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619m	99 C T ---				ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGACACAAGAC AGAGAAGGGCCAAATGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGTAAATTACATGG TGGCAGGAAGAAATGGGGCTTAAAGGGAGTGTGGGTCTGTCTCTCCCTTTTTCATCTTTTCTCT TCTCGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619l	189 T A ---				ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGACACAAGAC AGAGAAGGGCCAAATGGGTCATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGTAAATTACATGG CAGGAAGAAATGGGGCTTAAAGGGAGTGTGGGTCTGTCTCTCCCTTTTTCATCTTTTCTCTCT TCTCGCTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC

WI-7619k	90 C ---			---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAAGCACAAGAC AGAGAAAGGGCCCAATGGGGTCATCC[G]CTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTAC ATGGCAGGAAGATGGGGCTCTAAGGGGAGTGTTGGGCTGTCTCTCCCTTTTTCATCTTTTTCCT CTCTCGCTTTCTTTACACAGAAACATACATACCGAGAAACCTATTTC
WI-7619j	206 T G ---			---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAAGCACAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTAC ATGGCAGGAAGATGGGGCTCTAAGGGGAGTGTTGGGCTGTCTCTCCCTTTTTCATCTTTTTCCT CGCTGCTTTCTTTACACAGAAACATACATACCGAGAAACCTATTTC
WI-7619i	106 C G ---			---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAAGCACAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTAC ATGGCAGGAAGATGGGGCTCTAAGGGGAGTGTTGGGCTGTCTCTCCCTTTTTCATCTTTTTCCT CTCTCGCTTTCTTTACACAGAAACATACATACCGAGAAACCTATTTC
WI-7619h	150 T C ---			---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAAGCACAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGATGGGGCTCTAAGGGGAGTGTTGGGCTGTCTCTCCCTTTTTCATCTTTTTCCTC TCTCGCTTTCTTTACACAGAAACATACATACCGAGAAACCTATTTC
WI-7619g	228 A G ---			---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAAGCACAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGATGGGGCTCTAAGGGGAGTGTTGGGCTGTCTCTCCCTTTTTCATCTTTTTCCTCCT CGCTTTCTTTCTTTACACAGAAACATACATACCGAGAAACCTATTTC
WI-7619f	237 G C ---			---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAAGCACAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGATGGGGCTCTAAGGGGAGTGTTGGGCTGTCTCTCCCTTTTTCATCTTTTTCCTCCT CGCTTTCTTTCTTTACACAGAAACATACATACCGAGAAACCTATTTC
WI-7619e	99 C T ---			---	TGGCAGGAAGATGGGGCTCTAAGGGGAGTGTTGGGCTGTCTCTCCCTTTTTCATCTTTTTCCTC TCTCGCTTTCTTTACACAGAAACATACATACCGAGAAACCTATTTC
WI-7619d	189 T A ---			---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAAGCACAAGAC AGAGAAAGGGCCCAATGGGGTCATCCCTCCCTAACGAGACTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGATGGGGCTCTAAGGGGAGTGTTGGGCTGTCTCTCCCTTTTTCATCTTTTTCCTC TCTCGCTTTCTTTACACAGAAACATACATACCGAGAAACCTATTTC

WI-7619c	90 C G	---	---	ACAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGCCCAATGGGTCATCCGCTC/GCTCCCTAACGAGACTCTCTGTCTGGGGTGTCTAATTAC ATGGCAGGAAGAATGGGCTCTAAGGGAGTGTGGGTCTCTCCCTTTTCCATCTTTTCCATCTTTTCCCT CTCTCGCTTTCTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619b	206 T G	---	---	ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGCCCAATGGGTCATCCCTCCCTAACGAGACTCTCTGTCTGGGGTGTCTAATTACATGG CAGGAAGAATGGGCTCTAAGGGAGTGTGGGTCTCTCTCCCTTTTCCATCTTTTCCATCTTTTCCCTCTCT CGCT/GTCTCTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619	189 T A	---	---	ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAAGGCCCAATGGGTCATCCCTCCCTAACGAGACTCTCTGTCTGGGGTGTCTAATTACATGG CAGGAAGAATGGGCTCTAAGGGAGTGTGGGTCTCTCTCCCTTTTCCATCTTTTCCATCTTTTCCCTCTCT TCTCGCTTTCTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7626d	105 A G	---	---	CCTTTGATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACAAACAAAGCAACAGTAA TCTATGTGTTCTGTAAACAAATGGGATCTGTCTGGCA/GJTAAACACATCATGGACCAATGTG CCATACATGATGAGCATTTAGCACAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTTATATAGTAACCATTTTCCTTGGACTGTTCA
WI-7626c	155 C T	---	---	CCTTTGATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACAAACAAAGCAACAGTAA TCTATGTGTTCTGTAAACAAATGGGATCTGTCTGGCAATTAACACATCATGGACCAATGTGCCA TACTAATGATGAGCATTTAGC/TJACAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTTATATAGTAACCATTTTCCTTGGACTGTTCA
WI-7626b	28 T A	---	---	CCTTTGATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACAAACAAAGCAACAG TAATCTATGTGTTCTGTAAACAAATGGGATCTGTCTGGCAATTAACACATCATGGACCAATGTG CCATACATGATGAGCATTTAGCACAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTTATATAGTAACCATTTTCCTTGGACTGTTCA
WI-7626	144 T C	---	---	CCTTTGATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACAAACAAAGCAACAGTAA TCTATGTGTTCTGTAAACAAATGGGATCTGTCTGGCAATTAACACATCATGGACCAATGTGCCA TACTAATGAT/GJAGCATTTAGCACAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCCTGCTGTTATATAGTAACCATTTTCCTTGGACTGTTCA
WI-7689c	134 A G	---	---	TCCCATACCGCTGATTCAGGGTCTCTGCTGCCGCCCAACCCAGATGGGGAAAGCACAGGTGGGC TTCCAGTGGCTGCTGCCAGGCCAGACCTTCTAGGACGCCCAAGCAAGGTTGTTCTTAAAJA /GJTAAGGGCAGAGTCACACTGGGGCAGCTGATACAAATTCAGACTGTGTAAAAGAGAGCTTAAT GATAATATTGGTGGCCCAACAAATAAATGGATTATTAGAAATTTTATATGAC

WI-7689b	134	A G ---				TCCATAACCGCTGATTCAGGGTCTCTGCTGCGCGCCCAACCCAGATGGGGGAAAGCACAGGTGGGC TTCCAGTGGCTGCTGCCAGGGCCAGACCTTCTAGGACCCACCCAGCAAAAGGTTGTTCTCTAAAG /GJTAAGGGCAGAGTCACACTGGGGCAGCTGATACAAATTGCAGACTGTGTAAAGAGAGCTTAAT GATAATATTGGGTGCCACAAATAAAATGGATTATTAGAAATTCATATGAC
WI-7689	121	G A ---				TCCATAACCGCTGATTCAGGGTCTCTGCTGCGCGCCCAACCCAGATGGGGGAAAGCACAGGTGGGC TTCCAGTGGCTGCTGCCAGGGCCAGACCTTCTAGGACCCACCCAGCAAAAGGTTGTTCTCTAA AATAAGGGCAGAGTCACACTGGGGCAGCTGATACAAATTGCAGACTGTGTAAAGAGAGCTTAAT GATAATATTGGGTGCCACAAATAAAATGGATTATTAGAAATTCATATGAC
WI-7690	45	G A ---				TGGAGAACATTCAATCTTGCCGTCATCTTATCATCAATGAAGATTAG/AJCACTGAGATCCAGAGAGG CTGGATGACTTGCTCAAGTTCACCAAGCATGGTAGTGGCAAAGAGAGTCCAGAGTCTGGCCCTTGAT GCCAGCTCAGTGCCACAAAGCTCAGTAGGAGGATGTTCCAGTGGATGAGGGCCACCCAGGAAGCAC AGGTCCAAGGCTGGTCCACACTTATCAGCAGCAACAACCTGTCAGTTCATCC
WI-7703b	164	T C ---				ACAGAAAGTTGAATTTACATGGCTGGAGCTAGAATTTGATATGTGAACAGTTGTGTTGAAGCAC AGTGATCAAGTTATTTTAAATTTGGTTTTCACATTGGAACAAGTCAGTCAATTCAGATATGATTCAAA TGCTATAAACCAAACTGATGTAAAGTAAAT/CJGGTCTCTCAGTTGTTTATTAACTCTAAATTCT TTCAITTTAGGGGTAGCATTTGTGTGAAGAGGTTTTAAAGCTTCCATTGT
WI-7703	156	T C ---				ACAGAAAGTTGAATTTACATGGCTGGAGCTAGAATTTGATATGTGAACAGTTGTGTTGAAGCAC AGTGATCAAGTTATTTTAAATTTGGTTTTCACATTGGAACAAGTCAGTCAATTCAGATATGATTCAAA TGCTATAAACCAAACTGATGTAAAGTAAAT/CJAAAGTAAATGGTCTCTCAGTTGTTTATTAACTCTAAATTCT TTCAITTTAGGGGTAGCATTTGTGTGAAGAGGTTTTAAAGCTTCCATTGT
WI-7743e	106	C A ---				TTAAATGAGTGTGTTGTCAACCGTTGGGGATTGGGGAAGACTGTGGCTGCTGGCATTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCAAGCACTAAAGCAAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAAATCTGCTACCTCAGTGGGTCTGCGGCTCGGAGCCTATCCAGGAGGTCAGGAGAG GAGGGGCAGAACAGCGCTCTGTGTCAGCCAGCAGCAGCAGCTCTCAGCC
WI-7743d	275	C T ---				TTAAATGAGTGTGTTGTCAACCGTTGGGGATTGGGGAAGACTGTGGCTGCTGGCATTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCAAGCACTAAAGCAAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAAATCTGCTACCTCAGTGGGTCTGCGGCTCGGAGCCTATCCAGGAGGTCAGGAGAG GGGCAGAACAGCGCTCTGTGTCAGCCAGCAGCAGCAGCTCTCAGCCAAACG
WI-7743e	106	C A ---				TTAAATGAGTGTGTTGTCAACCGTTGGGGATTGGGGAAGACTGTGGCTGCTGGCATTGGAGCCAAAGG GTTTCAGAGACTCAGGGCCCAAGCACTAAAGCAAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAAATCTGCTACCTCAGTGGGTCTGCGGCTCGGAGCCTATCCAGGAGGTCAGGAGAG GAGGGGCAGAACAGCGCTCTGTGTCAGCCAGCAGCAGCAGCTCTCAGCC

WI-7743d	275 C T ---	---	---	TTAATGAGTGTGTTGTACACCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCAGCTTGAGGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGATTCTGCTACCTCACTGGGGTCTGGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAG GGGCAGAACAGCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAAACG
WI-7743e	106 C A ---	---	---	TTAATGAGTGTGTTGTACACCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCAGCTTGAGGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAAATCTGCTACCTCACTGGGGTCTGGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGA GAGGGCAGAACAGCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAAACG
WI-7743d	275 C T ---	---	---	TTAATGAGTGTGTTGTACACCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCAGCTTGAGGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATCTGCTACCTCACTGGGGTCTGGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAG GGGCAGAACAGCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAAACG
WI-7743c	106 C A ---	---	---	TTAATGAGTGTGTTGTACACCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCAGCTTGAGGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAAATCTGCTACCTCACTGGGGTCTGGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGA GAGGGCAGAACAGCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAAACG
WI-7743b	275 C T ---	---	---	TTAATGAGTGTGTTGTACACCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCAGCTTGAGGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATCTGCTACCTCACTGGGGTCTGGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAG GGGCAGAACAGCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAAACG
WI-7743	106 C A ---	---	---	TTAATGAGTGTGTTGTACACCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCAGCTTGAGGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAAATCTGCTACCTCACTGGGGTCTGGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGA GAGGGCAGAACAGCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAAACG
WI-7743	275 C T ---	---	---	TTAATGAGTGTGTTGTACACCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCAGCTTGAGGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATCTGCTACCTCACTGGGGTCTGGGGCTCGGAGCCTCATCCGAGGCAGGGTCAGGAGAG GGGCAGAACAGCGCTCTGTCTGCCAGCCAGCAGCCAGCTCTCAGCCAAACG
WI-7758	144 A G ---	---	---	TGACATTTATTCAAAGTTAAAGCAACACTTACAGAAATATGAAGAGGTATCTGTTTAAACATTTCC TCAGTCAAGTTTCAGAGCTTCAGAGACTTCGTAATTAAGGAACAGAGTGAGAGACATCATCAAGTG GAGAGAAATC[W/G]TAGTTTAAACTGCATTATAATTTTATAACAGAAATTAAGTAGATTTTAAAA GATAAAATGTGTAATTTTGTATTATTTCCCATTTGGAGTGTAACTGACTGCC

WI-7765b	126	GC	---			ACAGGCGCTTGGCAGGTGCAGCCCCCACTGCCCTTGACCTGCCCTTCATGCATGGAAATTCOCCT TCATCTGGAACCATCAGAAACCCCTCACACTGGGACTTGCAAAAGGGTCAGTATGG(G/C)TTAGG GAAACATTCATCCTTGAGTCAAAAATCTCAATCTCCCTATCTTTGCCACCCTCATGCTGTGTG ACTCAAAACCAATCACTGAACCTTGTGCTGAGCCTGTAAATAAAAGGICGGA
WI-7773b	237	CG	---			TTAATTTACTGATTCAGCAAGACCAATCATTTGTATCAGATTATTTTAAAGTTTATCCGTAGTTTT GATAAAGATTTTCTTATCTTGGTTCTGTGTCAGAGAACCTATAAGTGTCTATTTGCCATTAAAGCA GACTAGGGTTCTATCTTTTACCTTTNNNNNNNTGTAAAGTCTAGTTACCTACTTTTTCTTT GATTTTCGACGTTTACTAGCCATCTCAAGCA(G/C)TTTCGACGTTTGA
WI-7774b	170	TC	---			TGCAACCTCTTTTCGTGATGGCAGCCTGCTGGTCAGCACTCCAGTAGCGAGAGACGCCACCCAGAAT CAGATCCACAGCTTCGGCATTGATCAGACCAGAGTGTCTTCCGGGGAGGAAACACTTTTTTAA TTACCCCTTTTCGAGGCCACCCTTTAATCTGTTT/CJATACCTTGCTTATTAAATGAGCGACTAAA ATGATTGAAAATAATGCTGTCCTTTAGTAGCAAGTAAATGTCCTTGCT
WI-7785c	165	G	---			GCAGAGACCTTCCAAAGGACATATTGCAGGATTCCTGTAATAGTGAACATATGGAAAGTATTAGAAATA TTTATTGCTGTAATACTGTAATGCATTGGAATAAACTGTCTCCCCCATTCCTCTATGAAACTGC ACATTGGTCATTGTAATANNNNNNNNNGCCAAAGGCTAAATCAATATTATATCACAATTACCA TAATTTATTTGTCATTGATGATTATTTTGTAAATGATCTTGGTCTGC
WI-7785b	165	G	---			GCAGAGACCTTCCAAAGGACATATTGCAGGATTCCTGTAATAGTGAACATATGGAAAGTATTAGAAATA TTTATTGCTGTAATACTGTAATGCATTGGAATAAACTGTCTCCCCCATTCCTCTATGAAACTGC ACATTGGTCATTGTAATANNNNNNNNNGCCAAAGGCTAAATCAATATTATATCACAATTACCA TAATTTATTTGTCATTGATGATTATTTTGTAAATGATCTTGGTCTGC
WI-7785	156	T	---			GCAGAGACCTTCCAAAGGACATATTGCAGGATTCCTGTAATAGTGAACATATGGAAAGTATTAGAAATA TTTATTGCTGTAATACTGTAATGCATTGGAATAAACTGTCTCCCCCATTCCTCTATGAAACTGC ACATTGGTCATTGTAATANN- /JNNNNNNNGCCAAAGGCTAAATCAATATTATATCACAATTACCATAATTTATTTTGTCCATTGA TGATTTATTTTGTAAATGATCTTGGTG
WI-7789c	84	GA	---			TCTCCCTCATCCAACTCCGAAAGTCTGAATCTCCCAAGGAGGGCACCCTTACAGAGACTCTCCC TGACGGTGGAAATTTAA(G/A)TTAGGGTCCCTAAAGCATTTGACACACAGTTGTTGAATGACTGAC CCAAAATGTGAATGAAGCTAATGTGAATGTGAGTGAAGTCCCTCAGGCCCTGCCCTAGGATAT GCCCTCCTGCTGACTCGGGGGCTGTCTCAGACGACTAGGCCAGGACCCATCT
WI-7789b	84	GA	---			TCTCCCTCATCCAACTCCGAAAGTCTGAATCTCCCAAGGAGGGCACCCTTACAGAGACTCTCCC TGACGGTGGAAATTTAA(G/A)TTAGGGTCCCTAAAGCATTTGACACACAGTTGTTGAATGACTGAC CCAAAATGTGAATGAAGCTAATGTGAATGTGAGTGAAGTCCCTCAGGCCCTGCCCTAGGATAT GCCCTCCTGCTGACTCGGGGGCTGTCTCAGACGACTAGGCCAGGACCCATCT

WI-7789	73 GA ---	---	---	TCCTCCCTCATCCAACTCCGAAAGTCTGAATCTCCCAAGGAGGGACCACATCTTACAGAGACTCTCCC TGACG[G/A]TGAAATTTAAGTTAGGGTCCCTAAAGCAATTTGACACACAGTTGTTGAATGACTGAC CCAAATGTGAATGAAGCTAATGTGAATGTGAGTGAAGCTCCCTCAGGCCCGCTGCCCTAGGATAT GCOCTCCTGGTGAAGTGGGGCTGTCTCAGACGACTAGCCAGGACCCCATCT
WI-7790b	190 CT ---	---	---	AATTGTCAGTCACTCTTCAAAACCTTACAGTCTTCTCCTAAGGTTACTCTTCATGAGATTCATCCATT TACTAATACTGTATTTTGGTGGACTAGGCTTGCCTATGTCTTATGTGTAGCTTTTACTTTTATGG TGTGATTAATGGTGATCAAGGTAGGAAAGTTGTGTTCTATTTCTTGAAGTCTC[G/T]TCTATACTTT AAGATACCTCTATTTTAAACACTATCTGCAAACTCAGGACACTTTAAG
WI-7790	190 CT ---	---	---	AATTGTCAGTCACTCTTCAAAACCTTACAGTCTTCTCCTAAGGTTACTCTTCATGAGATTCATCCATT TACTAATACTGTATTTTGGTGGACTAGGCTTGCCTATGTCTTATGTGTAGCTTTTACTTTTATGG TGTGATTAATGGTGATCAAGGTAGGAAAGTTGTGTTCTATTTCTTGAAGTCTC[G/T]TCTATACTTT AAGATACCTCTATTTTAAACACTATCTGCAAACTCAGGACACTTTAAG
WI-7795b	81 CA ---	---	---	CAGATGTTCTGGTAAACTGATTGCTGGCAACAACAGATTCTCTGGCTCATATTTCTTTCTCTCAT CTTGATGATGAT[C/A]GTCAATCATCAAGAAATTTAATGATTAAATAGCATGCCCTTCTCTCTCTCT TAATAAGCCCAATATAAATGTACTTTTCTCCAGAAATCTCCTTGAGGAAAAATGTCCAAAA TAAGATGAATCACTTAATACCGTATCTTCTAAATTTGAAATATAATCTG
WI-7795	81 CA ---	---	---	CAGATGTTCTGGTAAACTGATTGCTGGCAACAACAGATTCTCTGGCTCATATTTCTTTCTCTCAT CTTGATGATGAT[C/A]GTCAATCATCAAGAAATTTAATGATTAAATAGCATGCCCTTCTCTCTCTCT TAATAAGCCCAATATAAATGTACTTTTCTCCAGAAATCTCCTTGAGGAAAAATGTCCAAAA TAAGATGAATCACTTAATACCGTATCTTCTAAATTTGAAATATAATCTG
WI-7814c	41 GA ---	---	---	TTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCC[G/A]TTTCATTTAGTCATGTGACCCTC TGCTTTGTGTTTCCACAGCCTGCAAGTTCAAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAAATCTTTAGAGAAGTATACATAAGTTTAGGATAAAATAATGGGATTTTC TTTTCTTTCTCTGGTAATATTGACTTGATATTTTAAAGAAATAACAGAA
WI-7814b	41 GA ---	---	---	TTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCC[G/A]TTTCATTTAGTCATGTGACCCTC TGCTTTGTGTTTCCACAGCCTGCAAGTTCAAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAAATCTTTAGAGAAGTATACATAAGTTTAGGATAAAATAATGGGATTTTC TTTTCTTTCTCTGGTAATATTGACTTGATATTTTAAAGAAATAACAGAA
WI-7814	28 GA ---	---	---	TTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCC[G/A]TTTCATTTAGTCATGTGACCCTC TGCTTTGTGTTTCCACAGCCTGCAAGTTCAAGTCCAGGATGCTAACATCTAAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGAAATCTTTAGAGAAGTATACATAAGTTTAGGATAAAATAATGGGATTTTC TTTTCTTTCTCTGGTAATATTGACTTGATATTTTAAAGAAATAACAGAA

WI-7830d	150 C T ---	---	---	GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGGTTTAGTAAGAGAAGTCTGTCTGTCTGATGA TGGATAGGGGGCAAATCTTTTCCCTTTCTGTTAATAGTATCATCACATTTCTATGCCAAACAGGAACG ATCCATAACTTTAGT[C/][T]TAATGTACACATTCGATTTTGATATAAATTAATTTGTTGTTCCCTTTG AGGTTGATCGTTGTGTTTGTCTGCACITTTTACTTTTTTGCCTGTGGA
WI-7830c	54 G A ---	---	---	GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGGTTTAGTAAGAGAAGTCTGTCTGTCTGATGA TGATGGATAGGGGGCAAATCTTTTCCCTTTCTGTTAATAGTATCATCACATTTCTATGCCAAACAGGA ACGATCCATAACTTTAGTCTTAATGTACACATTCGATTTTGATATAAATTAATTTGTTGTTCCCTTTG AGGTTGATCGTTGTGTTTGTCTGCACITTTTACTTTTTTGCCTGTGGA
WI-7830b	134 G A ---	---	---	GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGGTTTAGTAAGAGAAGTCTGTCTGTCTGATGA TGGATAGGGGGCAAATCTTTTCCCTTTCTGTTAATAGTATCATCACATTTCTATGCCAAACAGGAAC[ G/][ATCCATAACTTTAGTCTTAATGTACACATTCGATTTTGATATAAATTAATTTGTTGTTCCCTTTG AGGTTGATCGTTGTGTTTGTCTGCACITTTTACTTTTTTGCCTGTGGA
WI-7830	44 A G ---	---	---	GCAGGAAATAGTCACTCATCCCACTCCACATAAGGGGTTTAGTAAGAGAAGTCTGTCTGTCTGATGA TGATGGATAGGGGGCAAATCTTTTCCCTTTCTGTTAATAGTATCATCACATTTCTATGCCAAACAGGA ACGATCCATAACTTTAGTCTTAATGTACACATTCGATTTTGATATAAATTAATTTGTTGTTCCCTTTG AGGTTGATCGTTGTGTTTGTCTGCACITTTTACTTTTTTGCCTGTGGA
WI-7865e	25 C T ---	---	---	CCACTTCCTATCTGATTTTCCAG[C/][T]AAATGAGGAGGCAATCTAGTCTTCCACAAACATCTA GCCATCTAAATGGAGAGATGAATCTTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGG GGTATGCTACTATAAGATTCAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAAGGAAAGTGTCTATTCACCCAGTAAACCCAAA
WI-7865d	191 C T ---	---	---	CCACTTCCTATCTGATTTTCCAGCAAATGAGGAGGCAATCTAGTCTTCCACAAACATCTAGCC ATCTAAATGGAGAGATGAATCTTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGGGT ATGCTACTCATAAGATTCAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGT[C/][T]GAAAAAC CTGAAATCACATGCCTATGTAAGGAAAGTGTCTATTCACCCAGTAAACCCAAA
WI-7865c	25 C T ---	---	---	CCACTTCCTATCTGATTTTCCAGCAAATGAGGAGGCAATCTAGTCTTCCACAAACATCTA GCCATCTAAATGGAGAGATGAATCTTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGG GGTATGCTACTATAAGATTCAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAAGGAAAGTGTCTATTCACCCAGTAAACCCAAA
WI-7865b	191 C T ---	---	---	CCACTTCCTATCTGATTTTCCAGCAAATGAGGAGGCAATCTAGTCTTCCACAAACATCTAGCC ATCTAAATGGAGAGATGAATCTTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGGGT ATGCTACTCATAAGATTCAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGT[C/][T]GAAAAAC CTGAAATCACATGCCTATGTAAGGAAAGTGTCTATTCACCCAGTAAACCCAAA



WI-7865	25 C T ---			CCACTTCCTATCTGATTTTCCAG[C]/JAAATGAGGCGAGGCAATTCTAGTCTCCACAAAACATCTA GCCATCTAAAATGGAGAGATGAATCATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGG GGTATGCTACTCATAAGATTTTCCAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAAGGAAAGTGCTATTACCCAGTAAACCCAAA
WI-7865	191 C T ---			CCACTTCCTATCTGATTTTCCAGCAATGAGGCGAGGCAATTCTAGTCTCCACAAAACATCTAGCC ATCTAAAATGGAGAGATGAATCATCTACCTATACAAACAGCTAGCTATTAGAGGGTGGTTGGGT ATGCTACTCATAAGATTTTCCAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTA[C]/JGAAAAAC CTGAAATCACATGCCTATGTAAGGAAAGTGCTATTACCCAGTAAACCCAAA
WI-7867c	92 A C ---			TTCAAACACCTGTCTTCCACCTCCACCATCTGTGCAATCACTCACCTTCAGCCTCACTAGTCCCC CTAACAAATTACCTGTCAAGAG[C]/GAGTGCAGCTCAGGTGGATTAATGTGGGTTAATATGCG CTGTTGAGTTAATGTTAATGTTGATTTTCTTTAAGTAACCATTTCTGTTCTTGCTATAAATCTATGT CTATATGCTATGCTTAATTTGGATGATGAAGGCAACTGGATTTAAGG
WI-7867b	92 A C ---			TTCAAACACCTGTCTTCCACCTCCACCATCTGTGCAATCACTCACCTTCAGCCTCACTAGTCCCC CTAACAAATTACCTGTCAAGAG[C]/GAGTGCAGCTCAGGTGGATTAATGTGGGTTAATATGCG CTGTTGAGTTAATGTTAATGTTGATTTTCTTTAAGTAACCATTTCTGTTCTTGCTATAAATCTATGT CTATATGCTATGCTTAATTTGGATGATGAAGGCAACTGGATTTAAGG
WI-7868c	173 C T ---			TTGATCGATCTTTTCCACCTGTCACTCAACGTGGTCCCTAGAACAGAGGCTTAAACCGGGCTTT CACCCAACTGCTCCCTCTGATCCTCCATCAGGGCCAGATCTCCACGTCTCCATCTCAGTACACAAT CATTTAATATTTCCCTGTCTTACCCCTATTCAAGCA[C]/JTAGAGGCCAGAAAAATGGCAAAATTAT CACTAACAGGCTTTTGACTCAGGTTCCAGTAGTTCATTCTAATGCCTAGAT
WI-7868b	173 C T ---			TTGATCGATCTTTTCCACCTGTCACTCAACGTGGTCCCTAGAACAGAGGCTTAAACCGGGCTTT CACCCAACTGCTCCCTCTGATCCTCCATCAGGGCCAGATCTCCACGTCTCCATCTCAGTACACAAT CATTTAATATTTCCCTGTCTTACCCCTATTCAAGCA[C]/JTAGAGGCCAGAAAAATGGCAAAATTAT CACTAACAGGCTTTTGACTCAGGTTCCAGTAGTTCATTCTAATGCCTAGAT
WI-7868	66 T C ---			TTGATCGATCTTTTCCACCTGTCACTCAACGTGGTCCCTAGAACAGAGGCTTAAACCGGGCTTT /CTCACCCAACTGCTCCCTCTGATCCTCCATCAGGGCCAGATCTCCACGTCTCCATCTCAGTACAC AATCATTTAATATTTCCCTGTCTTACCCCTATTCAAGCAACTAGAGGCCAGAAAAATGGGCAAAATTAT CACTAACAGGCTTTTGACTCAGGTTCCAGTAGTTCATTCTAATGCCTAGAT
WI-7870b	85 T C ---			ATCTTTGCTCCCTGCAAGAAATCAGCCATAAGAAAGCACTATTAACTCTGCACTGATTAGAAGGG GTGGGGTGGCGGGAATCC[C]/JATTTATCAGACTCTGTAATGAATATAAATGTTTACTCAGAGGA GCTGCAAAATTGCCTGCAAAAATGAAATCCAATGAGCACTAGAAATTTTAAACATCATCTACTGCCAT CTTTATCATGAAGCACATCAATTACAAGCTGTAGACCACCTAATATCAATTTG

WI-7870	76 C T ---	---	---	ATCTTTGCTCCCTGCAAGAAATCAGCCATAAGAAAGCACTATTAACTACTCTGCAGTGATTAGAAAGG GTGGGTGG[C/TTGGGAATCCTATTATCAGACTCTGTAATGAATATAAATGTTTTACTCAGAGGAG CTGCAATTGCCCTGCAAAAATGAAATCCAATGAGCACTAGAAATATTTAAACATCATTACTGCCATC TTTATCATGAAGCACATCAATTACAAGCTGTAGACCACCTAATATCAATTTG
WI-7889c	54 C ---	---	---	TTAGGTCTCATGCCCACTCCCCAGGAGCAGCTGGCACTGACAGCCTGGGGGGCCGCTCTCCCCCTG CAGCCGTGCAGGACTCTAGCTCATGAGTGGAAAGTCACCTACAGGACTGGCCGGCCAGGGCCTCT GGCTTCCCTGCCCAATCCTCCCTGGAGAAGGACATGGGAATGAATTTGAAATGGGGCGCTGGACACC TACAGCAGCAGCATGTCCCTCCAAGGCTGCTTCTCCAGAGCACAAAG
WI-7889b	54 C ---	---	---	TTAGGTCTCATGCCCACTCCCCAGGAGCAGCTGGCACTGACAGCCTGGGGGGCCGCTCTCCCCCTG CAGCCGTGCAGGACTCTAGCTCATGAGTGGAAAGTCACCTACAGGACTGGCCGGCCAGGGCCTCT GGCTTCCCTGCCCAATCCTCCCTGGAGAAGGACATGGGAATGAATTTGAAATGGGGCGCTGGACACC TACAGCAGCAGCATGTCCCTCCAAGGCTGCTTCTCCAGAGCACAAAG
WI-7894c	142 A G ---	---	---	AGCCACCCCAATATAACTGTTATCCAGAAGCTGTTATGCTCTGTTCCATACATGTTTTGTACT TTTACTATATCTACATACATCAATTAACCTATGCTCTATTGTTTGAAATTTATTTGCGTATAC ATTATC[A/G]TATGTAAATTTGCAATTTTTTATTGAAATTAATGTTCTTGAGATTTATCCACATTG AAACATGGAGCTCTAAATCGTTAATTTAACCGCTATAGATATCCATA
WI-7894b	142 A G ---	---	---	AGCCACCCCAATATAACTGTTATCCAGAAGCTGTTATGCTCTGTTCCATACATGTTTTGTACT TTTACTATATCTACATACATCAATTAACCTATGCTCTATTGTTTGAAATTTATTTGCGTATAC ATTATC[A/G]TATGTAAATTTGCAATTTTTTATTGAAATTAATGTTCTTGAGATTTATCCACATTG AAACATGGAGCTCTAAATCGTTAATTTAACCGCTATAGATATCCATA
WI-7900e	84 C T ---	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG[C/TTCTGCCATTGAAACAGTGATTAAGTTTGATCAAGCCATGGTGACACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTTCTCAGATTTGAACCCAGTGAAA TATGATGTATTTCTGAGCTAAACTCAACTATAGAAGACATTTAAAGAAATC
WI-7900d	128 C T ---	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG[C/TTCTGCCATTGAAACAGTGATTAAGTTTGATCAAGCCATGGTGACACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTTCTCAGATTTGAACCCAGTGAAA TATGATGTATTTCTGAGCTAAACTCAACTATAGAAGACATTTAAAGAAATC
WI-7900e	84 C T ---	---	---	GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG[C/TTCTGCCATTGAAACAGTGATTAAGTTTGATCAAGCCATGGTGACACA AAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTTCTCAGATTTGAACCCAGTGAAA TATGATGTATTTCTGAGCTAAACTCAACTATAGAAGACATTTAAAGAAATC

WI-7900d	128 C T ---			GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGAAACAGTGATTAAGTTTGATCAAGCCATGGTGA(C/T)ACA AAAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCAGATTGAACCCAGTGAAA TATGATGATTTTCTGAGCTAAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900e	84 C T ---			GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGAAACAGTGATTAAGTTTGATCAAGCCATGGTGA(C/T)ACA AAAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCAGATTGAACCCAGTGAAA TATGATGATTTTCTGAGCTAAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900d	128 C T ---			GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGAAACAGTGATTAAGTTTGATCAAGCCATGGTGA(C/T)ACA AAAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCAGATTGAACCCAGTGAAA TATGATGATTTTCTGAGCTAAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900c	84 C T ---			GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGAAACAGTGATTAAGTTTGATCAAGCCATGGTGA(C/T)ACA AAAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCAGATTGAACCCAGTGAAA TATGATGATTTTCTGAGCTAAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900b	128 C T ---			GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGAAACAGTGATTAAGTTTGATCAAGCCATGGTGA(C/T)ACA AAAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCAGATTGAACCCAGTGAAA TATGATGATTTTCTGAGCTAAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900	84 C T ---			GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGAAACAGTGATTAAGTTTGATCAAGCCATGGTGA(C/T)ACA AAAAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCAGATTGAACCCAGTGAAA TATGATGATTTTCTGAGCTAAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7901c	33 C T ---			AGACTTAGGTACAATTGCTCCCCCTTTTATATA(C/T)AGACACACACAGGACACATATATTAAACAG ATTGTTTCATCATTCATCTATTTCCATATAGTCATCAAGAGACCATTTTATAAAACATGGTAAGAC CCTTTTAAACAACACTCCAGGCCCTTGGTTGGGGTGCTGGGTTATTGGGCAGCGCCGTGGTCTGT CACTCAGTCGCTCTGCATGCTCTCTGTCATACAGACAGGTAACCTAGTTCT
WI-7901b	33 C T ---			AGACTTAGGTACAATTGCTCCCCCTTTTATATA(C/T)AGACACACACAGGACACATATATTAAACAG ATTGTTTCATCATTCATCTATTTCCATATAGTCATCAAGAGACCATTTTATAAAACATGGTAAGAC CCTTTTAAACAACACTCCAGGCCCTTGGTTGGGGTGCTGGGTTATTGGGCAGCGCCGTGGTCTGT CACTCAGTCGCTCTGCATGCTCTCTGTCATACAGACAGGTAACCTAGTTCT

WI-7901	33 C T	---	---	AGACITTAGGTACAATTGCTCCCTTTTATATATAC/JAGACACACACAGGACACATATATTAAACAG ATTGTTTCATCATTTGCATCTATTTCCATATAGTCATCAAGAGACCATTTTATAAAACATGGTAAGAC CCTTTTAAAAACAACCTCCAGGCCCTGGTTGGGGTCTGGTTATTGGGCGAGCGCCGTGGTGGT CACTCAGTGGCTCTGCATGCTCTGTCTACACAGACAGGTAACCTAGTTCT
WI-7901	271 T G	---	---	AGACTTAGGTACAATTGCTCCCTTTTATATACAGACACACAGGACACATATATTAAACAGATT GTTTCATCATTTGCATCTATTTCCATATAGTCATCAAGAGACCATTTTATAAAACATGGTAAGACCCCT TTTTAAACAACCTCCAGGCCCTGGTTGGGGTCTGGTTATTGGGCGAGCGCCGTGGTGGTGCAC TCAGTGGCTCTGCATGCTCTGTCTACACAGACAGGTAACCTAGTTCTGTGT
WI-7926c	150 C A	---	---	CATTCCGCATCTGTCAACCAGGACAGAAAGCATGGACAAGGGATGAGCTTTACAAAGATGATGCACT TTGGAGATCAGAAATTCATATTTAAGCAAGTGATACAAACACAGTATTTGGGAATGCCTTCATT TACAATGCAATACTTAC/JAATTTTAACTCTTTGTAGGAGAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTTGCAACCTATATCAGAGAATTACACTGTGGGAA
WI-7926b	28 A T	---	---	CATTCCGCATCTGTCAACCAGGACAGAA/JGTCATGGACAAGGGATGAGCTTTACAAAGATGATGCACT TTGGAGATCAGAAATTCATATTTAAGCAAGTGATACAAACACAGTATTTGGGAATGCCTTCATT TACAATGCAATACTTAC/JAATTTTAACTCTTTGTAGGAGAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTTGCAACCTATATCAGAGAATTACACTGTGGGAA
WI-7926	150 C A	---	---	CATTCCGCATCTGTCAACCAGGACAGAAAGCATGGACAAGGGATGAGCTTTACAAAGATGATGCACT TTGGAGATCAGAAATTCATATTTAAGCAAGTGATACAAACACAGTATTTGGGAATGCCTTCATT TACAATGCAATACTTAC/JAATTTTAACTCTTTGTAGGAGAAAAGCAACTGTATAAATGAATGTA GAGTGACTTTCTGCAATATTTGCAACCTATATCAGAGAATTACACTGTGGGAA
WI-7947b	203 G T	---	---	AAGAGCCAGCAGGTCAAAAAGGCCAACACACCAATAGCAGCCAGCCACAAAGGCCAGGTCTGT GCTATCAGAGGTCACTCTTTTACAGTTAGAAACACAGCCAGGCCACAGATCCCATCCCTTTCC TGAGTCATGGCCTCAAAAATCAGGGCCACCATTTGTCATTTCAATCCATAGATTTTGAAGCCACA GA/GTJCTCTCCCTGGAGCAGCAGACTATGGGAGCCCGAGTCTGCCACCTG
WI-7947	203 G T	---	---	AAGAGCCAGCAGGTCAAAAAGGCCAACACACCAATAGCAGCCAGCCACAAAGGCCAGGTCTGT GCTATCAGAGGTCACTCTTTTACAGTTAGAAACACAGCCAGGCCACAGATCCCATCCCTTTCC TGAGTCATGGCCTCAAAAATCAGGGCCACCATTTGTCATTTCAATCCATAGATTTTGAAGCCACA GA/GTJCTCTCCCTGGAGCAGCAGACTATGGGAGCCCGAGTCTGCCACCTG
WI-7963b	145 T C	---	---	CATGTGCTGCATGAAGAGCTAAATTTAAAAAGCAAGTAAGACTAATTTAAAAATAAAATGCC ACAAATTCATTTCTCTCTAAGTATACAAATGGAGTTATCTCTGCTAAAAAGTGAAGAAAT TGAGTGAATGA/JCJAATTTTGTAAATTTAGGATAGATCCAAAGTTATTTCCCAACTCTTTGTTCC CCATAAAGTTAGGCATGAGGAGGAGCAGTCAATTAAGGCGAGAGACGGGAA

[illegible]

WI-8021b	57 C T ---	---	---	ACAACTCAGAAAGGACTGTGCAAGTCAATGAGTCGCTTGGAATCTCATCTGGAAA[C/T]GATCCC ACGCTTAGAACCTTACCACAAGGAGTTTCTTGTAGTGATTCTCAAAGTCTTGGTAGGCATTGGA ACTGGTCTTTACCTTGAGATTCTTTCTTTGGCCCTCTTATCAAGTCAGCACACACCTTTTCCAAAG GATTTAGGTTGGGCTTGTTAGGGGTGATTCGAATTCGGTGAATTGCCA
WI-8021	57 C T ---	---	---	ACAACTCAGAAAGGACTGTGCAAGTCAATGAGTCGCTTGGAATCTCATCTGGAAA[C/T]GATCCC ACGCTTAGAACCTTACCACAAGGAGTTTCTTGTAGTGATTCTCAAAGTCTTGGTAGGCATTGGA ACTGGTCTTTACCTTGAGATTCTTTCTTTGGCCCTCTTATCAAGTCAGCACACACCTTTTCCAAAG GATTTAGGTTGGGCTTGTTAGGGGTGATTCGAATTCGGTGAATTGCCA
WI-8024c	206 A G ---	---	---	CTGAAAATTTACTATGCTCTCCACAACAAGAGCTCCCATTTTCCACAGACACAGTCAATGTCACTCA GCTTGATTCAGGAGGACAGGGCAGAGGGATCCAGTGGCACTTCCCATGGGAAGACAGAAGAGAGT GGCCCCAGAGATGGAAGGACCCAGTGTATCACCACAACACCATTTAGCCGCTCTAGCCTCTAA TTCCC[AG/CT]CTAGAACAGCTGGCCCTGGTCGTCAGTACACAAGGAAGAGC
WI-8024b	206 A G ---	---	---	CTGAAAATTTACTATGCTCTCCACAACAAGAGCTCCCATTTTCCACAGACACAGTCAATGTCACTCA GCTTGATTCAGGAGGACAGGGCAGAGGGATCCAGTGGCACTTCCCATGGGAAGACAGAAGAGAGT GGCCCCAGAGATGGAAGGACCCAGTGTATCACCACAACACCATTTAGCCGCTCTAGCCTCTAA TTCCC[AG/CT]CTAGAACAGCTGGCCCTGGTCGTCAGTACACAAGGAAGAGC
WI-8077	167 A G ---	---	---	GAAATGAGCCTTCTAGCGCGAGGGACCTGCTGCTGTTGTTGGCCTGCACATGCTTCTATGGAATGC TTTTTGGCCAAAGCGGGCACTGAGGACTAAGCTCTGANNNNNNINATCGCCAAACTCCTTTCT AAGGAGTCTGGGTGTCATGCCCTACAAACC[AG/TA]AAATTTCTCATCAGATGGATTTTATTTAACGTT GTGATTGTGACTTACTTTCCAACTCTGACTCTGGCATAACAAGGGAAAAA
WI-8118f	114 G C ---	---	---	TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTTGGAAATGACCACCTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAACCTGGCAATACAGAATGAGCTTGT[GT/CT]TTTCTAGCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGAGACCAACAGTTTCTGATTTCCCTGCTCCTCTATTCCTTCCCT AAAAATCAGACTCAITGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118e	40 A G ---	---	---	TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTTGGAAATGACCACCTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAACCTGGCAATACAGAATGAGCTTGT[GT/CT]TTTCTAGCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGAGACCAACAGTTTCTGATTTCCCTGCTCCTCTATTCCTTCCCT AAAAATCAGACTCAITGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118d	118 T G ---	---	---	TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTTGGAAATGACCACCTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAACCTGGCAATACAGAATGAGCTTGT[GT/CT]TTTCTAGCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGAGACCAACAGTTTCTGATTTCCCTGCTCCTCTATTCCTTCCCT AAAAATCAGACTCAITGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA

WI-8118c	44 C T ---			TCTAGGTTTAAATCAAAAGCAATTTGCANTTTGGATTTTGGAAATGA[CT]CACTCCCTTGCTAAGGAAGC TATGTACTTCATGCTGTGGAAACTGGCAATACAGAATGTAGCTTGTGTTTCTTAGCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGAGACCAACAGTTTTCTGATTTCCCTGCTCCTCTATTCCTTCCCT AAAAATCAGACTCATTTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118b	88 T C ---			TCTAGGTTTAAATCAAAAGCAATTTGCANTTTGGATTTTGGAAATGACCACCTCCCTTGCTAAGGAAGCTAT GTACTTCATGCTGTGGAAACT[CT]GGCAATACAGAATGTAGCTTGTGTTTCTTAGCCTTGAAGA TGACCAGGTAGAGAGACAGAGTGAGACCAACAGTTTTCTGATTTCCCTGCTCCTCTATTCCTTCCCT AAAAATCAGACTCATTTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8171d	299 C T ---			TTTTCTCTCTCCGCGGGGACCAGGTACCTTCTGGGGCATACAACATGGCAGCAGGGCCTCGGGAAG AGGGGTAGGAGGACCGAGCAGCATTCCTGTAGAGGAAGACAGGAAGGAGACCCTCTTGGCACACA TTTATGGAGGTTGTCCCTGAAGAGAGAGGGCAGGTGGGGAGAGGTTCCCTGTTACTTAAGAGAAGGC ACCAAGTGGGCAAGAGACACAATGAAGAGGATGATGATAAAAACAATCACGGCA
WI-8171c	46 A G ---			TTTTCTCTCTCCGCGGGGACCAGGTACCTTCTGGGGCATACAAC[AG]TGGCAGCAGGGCCTCGGG AAGAGGGTAGGAGGACCGAGCAGCATTCCTGTAGAGGAAGACAGGAAGGAGACCCTCTTGGCAC ACATTTATGGAGGTTGTCCCTGAAGAGAGGGCAGGTGGGGAGAGGTTCCCTGTTACTTAAGAGAA GGCACCAAGTGGGCAAGAGACACAATGAAGAGGATGATGATAAAAACAATCAC
WI-8171a	46 A G ---			TTTTCTCTCTCCGCGGGGACCAGGTACCTTCTGGGGCATACAAC[AG]TGGCAGCAGGGCCTCGGG AAGAGGGTAGGAGGACCGAGCAGCATTCCTGTAGAGGAAGACAGGAAGGAGACCCTCTTGGCAC ACATTTATGGAGGTTGTCCCTGAAGAGAGGGCAGGTGGGGAGAGGTTCCCTGTTACTTAAGAGAA GGCACCAAGTGGGCAAGAGACACAATGAAGAGGATGATGATAAAAACAATCAC
WI-8171b	298 T C ---			TTTTCTCTCTCCGCGGGGACCAGGTACCTTCTGGGGCATACAACATGGCAGCAGGGCCTCGGGAAG AGGGGTAGGAGGACCGAGCAGCATTCCTGTAGAGGAAGACAGGAAGGAGACCCTCTTGGCACACA TTTATGGAGGTTGTCCCTGAAGAGAGGGCAGGTGGGGAGAGGTTCCCTGTTACTTAAGAGAAGGC ACCAGTGGGCAAGAGACACAATGAAGAGGATGATGATAAAAACAATCACGGCA
WI-8314b	85 G C ---			GAGGGGAAATGACATCTGGAGATCTAGGTATGTGCCCATTTGCAATTGAGCACATTTCTTGGGTCTGT TTCTCTATCTCTAAGGG[CT]AGTCTCAAAACCCAGCTCAAAATACGACACTAAGATGATGAACAT GCATGAGCTTTGAAAAGTGCTCTGTAGTCTTATGATGATCTAGAGAGCAGCTGTCCCAATAGAACTTTC TGTGATGATGAAAAGATTCTACTTCTGACCTATTCAATAGGGGTAACCACT
WI-8314	78 C G ---			GAGGGGAAATGACATCTGGAGATCTAGGTATGTGCCCATTTGCAATTGAGCACATTTCTTGGGTCTGT TTCTCTATCT[CT]GTTAAGGGAGTCTCAAAACCCAGCTCAAAATACGACACTAAGATGATGAACAT GCATGAGCTTTGAAAAGTGCTCTGTAGTCTTATGATGATCTAGAGAGCAGCTGTCCCAATAGAACTTTC TGTGATGATGAAAAGATTCTACTTCTGACCTATTCAATAGGGGTAACCACT

WI-8321	178	G A ---			TTTTAAATATGCCCCGTTAGAGCAGACACAGTCACAATAAAAGTTAAAAAGTTACAATGTGTCCAG TGATATACCCAGGNAATCCATTCTTGTTACTTTTCAAGAGCTGCTGTATTACTGAGTCTCTGAGAAG TCCCCTTAGATAATAGCTGCCACTTTTCAGTATGGTTCAGAAATG/AJAGTATCTTAGTATCTTTCTA TTTTGCTATGGTCTAGTTTATCAACCTACTTTATTAGCTGAACGTGTTGGC
WI-8321	178	G A ---			TTTTAAATATGCCCCGTTAGAGCAGACACAGTCACAATAAAAGTTAAAAAGTTACAATGTGTCCAG TGATATACCCAGGNAATCCATTCTTGTTACTTTTCAAGAGCTGCTGTATTACTGAGTCTCTGAGAAG TCCCCTTAGATAATAGCTGCCACTTTTCAGTATGGTTCAGAAATG/AJAGTATCTTAGTATCTTTCTA TTTTGCTATGGTCTAGTTTATCAACCTACTTTATTAGCTGAACGTGTTGGC
WI-8321	178	G A ---			TATGACTCACTTTCAGTTACCCCGTGCCTCCAGATCGCATGTTGCTCCACCTGGGGCGGATATA AATTACCTCTAGATTGTCCAAAGCCAGCTTTCCCTTCCCTGTGCAGCCTTAG/A/CJACTAAGTAG CAGTACTGTTGGTGTGTTGTTTCTTCCCGAGCAATGCCCTACTGCAGCTACTTAGTAACAACCTAG AGGTGGAGGNTCCGGGAAGCAGTTAGATGAGTTAAGTGTGATGCACA
WI-8332	123	A C ---			TATGACTCACTTTCAGTTACCCCGTGCCTCCAGATCGCATGTTGCTCCACCTGGGGCGGATATA AATTACCTCTAGATTGTCCAAAGCCAGCTTTCCCTTCCCTGTGCAGCCTTAG/A/CJACTAAGTAG CAGTACTGTTGGTGTGTTGTTTCTTCCCGAGCAATGCCCTACTGCAGCTACTTAGTAACAACCTAG AGGTGGAGGNTCCGGGAAGCAGTTAGATGAGTTAAGTGTGATGCACA
WI-8332	114	A C ---			TGCGGGCTTAACAGGAAGCATGACTGGAGGCCCTCAGGAAGCTTATAATCATGGCAGAAGCGAAGG GGAAGCAAGGACCTTCTTACATGGCAGCAGGAGAAAGAGAAGGAGGAGTCTACACACTTTT AAACAACAGATCTCATGAGANTCCATCGGGAGACAGCACTAGGGGGATGGCACTAAACCATTAGA AACTGCCCCCATGATCCCAATCACCTNTCACAGGCCCTCCTCCACACACGTGGGG
WI-8378b	311	T C ---			TGCGGGCTTAACAGGAAGCATGACTGGAGGCCCTCAGGAAGCTTATAATCATGGCAGAAGCGAAGG GGAAGCAAGGACCTTCTTACATGGCAGCAGGAGAAAGAGAAGGAGGAGTCTACACACTTTT AAACAACAGATCTCATGAGANTCCATCGGGAGACAGCACTAGGGGGATGGCACTAAACCATTAGA AACTGCCCCCATGATCCCAATCACCTNTCACAGGCCCTCCTCCACACACGTGGGG
WI-8378	308	T C ---			TTTAGCACATATTTAGCATTAAGCCTCAACGATACAGCAATATGTTACATCTCTTGTGAAAACAG TTGTTGTAGACTGTTAANNININININAAATGTAACCTCGACTTGGCCTAATAGGATTTGACCNNTAA GAGGNTCTTTGCTGTGGANGGGTGGCTTGTGCTGAACCTCCATCTGTG/GGCCCTGTAGCTGGTG AGGCTGGGAGTATGGANGNCCCGGGGCCCTTGGCNATGNATTCAGTGAG
WI-8426	184	T G ---			TTGAGCCTCCACAAATATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTC/AJCA TCTTCTCTATCTAGTCCAAAGTTTGTAGTTTCAATCCCAATTAACCAATCCATGTTATTTAAGA AAAAACCTTCCCAGTTATTGTCAAGAACTATGATTAGCTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTCAT
WI-8450h	61	C A ---			



WI-8450g	55 T C ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAAGGCCCTTCTACATTCACACTCCCAT CTTCTCTATCTTAGTTCCAAAGTTTGTAGTTTCAATCCCAATATACCAATTCATTGTTATTTTAAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450f	108 T A ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAAGGCCCTTCTACATACACTCCCATCTT CTCTATCTTAGTTCCAAAGTTTGTAGTTTCAATCCCAATATACCAATTCATTGTTATTCJTTTAAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450e	125 T C ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAAGGCCCTTCTACATACACTCCCATCTT CTCTATCTTAGTTCCAAAGTTTGTAGTTTCAATCCCAATATACCAATTCATTGTTATTCJTTTAAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450d	125 T C ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAAGGCCCTTCTACATACACTCCCATCTT CTCTATCTTAGTTCCAAAGTTTGTAGTTTCAATCCCAATATACCAATTCATTGTTATTCJTTTAAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450c	108 T A ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAAGGCCCTTCTACATACACTCCCATCTT CTCTATCTTAGTTCCAAAGTTTGTAGTTTCAATCCCAATATACCAATTCATTGTTATTTTAAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450b	61 C A ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAAGGCCCTTCTACATACACTCCCATCTT TCTTCTCTATCTTAGTTCCAAAGTTTGTAGTTTCAATCCCAATATACCAATTCATTGTTATTTTAAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450a	55 T C ---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAAGGCCCTTCTACATTCACACTCCCAT CTTCTCTATCTTAGTTCCAAAGTTTGTAGTTTCAATCCCAATATACCAATTCATTGTTATTTTAAAGA AAAAACCTTCCCAGTTATTGTCAGAAACTATGATTTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTAAATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8458b	60 A G ---			CAAGGAAAGCTGTCAGTCTTCATAAACTTTCAAAGAGTTTACAAAATACGATTTTTTAAJ/GJCTA CAATTCAGGATTAGCATCCAAACCTACAAACATGATGATACATTCGTCACACACCATACAACTTCAC ACCTGGCTACAGCAATGTTGACTTACATCACCATTGTTTATACCTTGTAAGAACTTTTATTGTGCACAGT GACATCCATTCCGCCAGACTTAATGTTATAAAGCAGCTGAGCAGAGTTCTCA

WI-8461c	105 A T ---	---	---	CTTCTCTCCAAAATCTACATGAATACITTTGAAGACAATAAATACTACAACCTTACAAATGCCAATTA GACAAAAGAGANTAAATGATATAATAATCATTTTTT[A/T]NNNNNNNNCCCTTGCTTATTACACAT TCAGGGAAGTCTAGCACCAGGACAGTNTTAAACAACATTAACAANTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461b	38 T C ---	---	---	CTTCTCTCCAAAATCTACATGAATACITTTGAAGACAATAAATACTACAACCTTACAAATGCCAA TTAGACAAAGAGANTAAATGATATAATAATCATTTTTTNNNNNNNNCCCTTGCTTATTACACAT TCAGGGAAGTCTAGCACCAGGACAGTNTTAAACAACATTAACAANTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461	38 T C ---	---	---	CTTCTCTCCAAAATCTACATGAATACITTTGAAGACAATAAATACTACAACCTTACAAATGCCAATTA GACAAAAGAGANTAAATGATATAATAATCATTTTTT[A/T]NNNNNNNNCCCTTGCTTATTACACAT TCAGGGAAGTCTAGCACCAGGACAGTNTTAAACAACATTAACAANTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461	105 A T ---	---	---	CTTCTCTCCAAAATCTACATGAATACITTTGAAGACAATAAATACTACAACCTTACAAATGCCAATTA GACAAAAGAGANTAAATGATATAATAATCATTTTTT[A/T]NNNNNNNNCCCTTGCTTATTACACAT TCAGGGAAGTCTAGCACCAGGACAGTNTTAAACAACATTAACAANTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAAAAANTCAAGGATTTGCAAAAAGGGGG
WI-9438	77 A G ---	---	---	AATAACATGTTATGAACAAGCTGTTACAAGTAGTAGGTAGATGACTTAATTTTGATAAAAAAAT TAAAAAGCAT[A/G]AACATGCATATAAAATAGATTATGTACAAAATACCAACAGTATTTACTTC TGCTCAGTAATTAATATCTCCCTTTGTTTGTCTTTTAAAAAACATTATTTCTGAAAAAATAA ATCAGAAAAACATGATCGTGGAGAGATTATTA
WI-9439b	101 C T ---	---	---	ACAGAAATGACCTTTATTTGTTGTACTAAAGCCTGTTTAACTTTTGATACAAAGTAACATTTTAGTA CAGAAATCCAGTCTGTGAGTCAAGTACCTGT[C/T]GTGCACACTGTACCATCTCAGTCCCACCTCT GCCTGTAACTTAGAAAACAGCCCTACCCAGAGGGTCTGCGAGTTAATACCTTGAGAAATAGTCTA CAGTTTTCATAGTTGTCTGAGCTAGAAAACCTGTACCTGTAAACAAAG
WI-9439a	76 C T ---	---	---	ACAGAAATGACCTTTATTTGTTGTACTAAAGCCTGTTTAACTTTTGATACAAAGTAACATTTTAGTA CAGAAAT[C/T]CCAGTCTGTGAGTCAAGTACCTGTCTGTGCACACTGTACCATCTCAGTCCCACCTCT GCCTGTAACTTAGAAAACAGCCCTACCCAGAGGGTCTGCGAGTTAATACCTTGAGAAATAGTCTA CAGTTTTCATAGTTGTCTGAGCTAGAAAACCTGTACCTGTAAACAAAG
WI-9446b	75 T C ---	---	---	GAGGCTTGATTAAAGGGAGGNTTTATTTGATGTNAACCTTACCATTCCATAGACTATAAAGANCATTA TAAAAAAAT[C/C]CTCTAAAGNGACACATGCCCCAAATGACCAANGNCATTAAGCAAAACCTTTTAAAT TACTCATCTTTCATATGTGTGTTTGTGTCCTTATATCACTGTGCTTCTGCTTTTGTCTACCTA TGNGAACTGCACACTATCTGTGGCAATATTGT

WI-9446	75	T C ---	---	GAAGGCTTGATTAAAGGAGGNTTATTGTGATGTNAACCTACCATCCATAGACTATAAAGANCATTA TAAAAAA[T/C]CTCTAAAGNGACACATGCCCAAATGACCANGNCATAGCAAAACCTTTTAAAT TACTCATCTTTTCATATGTGTGTTGTCNCCCCTACTNTTATCACTGTGCTCTTGTCTTTTGTCTACCTA TGNGAACTGCACACTATCTGTGGCAATATTGT
WI-9497b	185	A --- ---	---	ATTAATGTCAAGGTTTCATGTTTACATTTCTTATATCAAGTACAATGGTATATATACATTTTTTT GAGATAATTATCTAGATTCAGGCTTCTCTAGATGTAGTAAAGTAAAGCTTATAGTTTACATTTGA TATCTAGACATATATCTTAAACAGTCTCCAAATTNCTTTAATTAATCAAAAGTATGTTAATGTCACCTT GGAACTCTACATGGAAAAGCCCAACAAAATAACTAAAACTTGACTAATGAAG
WI-9497	185	A --- ---	---	ATTAATGTCAAGGTTTCATGTTTACATTTCTTATATCAAGTACAATGGTATATATACATTTTTTT GAGATAATTATCTAGATTCAGGCTTCTCTAGATGTAGTAAAGTAAAGCTTATAGTTTACATTTGA TATCTAGACATATATCTTAAACAGTCTCCAAATTNCTTTAATTAATCAAAAGTATGTTAATGTCACCTT GGAACTCTACATGGAAAAGCCCAACAAAATAACTAAAACTTGACTAATGAAG
WI-9523b	193	C A ---	---	GTGAAAAGTTTTCTATTCATTCCATCATACATAGATTGTGCTAAGGATCATTTTGGGAAGAATGTG CAGCATTCAGAAAGTTGTATCTCATCATGCAGTCACTCAGCAGCATTTTATCTAAAAAGTACGTGCACA GACTCAGACAATTACAAACTATTTCCAGCCATGATCTATGGTGATTTCCACACATTTGTA[C/A]AGTG AAAGCTCTTCAGCTTGGAAACAACCTTGTCAGGCGAGACTGCATGCACATATAT
WI-9523a	47	G A ---	---	GTGAAAAGTTTTCTATTCATTCCATCATACATAGATTGTGCTAAGTCAATCATTTTGGGAAGAAT GTGCAGCATTCAGAAAGTTGTATCTCATCATGCAGTCACTCAGCAGCATTTTATCTAAAGTACGTGCA CAGACTCAGACAATTACAAACTATTTCCAGCCATGATCTATGGTGATTTCCACACATTTGTACAGTGA AAGCTCTTCAGCTTGGAAACAACCTTGTCAGGCGAGACTGCATGCACATATAT
WI-9554	202	T C ---	---	AAAAACACAAGTTTCATACATCACAAAAAACCTTCCATTATAACACAGAAGTGATTATACCAGAC AAGCATCAGTGATGTATCTAGTCCCTTNTAGTTGTTATTGTACAATGCTGTAGATAATGCAGCCCATG CAATACACCCCAAGAACACTAGAGTCTCTACACCCCAAGTACAATATGATAAAGCAGCCCTCTGCAAGTG GT[C/G]CTGGATACCCTAAGAAAGTCTACTGCAGCCCATGTTGGTTATGATTTT
WI-9555	97	G A ---	---	CCAAAAGCCAAACCATTCATATGATGGATTTTCATAAACAATTTATGATCCTTTTGGGTAAGTAT AAATACCTTTACATGGCTAACCTTCTAAC[G/A]CTTGAAAAATCAATTTCAAGGGACTCTTTAATCA GTTAAATAATCTGCTTTAGAAGGCACAAATGATCATACTTCAGATTAAAAACAGGTAAGTATTCAG GGNTAAATGGTACAAAAAAGGCTGTAACCTTTTNTCTTCACATTGATCACA
WI-9625b	172	A T ---	---	TTGAACATTTAATGAATGACAAAGACATAACATCCTCTGAAAAATCTGCAAGTAAATCAATCATTTT TAAACAATAGCTACCATATATTTGTATCTNCTCTCTGGGAAAAAATTTGGAAAAAACAACACGCACA TAAGTATCATAACTGAGGGTTGTGGACAAGTTACTCT[AT/G]TTTACCAATTTTATATTGACATAA AGTAGCAGACACTAGTTATTTCAATTTAAAAAACAACACTGACAAATCTTTTC

WI-9625	172 A T ---	---	TTGAACATTTAATGAATGACAAAGACATAACATCCTCTGAAAAATCTGCAAGTAAATCAATCATTTT TAAACAATAGCTACCATATATTTGTATCTNCTCCTGGGAAAAACITTTGGAAAAAAAACACGCACA TAAGTATCATAACTGAGGGTTGTGGACAAGTTACTTCTATGTTTACCAATTTTATATTGACATAA AGTAGCACAGACTAGTTATTTCAATTTAAAAAACACACTGACAAATCTTTTC
WI-9647	144 C T ---	---	TTTTCTGAGATCAAGAGCTACATTTTGGTTAGTGATGTCTACTATACCTTTTTCATCCTTTTCA ACATCTTTTGTACATTTTAGTGATGCTCTGTAAACAGTGATTTGCTAGACCTAAAAATCCAAAGCT TACAACTGCTGTCCTTACCTGATACATTTATCCATTTACTTTTCAATTTGGATTTTAAAAATGTTA ACTTAATACGTCTCTTCAGATGTCCTGCTTTTGTAGTTAATGTGTTT
WI-9676n	114 A G ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCTCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAAATGCAGAGCA/GJGATGTGGCTTCTCTGCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTTGTTT
WI-9676m	184 G T ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCTCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTCTCTGCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTTGTTT
WI-9676l	84 A C ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCTCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTCTCTGCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTTGTTT
WI-9676k	202 C T ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCTCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTCTCTGCC C/TTCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTTGTTT
WI-9676j	92 C T ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCTCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTCTCTGCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTTGTTT
WI-9676i	173 T C ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCTCCATATGGCAAGATGAAGAAAAATGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAAATGCAGAGCAAGATGTGGCTTCTCTGCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTTGTTT

WI-9676h	134	C A	---			GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTCGCCCG C/AJTTCACCTCAAGGCATCTCAGCAACCCACATGGCTTCCCTCTGTGGCAGTGAATAACTTG AGGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676g	202	C T	---			GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTCGCCCG ATTTCACTCAAGGCATCTCAGCAACCCACATGGCTTCCCTCTGTGGCAGTGAATAACTTGAGG C/TJAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676f	184	G T	---			GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTCGCCCG ATTTCACTCAAGGCATCTCAGCAACCCACATGGCTTCCCTCTGTGGCAGTGAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676e	173	T C	---			GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTCGCCCG ATTTCACTCAAGGCATCTCAGCAACCCACATGGCTTCCCTCTGTGGCAGTGAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676d	134	C A	---			GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTCGCCCG C/AJTTCACCTCAAGGCATCTCAGCAACCCACATGGCTTCCCTCTGTGGCAGTGAATAACTTG AGGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676c	114	A G	---			GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTCGCCCG CCCATTTACCTCAAGGCATCTCAGCAACCCACATGGCTTCCCTCTGTGGCAGTGAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676b	92	C T	---			GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTCGCCCG CCCATTTACCTCAAGGCATCTCAGCAACCCACATGGCTTCCCTCTGTGGCAGTGAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT
WI-9676a	84	A C	---			GGCCACTGTCCAAAGTCTGCACAGTCTCCATATGGCAAAGATGAAGAAATGGCAATCTTTTA GGGGTACCAAGGNTCTGAGTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTCGCCCG CCCATTTACCTCAAGGCATCTCAGCAACCCACATGGCTTCCCTCTGTGGCAGTGAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAAATCCTATGCATTGTTGTTT

WI-9738b	40 C A ---	---	TGGACCAACACAGACAGATGATTCCTGGTGGCTGTGTA/C/AJATTACAACACTATTGATCACATGC AGCAACATCAACATCTCAAGGAGTCCATTGTTCAAACACAGTAATGACTCCACATTTCCCTTT GAGTCAACAAAAGACTCTGCTTGTCACCTTGCTGGAGCGGGTGTGTTTCACTATGTGAGTATCTA TCTTTTATTCTGTCCCTTATGTTGGTGGCACATGCTGTATTGCTGTC
WI-9738	40 C A ---	---	TGGACCAACACAGACAGATGATTCCTGGTGGCTGTGTA/C/AJATTACAACACTATTGATCACATGC AGCAACATCAACATCTCAAGGAGTCCATTGTTCAAACACAGTAATGACTCCACATTTCCCTTT GAGTCAACAAAAGACTCTGCTTGTCACCTTGCTGGAGCGGGTGTGTTTCACTATGTGAGTATCTA TCTTTTATTCTGTCCCTTATGTTGGTGGCACATGCTGTATTGCTGTC
WI-9756	47 A ---	---	ACTGAAATGTAAATGGCCAAAGCCAGGCCCTTAAAAATCATAAGAGTTAATCTGTGGGAAAA GAGTAACTACAAAAGCATCTAAACAAGAGCAGGATGTGATGTAATGTGTCCTTATCACTTTAGTC AGTAAAGATAAGAAAGCCCTGGTGAGTATCCACTCCACAAACACAGAAATATACACTTTTGGAAAG ATTCCACTTAACCACTTGATTCCTCACTTTTATGATTTAAACCTCCGTGG
WI-9758	135 A G ---	---	GATGGTCCCTTAAGGATTTGCATTGGTTAATGGGCAGACTGGTGCAAAAGAGGCTGAATTGAATAAT TAGGAACTGGGAGAAATCAATTCAAAGAAATCTTGTCGCAAGGTCAATTTTATACTATTTA A/A/GTAAATAACTCTGGTAGGTTCTATAGCAAAATGCTAAGTAAAGTAACCGCTGTTTCTAAAT ATTACG
WI-9778	127 G A ---	---	ATTTAAATCCAGGCAGCGGGGAAATGGATACCTTCATATGTCTGTACCCAACTATAAATTTTG GTTCTCATGCACCATTTTCAATTTGCTTCTCACTCCAAAGTACCAGTATTTACCAATT[G/A]CTCTC ATAATTGACTTTGCTACTGGAAAGAACTCTTAGAATGTTGGAATTTCTCTATTACACACTTTGCCTCA AAGAAATGTCAGTCAGGACTAAAGGCAATAGTCTCAGGGCAGACAGCC
WI-9832	116 C A ---	---	TCTCCCTTTGCCTCCTCATGCCCACTCCCTCAGCCTGCACAGAGCGTTTCTCCAGTGTAGTCTCTGGT CCATCTGCATCAAAATCACCTGCAGGACTTGCTGACAATGCAGTTT[C/A]TGGATCCCAAGGAGG CTCAAAAAAAGTGGAAATGGGAGAGAGGAGGACCTGGAATCGGTGTTGCTAGCAAGCCCAAGGTGG TTTGTAAAGTGGACTAAAGTTTGAGGACCAGACATGGAAGGTTGGCTTTGGC
WI-9841	101 A G ---	---	TGGAAAAATAGCTTTTATCAATCTCTGATATGCTACATATGCTATGGAGAAATGCAGAAATGGCATGA TATGAAATTCATTTTGAATGAATAAATATACI/A/GTGTGTATGATATATATATATTAACACTT AGGATTATACACACAATAAAAGTCTGTAGGATAAATAAGGTTCTATCAGTGGGAAATGAGA TTGAAAGAGGGGATGTTACTTTGATATGCTGTTG
WI-9880c	222 G A ---	---	GAACCTAACACCTTTCTGCATGGATTTTCTTGATTTGGCAGTTAACAAATAAAATGTTATTAGATC ACTGGTCTTCTGTGGGTTGAGTTTTTATGATATCTCTGTAGACCCATAAGGGAGGCTGTGA GTTGTTTTCTACATCCTTGGACTATATAAGATCCCTTTTAAAAATTATTTTATATAAGCACATGAA AATGGAATGAAATAATGA/G/ATTGACATAGGAATTACCTACATATTTTG

WI-9880b	157	C A ---	---	GAACAAACACCTTTCTTGCATGGATTTTCTTGATTATTGGCAGTTAACAAATAAAATGTTATTAGATC ACTGGTGTCTCTGTGGGGTGGATTTTATGATATCTCTGTAGACCCATAAGGGAGGCTGTGA GTTGTTTCTACATCCTTGA[C/A]TATATAAGATCCTCTTTTAAATTTATATTTATATAAGCACAT GAAATGGAATGAAATAATGAGTTGACATAGGAATTACCTACATATTTTG
WI-9880a	108	C T ---	---	GAACAAACACCTTTCTTGCATGGATTTTCTTGATTATTGGCAGTTAACAAATAAAATGTTATTAGATC ACTGGTGTCTCTGTGGGGTGGATTTTATGATATCTCTGTAGACCCATAAGGGAGGCTG TGAGTTGTTTCTACATCCTTGGACTATATAAGATCCTCTTTTAAATTTATATTTATATAAGCACAT GAAATGGAATGAAATAATGAGTTGACATAGGAATTACCTACATATTTTG
WI-10183	127	C T ---	---	ACACTGCAGGCACTCCAAATCCTNACAGACATATGCACCTCGGAATCAACTCAGGCATGCACAGCAT CCCTGTGCTGGAGTTATTTTAAAAACAACGCCCCAGTTATCACAGTTCTNTTTTGT[C/T]CACC ATTTCCATAACAAAGAAGCTACACAAAATTNGGGGGGAGANACTCTCTTTGGAGACTGACACATT TGCAGAGGGGTCATGAATAATGATTCCAAA
FB25G10b	109	A G ---	---	TCCCTCAATGACAGATGAACATAAATTTCTCTTGGTAAGAAATACITTTATGTCCATTGTGATTAAA AAGTCAGATTCAAGACACTGCTTTATGTACAAGAAATGGAA[A/G]TGATTTTAGATCCTCCCCCAG TGACAAAGTAAACTGAACCTGACCATAATTTATACATAAAATGGAATGTAAGAACCCTATTTGGATATCC CGGAC
FB25G10	109	A G ---	---	TCCCTCAATGACAGATGAACATAAATTTCTCTTGGTAAGAAATACITTTATGTCCATTGTGATTAAA AAGTCAGATTCAAGACACTGCTTTATGTACAAGAAATGGAA[A/G]TGATTTTAGATCCTCCCCCAG TGACAAAGTAAACTGAACCTGACCATAATTTATACATAAAATGGAATGTAAGAACCCTATTTGGATATCC CGGAC
IB3071	102	C A ---	---	ACAACGCTGAACCTCCATAACAGTCAATGGTACAGTCAACATCACATGTACAGAACACACAATTTA GATGAACCTGAAATTAAGNTAAATAAAATAAAAT[C/A]CAATTTTCAGNAAACAAAAATCAAAAC ATTAAGGNTCCCTGNNATATTTCTAAACCCTAATGAGATTTCACTGGNCTCAAGTCATTTTGTAGTGA GGCATTCAACAATATGACCCCTATTACCCAGTCTAGGGATTCTG
NIB551	161	C T ---	---	CGTCTTTCTTTTGGATTGCAATTAAGTAGATAATATGAGAGAGAACTGACAATTTGGGTGTCCC TACTGAGCTTGGGGCCAGGTGTGACTTAGAACCCCAATCCACCCAGAGAGACTCATCTATGTTA ACACTAAGGATGCCCTGGAGGAGGT[C/T]TGACCACATACATGCGGCCATTGGTTGATTTTCAGCTTT GCAAGCAGCGTAGTGAGAAACCAAAAGCTTGTC
S72904	51	G T ---	---	AGCATAGAAAGTGATTATATTTTAAATGGTTTCAAGTGAAGTCTCTT[G/T]AATTTGTCAGTTC ATTCTTGAAATCTTTTGTAGTTAAATAAGGATCTAGGACAGCACCTCGAACTACAGGCCCTAAA GAGAAATTTGCTCAAAACCAAGTGCTGTAACCTCTCCCTTTCTGTCAATTTGGTTGCTCTTAAATA TTGCAAAAGTCTGATGCTAAACAGATTTTGGAGTGTTCAGTGTCTGTA

UTR-00481	115	CT	---	---	TATCTTTTATCTGGGCCACAGTCTTGATTATCCTCTGTGGTTAAAGACTGAATTTGTAAACC CATTCAGATAAATGGCAGTACTTTAGGACACACACACACAGAGCTACACCTTTTGATATGTA AGCTTGACCTAAAGTCAAAGGGACCTGTGTAGCATTTAGATTGAGC
ESTC1	33	---	---	---	CCCTGTAGCAGTCTTACGCCTCTACCTACNAGATCTGGAGCAACAGCTAGGAAA
ESTC102	37	---	---	---	GCTACTACCACGGCTGCTTCGTTGGACAAAAATAACNAGGAGGCATCCACGGGATTAGTTA
ESTC103	21	---	---	---	GCCATCAAAATTTCTTCACANTCAATACTGTTGAACAACAAGATAACACATCTCTTGCTCATCCC ACTTGAA
ESTC107	20	---	---	---	TGCTGGCTCACTTCCTCACANGCTGTATTACCTTTACAGAGCTGAGTGAGGCTGTGCT
ESTC109	35	---	---	---	AAACCAGGAAGGCCCTGCCCGCAGAGGCACATGNACAGGGCAGTGCACAGTGAOC
ESTC110	23	---	---	---	AAACCTCACACAGAAAAAGAGGANAACACTCAGAAATGTGATTACAGATTAGGCA
ESTC113	37	---	---	---	AAGGCACACAGTGTGCTGACAAGGTGACACTGAACANACAGTTTCTTTAATTGTAAGCGGG CATCG
ESTC117	24	---	---	---	AATTGGCTCTCTCCACATGATACNTAAGTTCAAGGTCCTATCACAAATTTACAAAAAGC CTCCA
ESTC119	24	---	---	---	TGTCAAGCAGATCTTGAGGGTTATNGTTAAGCCTGATAACAGCCTCTTT
ESTC122	34	---	---	---	GACAATAAACAGCTAAGCTACTGACATAAAATATNCAATAAATTTATGAGATATAAGGTACAGATG AGAAAAATCTGAAA
ESTC123	21	---	---	---	GAAGCCAGTATGTTGTGGCAANATTCGAGAAAAACACACTGAAAAA
ESTC128	42	---	---	---	GCAGAGGCATCAGATAAGGCCTCAGAAAGCCAGGCCATCATNTCCATGGGACCAGGCTGGCTCAA TGTGGAAGTGG
ESTC129	20	---	---	---	AGTCACCATGCCAGCCTAGNATGAGTTAGTAAGATTGGTTATGCTGGGGAG
ESTC13	46	---	---	---	GTGTATCTGGGCTTCATGGGATGCATAAAATTTCCAGTTGGTAAGNAGCAGGTGCCGAGGGTCTGGA TCAGAAA
ESTC130	49	---	---	---	GCCTGCTCACAAGGTAGACAAAAACATAAATCTTCAGGAAATGAAACANGAGAAGCTGAAACAAT CTACACCTGAATG



ESTC132	30	---	---	---	GGTAAAGTCTAAATTACTGCCCTTAGCAAACNCTATGTTGTCAAGGTTTTCTGCTGCA
ESTC137	21	---	---	---	CCAGTTTGGCTTCTGTCTCANAGTCTCTCTCCATGTGGCAAACA
ESTC139	45	---	---	---	AGGAGCACAGCCTAAGGACATGAAGTCAAGGTTCTCAGAGAGNGGGCTGGTCCCTGAGCTAG GAGGAGG
ESTC14	20	---	---	---	CCCATTTGGTTCACAGGAAGNAGAGGAGGCCACGTTCTTACTAGTTCCCTTGCATGGTTAGAAAGC TTGCCCTGGTG
ESTC142	72	---	---	---	CCTAGGCTCATAACAATACAGTCTCAATACAAAAGACGTAATACTATTTTATTCATTTTAAATC AAAGANACCATTCCTTAACAACA
ESTC143	29	---	---	---	GTTTACGAAAGTACTGAAAATGCTATTANTAGCTGAATTTGTGATTTCTCTTTTG
ESTC144	26	---	---	---	AAATCCATATTTTCTTGACATGAGGTGCTTTTATAGCAGCATTTCCGG
ESTC146	20	---	---	---	CATGTCAGGATAAGGAGCANACACCAGGATTTATACACGGTGGCAGCG
ESTC148	42	---	---	---	TCCTTGGTGTCTACACAGACACTTAAGTACTGTATCGCTGTNATGCAGCGGCTGTGGAGGCCCTG GGGGTGGCTGGGCTGTGCTGAG
ESTC149	28	---	---	---	TCAGTTCAATTTGCTTTAAGAGTTANATACCATGAGACACACAGTTCTGG
ESTC15	28	---	---	---	GGATTGTAATATTGCCAGCTTTGTAAAGNCATTAAAGCAGAAGTTTCTTCAGTGATCTT
ESTC150	20	---	---	---	CCAGGAAAACAAAGCACACANACTTATAGAATACTTTGGTTTAAAAATTATTCATAATCAATATT AAACCTGATGTTTAAAGAACCTAATGAGA
ESTC151	49	---	---	---	GAAGCTAAGGCCCAATTTTTTCTTTTAAATACAAATCTACTGGTGTCTNAAAACCTCAGAGCTTAGGA AACACAGCC
ESTC155	37	---	---	---	TTTTTAATTGACAACTCAATCTCTACATACAGTNTTGCACGAATTATAAGTGGATCAACAATT ATATTATTGATACAACTCATGAGCAATTACA
ESTC156	32	---	---	---	GCAGCATTTGTGACAGGAGCGCAAAACAAANCCCTGGCTGCCGCGGATGGAGCGGGGGGCGCTCA CCACCACCTGCAT
ESTC158	35	---	---	---	ACCAAGCCCTGGGATTTACTGTCTTGATGACTACANGGCTTTGCACAGTCTGAGATGCTTCAGTGTGC AA
ESTC159	31	---	---	---	AGCTGGCAAGAGACTTCTCTGAGGCACATCAGNTACGTTGGTCAATTTAGGGCACGGTCTGGTTCTGCA GCTTGAAGG

ESTC16	23	---	---	---	---	CACTGAATGCTCTGCCATGAGCCNAGCAGCACAGTGATCATCAACCCACAAGGACAGGTT
ESTC160	38	---	---	---	---	TTCTAGCATTGGTGCAGTGGGGCCTGAGCTGGGNGCAGTCGGCAGTGCTCACTGGGCCCCGTTTG GGACTGGGTTGA
ESTC162	36	---	---	---	---	CTCTTCGTCGGTTTGCAGTTGCTGTTTGTTCAGNTACACAGTCAGAGCTCCACAG
ESTC164	31	---	---	---	---	TCATTCTCCATAGAATATTGGTTTTGTAAACANCGAATACAATCCAAATATATAACATTAAACAATCC GATACATACCA
ESTC169	22	---	---	---	---	GTCTCTGGTGTGCAGGGAATCANTTTGCTGGATTAGAGGAAAGGTGCCCGCTGTTTCCATGACTT
ESTC176	23	---	---	---	---	CACCTCCTCCCTGAGCTACCCANGTAGTGTCTGGGAGCTGGCA
ESTC177	42	---	---	---	---	TGGGTGGCTCTTTAAATACCTTCCATTATATTTCAAAATTTTNCITTTATCTATTAAATACCTTTTAT TCTCTTTATTCCCATAAAAAGGCAACCAA
ESTC18	29	---	---	---	---	TCAGACACTGCCGACATCAGCATTGTCTCNTGTACAGCTCCCTGCCAGGGGCGCCCTGGGAGAC AACTGGACAAGA
ESTC181	21	---	---	---	---	TAGGGATTCCAAAGTTGCCTGGNTTAAATATAATACATAITTCACAAAAATTTACACAGCTCATGCATAC CA
ESTC186	43	---	---	---	---	GCTTGACTAGGGGCTACATCACAAATTTATAAGTGCCAGATNAGTGCTAATTTGTCATTCAGCTTG ATTTTTCACCTCA
ESTC187	24	---	---	---	---	ACCATGATTGCTCACAACAAGCATNATCAATCGCCACGAGAGACTGGATGCCAAAGAGTATGGCTGG TCTATTAAACAGGGTTATGTCACACCNCTGTCAACCTCAAAACAGATGATCACTCATCTTGTCTTCCAT CTTGC
ESTC189	27	---	---	---	---	AAAGTACAATCCAGTATATGCAGAAAGNTACTCAGCATCACACTCGTGATCA
ESTC196	42	---	---	---	---	TCCTCAAATACCACTTTCCCTTAACCTTATCAGTCTAGTAGCNTTTCAAAGGAGGAAAATGGGTTAC CTTTCAGGGG
ESTC197	26	---	---	---	---	ATCTCCAGTGTCTGCTGCCTCCTCCNCGCAAAGTCTCCACAAGCACA
ESTC20	33	---	---	---	---	AAGATTAGGACAGACCGGTATAGTAAGCTCTGNGGAACTCCAAAGATCTAGAGGGGGCTGTGGGAA CGCTGCTTAGATC
ESTC200	44	---	---	---	---	TTTGGTGAAATCCCAATATATGAGTTTTAAAAAATAATCATTANCATCATTAAACAGTACTTTAAAT CAATTACTCCTTTTGCCTGCAACAG

ESTC201	35	---	---	---	---	TCCTACTTGGGTAGTTAGCAACATTTTAAANCCACATCCACAGATTGGTT
ESTC202	22	---	---	---	---	CTGCTGGAGGGAGACAGCGNCGCGCTGGGTGGCGCCAGAAAGGCTGGCGTGATGTT
ESTC203	27	---	---	---	---	CGAGATGAGCC
ESTC208	43	---	---	---	---	ACACTTAACAGGTTAAATATCCAAATNAATTTACTGCAACTTTTGTAGAAATTTTATTGTGCTAC
ESTC210	29	---	---	---	---	AAGACACGTTGCA
ESTC212	27	---	---	---	---	TATAGCCCCATCGCTCTCAGTTATTAGAACTCTGAGAGGGATAANAGCAATACTATTGTTTAAAGC
ESTC214	21	---	---	---	---	CTAAGAGTGAAAA
ESTC216	49	---	---	---	---	GATGAAGTGGCTTCCTTTGGCGAAAGGATNAAGAGTGAGTGACGGTGACCTGTG
ESTC217	28	---	---	---	---	GGGTAACCTGATGAGGAAGCTCTAGTGNAGAAATTCAGGACGCGTCTCAGAGCAGAGGGCTTGGT
ESTC219	32	---	---	---	---	TCAAGTC
ESTC22	41	---	---	---	---	CTCCAGAGTCCCTCCTCANACCAGGGGCGAGGGAGTTAGGGAAT
ESTC223	27	---	---	---	---	TGGCAAGAAATTTATTACACTAACAAATTAATTAATCAGAGGTATNTTAGATTGGTCAGAAAA
ESTC224	37	---	---	---	---	CAAAAGACCA
ESTC225	20	---	---	---	---	TTTTGTCAATGAGCAATACACTGANTGGAATCTGCATGATTAATAACATTAAACAAGTTCAT
ESTC23	27	---	---	---	---	AAACACACCCCA
ESTC230	43	---	---	---	---	GTACACATCTGGGGTGAGCACACAGCAAAANGGGTGGGACGTGCAGAGAGGTATAGGGTAAAG
ESTC231	24	---	---	---	---	GCAAAGGAAGC
						TCATTGAAGAAAAATTATGGGTTTTATTCTTATTCTAATTGNGAGAATGCTTAATGTACAGGCTACA
						TAAGGGCC
						CTTCTGAAGCCCAAGAGAGGGGCGAGAANGTAGTCTTGATTTAAAAAACAGAAAGGGGAGGAGGA
						CGAAGTAGATTCCCTCACATATTACAAAATACACANAACACACACACACACACACACA
						TGCACGTGTTACTCCCCAGACNGAGAGCTTACATACCATATAGAAAGAGCATAAGTGCTTCAGAAAGGA
						ATGTGTAGGATCG
						TTCTACTTTATTTCATATTTCCACCACNATAACGACTCCTTTAATTTAACTAAAAACCATACAGGGT
						TCCTGAAAGGG
						GCTTCTCCACGAATTTGAAAGACATATTGGCTGACCTGATACNTAAGGAGCAGGCCAGAAATTAAGA
						CAAAAGGGTTAGTCATATTCCCCANCAACAGCATGATAAAATAATTCAAC

ESTC28	23	---	---	---	---	GAAGAGCTGGGCACGCATCTGACNITTTCTTCTCTATTCTCTATAAAAAATAAAGGAAGCAGAAATCT GC
ESTC3	20	---	---	---	---	CAGACATGACCTACCGTCCCGCCCTCAATTCATATTTTATCTTGAGCCGCTTGGTCAGGTTTGAT TCGCACACTCC
ESTC31	32	---	---	---	---	ACAGCCCCACAGAACTATTGTAAACAATAATNTCAGTCGGTGATCATTTGTAATATACAATACAAAG CAATTCCTCAGA
ESTC33	25	---	---	---	---	AGCACTTCCAGCTCCTTGACGTTGTNGGACCCAGGAACTTCCGGAA
ESTC39	26	---	---	---	---	AAGGAAAGGGAACCCACCTGGGCTTTNGGTACAGAACTCAGAGCCTGGGCATTA
ESTC4	23	---	---	---	---	CCACTGAATCACACAACATGGACNAATCTCAAATCATTATGCTGATGGAAAGAAACCAATT
ESTC40	22	---	---	---	---	GGCATGCTAGACAGAGGCATTANTTTTGAAGATCTTTTAAAAATATTTTGACTTGTTCCTCCCTTCAC
ESTC45	37	---	---	---	---	TTTGGAGGTTTGTGCTGGAGTTTGTCTTTGTAAACNCTCTCATCTCAGGCTATATATTA CTGTCGCTGGTGAGCCCTGCCGCTGTCCCATGGGCCAGGGAGCCACTGGTGGGANCCGGGCAGATG TTTACCCCTGT
ESTC50	56	---	---	---	---	GTGCCCTGAAGATTAGCAGCAGCAGCAGCAGGTTGGCAGGAAGNAGTGGAGGGAAGGACACCA AGT
ESTC57	20	---	---	---	---	AAGTGGCCCTCCCAGTCCCTCTCTGGGCACAGATCCCACAGTCGTCTC
ESTC59	38	---	---	---	---	GAAACACAAAAAGTGTGAGAAAAAACTTCTCAAAATTTNGTCCAGACTTCAGGAAAAATGATTTCC ACATGGTAAGGCC
ESTC6	27	---	---	---	---	TCTGCAGCACTTCACTACCAAAATGAGCNITTAGCTACTTTTCAGAAATTGAAGGAGAAAAATGCATTATG TGGACTGAACCG
ESTC61	57	---	---	---	---	AGTGATTTTGGTAGCGGTGTTCTCATCTGTGAAATTCACAGCGCAATGACAGCANCCTCTCTCCC ACCCACTCAAG
ESTC63	20	---	---	---	---	ACAGACACAGCATCACACCANAGGCCACCGGAGGTGCGGGAGACGACACTTTTCCCTGGGAAA GGCAGCTCTAATC
ESTC69	20	---	---	---	---	GAGAGGCTAGTCAGGAGGGANACCCCTCAAGTTTAAATCCACACTTACTTACTGCTCATCCGT CACTTTCGCTAA
ESTC7	45	---	---	---	---	AGTTTCCCTAGAGCTGTGGGCCAGATAGCTGTTCTCTGAGTTGCANGCACGATGGAGATTTGGACACT G

[illegible]



EST10398 2a	147 C T ---			TGCCTGGGTGGCAAGGCTGCAACAAGGAGGCAACCCAGGAGGCTTTTATGAAGCGGCGCATGGTA AGATGCTGCCACCTCTTATCTACTTGATGATGTTACATTTGGGCTTGACTTTCCAACACGGAGAAG CAITGTTTCTTCTGTTGGCCAAGAGGTATCTACCAATAGTCTATTAGGCATTTG
ESTD-C7	14 G C ---			ATATCGTGGCCTTA[G/C]TTACCTAGAGCTGGACAATCCTGCTGGA
ESTD- D4S95	90 T C ---			CTTTCATGCACGATAGGCTTTCTCTACTAATCACAGAAATTTGAGAAGAGCAAAACAACCTTTCAAGG ATAATGGGGCAATCACTTCTTTT[C/T]CTTTAGAGTCTACCGG
ESTD- GPPK2L	38 G A ---			AGTCTCATCTGCGGTGTCAGGTAGATCCCTTTTACCC[G/A]CCGAGAACTGCTCGATATC
ESTD- HRASb	82 A G ---			CTGGGCTGCCCGCAGCAGCTGCTGGCACCTGGACGGCGCGCCAGGCTCACTCTATAGTGGGTGCG TATTCGTCCACAAA[A/G]TGCATCTGGATCAGCT
ESTD- HRASa	37 C T ---			CTGGGCTGCCCGCAGCAGCTGCTGGCACCTGGACGG[C/T]GGCGCCAGGCTCACCTCTATAGTGGGG TCGTATTCGTCCACAAAATGCATCTGGATCAGCT
ESTD- NRAMP	81 A G ---			GGAGCAGGAGGTGGGAGGGGTCTGTCTGCTCCAGGTCCACAGACCCAGAGAGCGGCTCAGTG TATCCCCACCCCCA[A/G]TGGGGCTGGGAGATGAAGAGGAGTTGATGCAGGT
ESTD-OTC	18 A G ---			GTGACCTTCTCACTTTAA[A/G]AACTTTACCGGAGAGAAATTAATATATGCTATGGCTATCAGC AGATCTGAATTTAGGATAAACAGAAAGGAGGATGTAAACA
EST36751 7	36 C T ---			CCAACTGTTTCAATTTTAGCTTTGCAGGTTTAACT[C/T]GATTACTTTTCTATTCAAATCTCTGTA AAATTGAATATGAACCTTAGTTTCTGATCTATGGTTTCAAGTTAAACAG
EST40562	109 A G ---			CACGTGGAAGGAGCTATTTTGGAGGCTTAAAGAGTAAAGAACTGTGCCCCAAACTTGTGGCTGAC TTTATGGCTAAGAAATTTCACTGGATGCATTAAACAAAT[A/G]TTTACCTTTTGAAAAAATAA ATGAAGGATTGACCTGCTTGGCTCTGGAAGAGATCCGTACCGTCTGACGTTTTGAAACAATACA GATGCTTCCCTTGTACAGTTTTACGCTCTCTACCTA
EST18288 3	121 C T ---			GCTCTATACCCCTGTGGTCTCCACGCTCTCTGGACTTTCACAGAACTGGATGTTGCTGCTGAGAA GATTGACAGGTTTCATGACGGCTGTGACAGGATGGAAGACTGGCTGCTCCCTGA[C/T]GGGAGCCAGT GTGGACAGCACCCCTGGCTTTCAACACCTACGTCCACTTCCAAGGTAAGGCAAACTCTCTGCTGGCTC TGGCCCTAGGACTTAGTATCC
ESTD-AK- 168	31 C T ---			GGGAGTGACAGCTAGAGCACCAAGGGGGGCT[C/T]TACAGCTGTGTTCTCATGGAGGACAGGCTTCT GCTCATCTGG
ESTD-ALB	180 A G ---			AATCCCAGCACCTTTAGGAGCTGAGGCAGGCATATCACAGAGGTGAGGATTTGAGACCAGTCTGA CCAAACATGGTGAACCCCATCTCTACTATAAAATACAAATTAGCCAGGCATGGTGGTGCATGCCTGT AATCCCAGGAGGCTGAGGCAGGAGAAATCGCTTGAACCTGGGAGCGG[A/G]AGGTTGTGGTGAGCCGA GATGGCACCAATTGCACTCCAGCTGGGCAACAAGAGTAAAACTCTGTCTTC

EST70523 3	182 G T ---	---	TTCCGCCAGCCCCCATCTTGGACCCCTGGTCCCTCAGGGGCCACCCCGGGGCACTCACCGCTCT CGCTCTGGTAACATCCGGCCGGGCGCCGCTCTTGAACACATAGCTGGACCGTTTCCGTATAGGAGG ACCGTGTAGGCCCTTCTGTCCGGGCCCTTGCAGGGGCCAGCCCT[G/T]CAGAGAGGGGTCCCTGT GGTTGAGCTGAACACACAGCTGTGGAGTGTCTCCACGTG
ESTD- APOA2	101 C T ---	---	CCAGGTGTTGTGGCACGTGCCTGTAATCCACGTACTCGGGGAGACTGAGGCATGAGAATCTTTTGAAC CGGGGAGGGCGGAGGTTGCAGTGAGCTGACATCG[C/T]GCCACTGCCTCCAGCCTAGGTGACAGAGC AAGACTCC
EST58707 7	112 C T ---	---	CAGTGTATCTGAAAGCCTACAGGACACCAAAATACCTTAATCATCAATTGTTACAGGAGGCTTT AAGTTACGACATCTTTGGCTACATGAAGGCCAAATTCGAGAGAC[C/T]CTAGAAGATACACGAGAC CGAATGTATCAAATGGACATTGACGAGGAACCTTCAACGATACCTGTCTGGTAGGCCAGGTTTATA GCACACTTGTCACTACATTCTGATTGGTGGACTCTTGTGCTAAGAACCTT
EST74167 6	137 C -- ---	---	AGACCATGAAGGAGTTGAAGGCCTACAAATCGGAACCTGGAGGAACAACCTGACCCCGGTGGCGGAGG AGACGGGGCACGGCTGTCCAAGGAGCTGCAGGGCGGCGAGCCCGGCTGGGGGCGGACATGGAGGA CGTGGGGCGCGCTGGTGCAGTACCGGGCGAGGTGCAGGCCATGCTCGGCCAGAGCACCGGAGGAGC TGCGGGTGGCCCTCGCTCCACCTCGCAAGCTGCGTAAGCGGCTCTC
EST43211 8	132 C -- ---	---	CGCTGGTGCAGTACCGGGCGAGGTGCAGGCCATGCTCGGCCAGACACCGAGGAGCTGGGGTGCG CCTCGCTCCACCTGGCAAGCTGCGTAAGCGGCTCTCCGCGATCCGATGACCTGCAGAGCGCC TGGCAGTGTACAGGCCGGGCCCGGAGGGCGCGAGCGGCTCAGCGCCATCCCGGAGCGGCTG GGGCCCTGGTGAACAGGGCGCGTCCGGGGCGCCACTGTGGGCTC
ESTD- ARSB	126 A -- ---	---	GGAAGAAATGGAGCCTGTGGGAAGGAGCGCTCGAGGGTGGCTTTGTGGCAAGCCCTTGCTGA AGCAGAAAGGGGTGAAGAACCGGGAGCTCATCCACATCTCTGACTGGCTGCCAACACTCATGAAGCT GGCCAGGGGACACACCAATGGCACAAAGCCTCTGGATGGCTTCGAGGTGTGGAAACCACATCAGTGAA GGAAGCCCATCCCCCAGAATTGAGCTGCTGCATAATATTGACCCAAAC
EST36770 4	144 C -- ---	---	TGTAGCCAAAGTCACCTGCATCATCTTTGGCTGCTGGCAGGCTTGGCCAGTTTGGCAGCTATAATCC ATCGAAATGTATTTTCATTGAGAACACCAATATTACAGTTGTGCTTTCCATTATGATCCCAAAAT TCAACCCCTCCGATAGGGCTGGGCTGACCAAAATATACTGGGTTCCCTTTCTCTGATCAT TCTTACAAGTTACTCTTATTGGAAAGGCCCTAAAGAAGGCTTATG
EST26021 1	137 A -- ---	---	TAATGTAAAGCTCATCCCAAGAAGCCTGCACCATTGTTTGAGGTTGAGTGACATGTTCCGAAACCTGT CCATAAAGTAATTTTGTAAAGAAGGAGCAAGAGAACATTCTCTGCAGCACCTTCACTACCAATGA GCATTAGCTACTTTTCAGAAATTGAAGGAGAAATGCATTATGTGGACTGAACCGACTTTTCTAAAGC TCTGAACAAAAGCTTTTCTTCTTTTTCCTTTTGAACAAGACAAAGCAAGGCC
ESTD- BA511	29 A G ---	---	GGGCAACATAGTGAACCCCATCTCTACA/GJAAAAATACAAAAATTAGCCAGGTGTGGTAGCAAG TGCCTGTAGTCCAGCTACTTGGGAGGCTGAAGTGGGAGGATCCCTTAAGCCTGGGAGGTGGAGGCTG CAGTGAGCCAAAGATGGTGCCACTGCA



ESTD- BCL2	116 A G ---	---	AGCTGGATTATAACTCCTCTCTCTGGGGCGCGTGGGGTGGGAGCTGGGGCGAGAGTGCGCGTT GGCCCCGGTTGCTTTCTCTGGGAAGGATGGCGCACGCTGGGAGAAC/A/GJGGGTACGACAACCGGG AGATAGTGATGAAGTACATCCATTATAAGCTGTGCGAGAGGGGCTACGAGTGGGATGCGGGAGATGT GGGCGCGCGCGCCCGGGCGCGCCCGCCGACCGGCGATCTTCTCTCTCCCA
ESTD-BCR	69 C T ---	---	CAGTGGCTGAGTGGACGATGACATTCAGAAACCCATAGAGCCCCGGAGACTCATCTCGCGCAAGA GA/C/TCAAAGAGGTGAGCTTCTGTTGCCGGGAAAGGGAGCGAGTGACAAAGCTAACTCTGCTTC AAATCAACCATCCGGTGGACACTGTGTGGCTGCCATCTGCGCTGGCACA
ESTD- BRCA1aa	119 C T ---	---	AAGAAGAGAAACTAGAAACAGTTAAAGTGTCTAATAATGCTGAAGACCCCAAGATCTCATGTTAA GTGGAGAAAGGGTTTTCGAAACTGAAAGATCTGTAGAGAGTAGCAGTATTTCA/C/TJTGGTACCTGG TACTGATTATGGCACTCAGGAAAGTATCTGTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAAACA GAACCAATAAAT
ESTD- BRCA1bb	139 A G ---	---	ACTAAATGTAAGAAATCTGCTAGAGGAAACTTTGAGGAACATTCATGTACCTGAAAAGAGAA ATGGAAATGAGAACATTCCAAGTACAGTGAGCACAATTAGCCGTAATAACATTAGAGAAAAATGTT TTTAAAG/A/GJAGCCAGCTCAAGCAATATTATGAAGTAGGTTCCAGTACTAATGAAGTGGGTCCA GTATTAAIGAAA
ESTD- BRCA1cc	126 A G ---	---	ATGCATCTCAGGTTTCTGAGACACCTGATGACCTGTTAGATGATGGTGAATAAAGGAAGATAC TAGTTTTCGTGAAATGACATTAGGAAAGTTCTGCTGTTTTAGCAAAAGCGTCCAGAA/GJAGGA GAGCTTAGCAGGAGTCTAGCCCTTCCACCATACACATTTGGCTCAGGGTTACCGAAGAGGGGCCA AGAAATTAGAGTCTCAGAAAGAGAACTTATCTAGTGAGGATGAAGAGCTTCCC
EST51212 0	122 A C ---	---	ATCCTGAGCTCGCCATAAGCTTCTTGTTCTACTTCTCTCTCCACAAGCCCCAATTCACTTTCTCA GAGGAAATCCCAAGCTTAGGAGCCCTGGAGCCCTTGTGCTCCCACTCAATACA/A/CJAAAGGCCCT CTCTACATCT
ESTD-C1R	40 A G ---	---	ACACAGGTGCTGGCACTGGGGCTGGGGATCCTCCTCCCTJAG/JATTTGCTCCGGGAAGCACATTCTAT CAA
ESTD-C1R	40 A G ---	---	ACACAGGTGCTGGCACTGGGGCTGGGGATCCTCCTCCCTJAG/JATTTGCTCCGGGAAGCACATTCTAT CAA
ESTD-C6	31 A C ---	---	CCAGTCAGTTTGGGGACAGCCATGCACTG/A/CJGCCTCTGTGTAGCCTTCAACCATGCATTCCATC TAAGCTCTGCAAAAT
EST20118 2	119 C ---	---	GTCCGAATCCTCCTCTGAAAGTGGCCGGGTTTAACTGCTCATGACGCTGCGGCTGTGGTCCAGCT GAGGTGAGGGGCTTGAAGCTGGGAGTGGGTTTAGGACGCGGGTCTGCGTGCATCCTAAGCTCT GAGAGAAACCTCCCTTGAAGCTGGGAGTGGGTTTAGGACGCGGGTCTGCGTGCATCCTAAGCT CTGAGA
EST53018 6	67 A G ---	---	ACATCCAGGTACACATTCAGAAAGAGGAGGGGTGTCAGTGAGCCTGGGTAGGTCCAGTAATCCA JAG/JGGATTCAAGGAAGGAGGCCACGAGGATCGAAGTTAGTGAAGTC

ESTD- CB22	119 C T ---	---	---	GGCAAGTTTATTGATAGAGAGGAATCAATAATGGCAATGAGGAGACATCACCTGGAATGTTAG GCAGTGCCTAACTGGGGATGGACAGACAATGGCAGTGGCAACCCATAGGG[C/T]GGATACAAAAG ACAGGCAAGGAAGGGTAGAACCATCAAGAGAGTAGGCTGGTACCACCAAGCAAGGAGGACCT AGTAACATAATTGTCTTATTATGGTCTTCCCGGCTTCTCTCTCACACAC
ESTD- CB23	136 C ---	---	---	TAGAACCATCAAGAGGAATAGGCTGGTACCCCAAGCAAGGAGGACCTAGTAACATAATTGTGC TTCAATTATGGTCTTCCCGGCTTCTCTCACACATACAGAGCCCTACAGGACCAGACAGCT CTCAGAGCAACCTAGCCCCATTACCTTCCCTTCCAGAGGACCTGAAAACGTGTCCCACCCGA GGTCGCTGTGTTGAGCCATCAGAAAGCAGAGATCICCCACACCCAAA
ESTD- CB24	145 A ---	---	---	ACCAGGACCAGACAGCTCTCAGAGCAACCTAGCCCCATTACCTTCCCTTCCAGAGGACCTGAA AAACGTGTCCCAACCGAGGTCGCTGTTTGAGCCATCAGAAGCAGAGATCTCCACACCCAAAAG GCCACACTGGTATGCCCTGGCCACAGGCTTCTACCCCGACCACTGGAGCTGAGCTGGTGGTGAATGG GAAGGAGGTGCACAGTGGGTACAGACAGACCCGACGCCCTCAAGGAG
ESTD- CB25	146 A G ---	---	---	GTTTCTTTCAGACTGTGGCTTCACTCCGGTAAGTGTCTCTCTTCTCTCTATCTTTCGGCGTC TCTGCTCGAACCCAGGGCATGGAGATCCACGGACACAGGGCGTGAGGGAGGCCAGAGCCACCTG TGCACAGGTA/GJCTTACATGCTCTGTTCTTGTCAACAGAGCTTACCAGCAAGGGTCTGCTGCC ACCATCCTCTATGAGATCTGTAGGGAAGGCCACCTGTATGCCGTG
ESTD- CB27	125 C T ---	---	---	TTTTCTGTTCCCTGAAGATTGAGCTCCCAACCCCAAGTACGAAATAGGCTAAACCAATAAAAAAT TGTGTGTTGGGCTGGTGCATTTGAGGAGTGTCTGTGGAGTCTGCTCATCTACCTGAC[C/T]ATCTTC TGATTTAGGGAAGCAGCATTCCTTGGACATCTGAAGTGACAGCCCTCTTCTCTCCACCCAAATGCT GCTTCTCCTGTTTCATCTGATGGAAGTCTCTCAACACCATTTCCATACC
ESTD- D4S338	59 A T ---	---	---	TTTTCTGTTTACCTTGTTCAGATCCTTCAGAGGAATCCCTATATATGGCAGGATATGA[A/T]ATGTA TTTTCTTAACAATAAACTTGAAGTCCAAATTAATCTCTTGAATCCATGGACTGCAGATAAATGTTA TTTTAGCTGTCAAGAAAACAATACTAATCTTGCATATGTTTCATCAGAGCCCTTGGGTGACCAGGTGA TTGCCAATAAGCAGTAATATTTGAGAGGAATCTTGTTCATGCAAGTAG
ESTD- CYP2D6	61 A G ---	---	---	CAGGCCAGCGTGGTGGTGCACCATCCGGCAGAGAACAGGTACGCCACCACTATGC[A/G]CA GGTCTCATCATTTGAAGCTGCTCTCAGGGTCCCTTGGCTGAGCAGGGCCGAGAGCATACTCGG
ESTD- D11S1873	40 A C ---	---	---	AAAAAACATTTAACACCTTTTCAATCATATACACCA[A/G]ATTTCCATTTTTCACATAAGTCA GTTTGAGCTGAGTTTCCAACTTACTGCAATCTAAATGTCACTAATGATTAATGCAAGTTCAACAG ACAACITTTCCCAAGCATCTACGATCAGAAAGGTCAAAATATTACATACTGGATTAAATTATGCCCA TATCTGCATGTC
ESTD- D17S33b	169 C T ---	---	---	CATCCCAAGCCCATCCTTTAGCCACTGGCATTTTTCGCCCTCTGACAGATACACTCAGGGCGGT CATGCTGCACACATCCAGGGGCGCCCTACCTTTGTAGTCCATGGAAAGGCTCTCTGCGGGCGGTG GGGTTGTGGCTATGTGGTGGTCTTGTGTAGA[C/T]GGGGGCTTGGTTTCAGTTGCACCTATTGCGTT ATTGCAGATTGCTTGTCTTCCACCTTGAGCGAGCCCTC

ESTD- D17S33a	75 C T ---				CATCCCAAGCCCATCTTAGCCACTGGCATTTTGGCCCTCTGACAGATACACTCAGGGCCGT CATGCTGCTACACATCCAGGGGCGCCCTACCTTTGTAGTCCATGGAAAGGCTCTCTGGGGCG GTGGGTGTGGCTATGTGGTGTCTTGTAGAGGGGGCTTTGGTTTCAGTTGCATATTGCGTT ATTGCAGATTGCTTTGCTTTCCACCTGAGCGAGCCTC
ESTD- D18S8	133 A G ---				TTTGAGACCACCCCTGGCCACATGGCGAAATCACATCTCTACCAAAATACAAAATTAGCTGGGTGT GGTGTACATGCCTATCGTAATCCAGCTACATCGGGAGGCTGAGGCAGGAGATTGCTTGAACCC/A /GJGGAGGCAGAGCTTGACGTGAGCCAAAGATCACACCCTGCACCTACAGCCTGGGTGACACAGTGA GACTCTGCTCAA
ESTD- D3S11	44 G ---				AACTGATTAGAACCTGAAATACATATTTATCTGAAAAAGTCGAGTTATTGGCTCATCACATTGG AATTTTGCATCATTAATAAAATCCAAATAAGTACACTGTAATAAGAAATTTAACAGAAATATCATTTGT TTATCAAACATTTATCACATTATTTATTGGTAAGCCATATAAATTTCTAAAGCATGTTTCTGAAAG TTTA
ESTD- D3S12	37 A G ---				AGGTTCCACATTATGCTGATTTTGGCTGATGTTTCC/AJGGGAGCCCTTGATGTCATCTGATCTCCT CAGGTATCCACCTTGAGACGTACTTTTCAAAAACCTCTACAGCCGTTGTTGTTATTATTTCAAGGT TGAACATAAAGTA
ESTD- D3S2b	247 C T ---				GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTTCCCTGC TGAGTCTTATTCAAACCTGACAGCCATTTATGCCACCTGAAATATGGTCAGGTTACAGCTGTATTCCTC AGAGTGAACATACCTGCTCTAGAACCCAGAGTCATACGATGTTCTGTTTCGGTCTTCACGATGG CAGGTATGAATATAATAATCTGICCTTTATTGGGAAGGATGCTGTTGGT
ESTD- D3S2a	248 G ---				GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTTCCCTGC TGAGTCTTATTCAAACCTGACAGCCATTTATGCCACCTGAAATATGGTCAGGTTACAGCTGTATTCCTC AGAGTGAACATACCTGCTCTAGAACCCAGAGTCATACGATGTTCTGTTTCGGTCTTCACGATGG CAGGTATGAATATAATAATCTGCTCTTTATTGGGAAGGATGCCGGTATGT
ESTD- D7S399	83 A G ---				TGAATCTTAATTGCTATCTACAAAATGTATAATCCTGAATCTGACATCTAGCCACCTCCCATAGAT AACTGCTAGAGACCC/AJGJGCTCTCTACATCATCTTTTCAAAACATTTTCATCCATGGACTCCATAC TAGAATATTTGAAAGAAACAACATGACAAACATTTTC
ESTD-DMb	146 A C ---				GTGGGACACCGAGGCTCCAGGCTGGGGCTTGCACGTGTGGCTCAAGCAGCTGCTCGGCCCTCCACT TCCATGGGTGTGGGGCTGGGACCTCACTGTCCCTGGGGAGAGGAGGAGTGGGGAGGAGACA GAATGCTGATT/AJCTCTGGTGAGAACCAAGAACCTTCTGGCCTGTGGGTAGGGGAGCTGCTTCCAAAG ACCTCCTGATTTGAGGAAGGGGAGCAGCAGAGAGGAGAACAGAGT
ESTD-DMa	66 C G ---				GTGGGACACCGAGGCTCCAGGCTGGGGCTTGCACGTGTGGCTCAAGCAGCTGCTCGGCCCTCCAC/ GJTCCATGGGTGTGGGGCTGGGACCTCACTGTCCCTGGGGAGAGGAGGAGTGGGGAGGAGAGA CAGAAATGCTGATTATCTGGTGAGAACCAAGAACCTTCTGGCCTGTGGGTAGGGGAGCTGCTTCCAAAGA CCTCCTGATTGAGGAAGGGGAGCAGCAGAGAGGAGAACAGAGT

ESTD- DRD1	154 C T ---			TCCCCAGCCCTATCGGTGCATATTGGACTATGACACTGACGTCTCTCTGGAGAAGATCCAAACCCATCAC ACAAACGGTCAGCACCCCAACCTGAACCTGCAGATGAATCTCTGCCACACATGCTCATCCCCAAAGCT AGAGGAGATTGCTCTGGGGC/TTTCGCTATTAAAGAACTAAGGTAC
ESTD- DRD2	144 C ---			TCTGCCCTTTGTGCAGGAGGCTGCCGGCAGCCAGGAGCTGGAGATGGATGCTCTCCAGCACCA GCCACCCGAGAGGACCCGGTACAGCCCCATCCACCCAGCCACCCAGCTGACTCTCCCCGACCCG TCCCACACGGTCTCCAGCACTCCGACAGCCCGCAACCCAGAGAAATGGGCATGCCAAAG ACACCCCAAGATTGCCAAGATCTTTGAGATCCAGACCATGCCCAATG
ESTD- DRD3	109 C T ---			AAGAGGATGGCCAGGATGAGCGCGCAGTAGGAGAGGGCATAGTAGGCATGTGGCGGGCCTGGCTGG CACCTGTGGAGTTCTCTGCCCCACAGGTGTAGTTGAGGTGGC/TAJCTCAGCTGGCTCAGAGATGCC ATAGCCAGAGGGAGGTGCGTGATGCCAAGGGCTTCTGTGAGGAGA
ESTD- ERB2	93 C T ---			TCTTTCAGGATCCGCATCTGCGCTGGTTGGGCATCGCTCCGTAGGTGTCAGCGGCTCCACCAAGCTGG GGTGAGGGGTGGTGGTCAGTGC/TTGGGGCGCGTGCAGACCCACGCGGGCTGGGAGGACTTCA CCCCGCTCACCTCGTTTCTCGACGAGTCTCGCATCGTGACT
ESTD- ETS2	43 A G ---			ACTCACAGTGTCTTTAAGTGAAATGGTCGAGAAAGAGGCACC[A/G]GGAAGCCGCTCTGGCGCCTG GCAGTCCGTGGGACGGATGTTCTGGCTGTTGAGATCTCAAAGGAGCGAGCATGTCGTGGACACA CACAGACTATTTTAGATTTCTTTTGCCCTTTTGCACCCAGAACAGCAATGCAAAAACCTCTTTGAG AGGGTAGGAGGGTGGGAAGGAACACCATGTCATTTCAGAAAGTTAGTTG
ESTD-F9	111 A G ---			AGATCCTGATGATTTTCTCTATTTTCTAAATGTTTACAGTTTGAAGTTTATAGATTTATGCCCA TGCTCCATTTGAGTTAATATTGTAAAGTATGATGTTT[A/G]GTCAAACCTTCATTTTTTTTTTCG ATAGGTATGTCCAATTTATCCAGCACAAATTTGTTAAACAAAAAAC
EST68787 5	144 A ---			CTTCTATGGGATTTGACTTTATTTTCTCCATTGCTTACCTTTTACAGGTGTTAATATAGTGAAAG GAAGCTTGCAAGCTCATGACAAATTTGAAGCTGACAAATACACAAGAGGAAATAAATTCACAGTCAA AGAATCAAGCACTTTTCGAAACATTGAAGTTGTTTTGAACCTTGGTGTACCTTTAATTACAAACCTAG CAGACGGAACCTGAACCTCAGGGTAAGAAT
ESTD- GODH	200 C G ---			CGCAGACCGGTGAGTGGGGTGGGAGTGGAGGGAAGGAGGAACTGGGGGTTTAGGGACT TTCCGGGTGACTTCCCGTTCTGTCTTGACAGAAAGGCGGGAGAACACAGAGCCAACCTGGCTAA GTGAAGGACCTCTGGTCGACCGTGTGTCTGCTGCCCCCTGTTACAGCTGCTGTCTGCGCGCAGTC/ G/GACTCTGTCCCGAAATCCGAGAGCT
ESTD-GOK	88 A G ---			GTTTTATGCATGGCAGCTCTAATGACAGGATGGTCAGCCCTGCTGAGGCCACTCTCTGGTCAACATGAC AACCACAGGCCCTCTCAGGA[A/G]CACAGTAAGCCCTGGCAGGAGAAATCCCCACCCACACCTGGC TGGAGCAGGAATGCCGAGCGCGCCTGAGCCCGAGGAGCAGGCTAGGATGTGAGAGACACAGTTC ACCTGCAGCCTAATTACTCAAAAGCTGTCCCCAGGGTCACAG

EST34088 2	62 A T ---	---	GTGGGGCAACAGTGGGAGAGAAAGGGCCAGGGTATAAAGGGGGCCCAAGAGACCGGCTC[AT] AGGATCCCAAGGCCCAACTCCCCGAACCACTCAGGGTCTGTGGACAGCTCACTAGCTGCAATGGCT ACAGGTAAG
ESTD- GNAT2	56 A G ---	---	GACCTGAGTACCTCCCTAGTGAGCAAGATGTGCTCCGATCCAGGGTCAAAACCAAC[AG]GGCATCA TTGAAACCAAGTTTTCGTCAAGACTTGAATTCAGGTAAGTGCATGGTCCCTAGG
ESTD-HT2	154 G ---	---	GGGCTAAATTCGAGCAACTTTCATAGACTGTTTATTTGACTTGACAGGATTGCTAGAGATAGG CAGGAGAGGAAGATGTACAGTTTGTACAGAGAAATAAAGGATAACCTGGGGTTTCTGTGC TTTGCTTTCACATCCCTGGGAGTTAATAGTGCATTTTCAAGAACGGTATACAGGGACAGCA AAGCGCAGTCGTGAAGTTTTCAAACAAGACACACTT
ESTD-HT5	149 C ---	---	AACACAAAGCCCCAGCGAGAAATGAACTCGCGACCCCTGGTTTACAAGACCAGTCTTAACCCCT GAGCTATGGAGCCCTCGTCTGCTGTTGGTTTCTTCTTCTTCAITCTATAGATTGATTATGCTCCTA GCATTCGGGCTACCGAATAGGATGTTAGCTTGAGTAAATTCAGGATATTCTCTACAAAATGAAA ACATTTCTGCTCTGTAATCCCTCGAAAAGTTCT
EST37382 5	124 A G ---	---	CTGAGAAACAATTGGCAAAATAAGGAATTTGGCACTCCCCACCCCTCTTCTCTCTCCCTTGGA CTTTGAGTCAATTTGGCCTGGACTTGAGTCCCTGAACCAAGCAAGAGAAAGAAAGG[AG]CCCCAGA AATCACAGGTGGCAGCTCGCTACCGCTACCGCTCTCAGGGAAATTTTCAGGGTAAACT ACCCAGTGGAGCCGCTCATTCGACGGTCTGGCAGGAGTG[C/T]CTGGGAGAAAGGAAGATG TTCCAGGGCACATAGCTTAGTGAGACTC
ESTD- IGHV4-6	120 C ---	---	TTTACTATTTCATGGATACAGAAATGTGGGAGTCACTATATCTATGAACAAAAATTCAGATTT CAGTGTAAAGTAATGTGCCTACATTGTGTAGTGACGGGAGTGGTGGATCCGAGAGTGGTGGG TGCACGGACATAATGATTCAGAAAGCAATATGGAAGATGAGTATCTATGGATACGAACTGAAAGT ATGTAATACTTCACAAAATACTAATAACGGAGTTGAATATAAACCCA
ESTD-IL1A	110 A G ---	---	CAAAGTAAGCACCCCAATAATGTAGCTATTACTATCATTAATTATTATTATTTATTTTGTG AGATGGAGTCTGGCTGTCAACCCAGGCTGGAGTGCAGTGG[AG]CAATCTCGGCTCACTGCAAGCT CTGCTCTGGGTTTCATGCCATCTCTGCTGCCCTCAGCCTCCGAGTAGTGGGAATACAGGCACCCGCC ACTGTTCCCGGCTAATTTTGTATTTTGTAGTACAGGAGTTCACCGT
ESTD-IL1B	99 A G ---	---	CCACTTACAGATGGATAAATGGGTACAATGAAGGGCCAATAGCCCTCCCTGTCTGTATTGAGGGTGT GGGTCTCTACCTTGGGTGCTGTTCTCTGCCTC[AG]GGAGCTCTCTGTCAATTGCAGG
EST74082	134 A T ---	---	TCCAGGTGGCTGGACCCAGGCCCAAGCTCTGCAGCAGGAGGAGCGTGGCTGGCTGTGAAGCATG TGGGGTGAGCCCAAGGGGCCCAAGGCAGGCACTGGCTTACGCTTGCCTCAGCCCTGCCTGTCT[AG] TCCCAGATCACTGTCTTCTGCCATGGCCCTGTGGATGCGCTCTCTGCCCTGTCTGGCGCTGCTGGCC CTCTGGGGACCTGACCCAGCCGACGCTTTGTGAACCAACACCTGTGCG

EST45311 0	151 C T ---				GCCCTCCTCTCTCCAAATTCGTGCCCTATAGTTTTCTCTATTAAAGTGAACATACATGCATCTTTTAGT GGATAGATGCACACAAACACACAGCCATTATGGGAAGGATCCACGTGTGGCCATATTGTAACA CATTTTCTGCAAAATC/TJACCCTCTTTCAATTAACAGCCCTTATCAATGGCCCTTTTCTTTTTCAGTA GTACATACACATCTGTGTCAATTTGTTGAAT
EST65258 8	80 A G ---				TGCCCCATACGCGCGGAGACATGGCTTGCCACAGCTCTTGAGGATGTCACCAATTAACCAGAAAT CCAGTTATTTCCJ/GJCCCTCAAAATGACAGCCATGGCCGCGGCTCTCTGGGGGCTCGTCGGG GGGACAGCTCCACTCTGACTGGCAGATCTTTGTCATGGAGACTTGAGGAGGAGGCTTGAGGTTGGT GAGGTTAGGTGCGTGTTCCTGTGCAAGTCAGGACATCAGTCTGATTAAT
EST38216 3	26 A T ---				ATGCAGGATGAAGGTGGACAGGAGGJ/TJGAGGGCCCAACCTGTCAATCCAGGGCCTGCAGATGTCTG CTGGACTATGGGTTGTGACCCCACTGACCTCCATGAGCATCAGGG
EST62782 149 G T ---					ATACTAGTACAAAGTGGTAATTTTGTACATTACACTAAATTTAGCATTTGTTTAGCATTAACCTAA TTTTTCTCTGCTCCATGCAGACTGTAGCTTTTACCTAAATGCTTATTTTAAATGACAGTGGAAAG TTTTTTTCTCTC/TJAAAGTGCCAGTATCCAGAGTTTGGTTTTTGAAGTACATGCAATGCCTGTGAA AAAGAACTGAATACCTAAGATTTCTGTCTGGGGTTTTTGGTGCAATGCA
ESTD- KRT10b	183 C T ---				CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTTCCATGTCAGTGTACCTTTTGGCAATATT AAAGGAAGAAATGCATTTTAAAGTAAGTCTAAGGTTTTTCCATTAAACCACATATTACTTCTAAG AGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGC/TJTGCTTTTAAATAGT CTCTGCCAGATACATCTCCCTATATAAGTTATAACCCAGTATTGATA
ESTD- KRT10a	133 A G ---				CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTTCCATGTCAGTGTACCTTTTGGCAATATT AAAGGAAGAAATGCATTTTAAAGTAAGTCTAAGGTTTTTCCATTAAACCACATATTACTTCTAAG GJGAGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGTGTCTTTTAAATAGT TCTGCCAGATACATCTCCCTATATAAGTTATAACCCAGTATTGATA
ESTD- KRT8b	231 C T ---				ACCTCACCCCTCCCTAGCCCGTGGGAGCAGGAAATCTCTCCAAATCCATGAATACACATCGG ATTGGACACCTTGAGAGTCTTAACAGCAGGCGCTGACATGAGACCTCAGACAGAACTTTCTAGAGTT TGCTAGAGGTCAAGGGTCAAGACTAAAGAGGGGCCAGAAATGTTAAGTACAAAAGTGAGGCCCATAG GCTGCTATCTCTCCCGTCTCAGGTTTACCA/C/TJGTCAACATTGACACA
ESTD- KRT8a	21 C T ---				ACCTCACCCCTCCCTAGCC/C/TJGTGGGAAGCAGGAAATCTCTCCAAATCCATGAATACACATC GGATTGGACACCTTGAGAGTCTTAACAGCAGGCGCTGACATGAGACCTCAGACAGAACTTTCTAGAG TTTGCTAGAGGTCAAGGGTCAAGACTAAAGAGGGGCCAGAAATGTTAAGTACAAAAGTGAGGCCCAT GGCTGCTATCTCTCCCGTCTCAGGTTTACCACGTCAACATTGACACA
EST75099 6	82 C T ---				CACCTGTGTGTAGATCTCCTCAGTGGCGCCCTCTACTGGGTTGACTCCAAACTTCACTCCATCTCA AGCATCGATGTCAA/C/TJGGGGGCAACCGGAAGACCATCTTGGAGGATGAAAAGAGGCTGGCCCCACC CCTTCTCCTTGGCGGCTTTGAGGTGGG

ESTD- LF79	142 A G ---	---	GGGTGATTTGAGGCTCAGTTAATATTTCAAATGTAAACGTAGCAAAACGTCATTGGTATTTAGA AAAAATAAAATTTCCAATATGTAGTGCTGTATTACCTGCCTCTGCCATGCAGCATCATAGCCTGT GGGAACCA/G/GGGAGGGCTTCCCTTACCACCCAGA
EST35879 9	142 A C ---	---	GAGATCGGTGTGTGAGTTATTAGGCATGGTTACCTGTGATTCTCCCAATCTTGTGCGTTCCACCGATG GAACTGCCGGCAAATCCTGACACGTGTGCACCCAGGCTGTACCCAAATTAGGTGAACATGGCTTCGAG AGAGTTG/C/CACAGATTCTCTGGAAGACAGCAGCGGGATGGGGCAGGAGAGAGCTGCCTGGATGA A
ESTD- LMP2	35 C G ---	---	TACACACTTTCCTTACCCATTCACTGAAAACGACTC/G/GCAAACTGGAGCCTTGTAGGAATGGAGT TGACCTTCCCCAAAAGCCACTATGATAAGCTATTGGTG
ESTD-LPL	113 C T ---	---	TGTCAGTGTCCCTAGGGGCACCTCACACTCCAGCTTCTCAGCTCTGGCCTGTCTGCTGCCTGCA AGGGTTTGTCTAAATCTCAATCAATGTCTCTCATCTTTAG/C/AGCTGTGGGGTTTTGTGTTG TTCTCTGTTTTGCTTAGTATCTGACTACTTTTAAATTATAAAAGAGATGTATCTAAACAAATAG AGATTGTTATCAGAAGTTCACAACATTATTAAAAATTTTTCACTG
ESTD-MOC	45 C T ---	---	TTGTCAGGAGTGTGCTGATGCTGCCTCCCGAGCTCTGTCCCTAGC/C/AGAACTTCAGGACAACGTGC AG
ESTD- METH	118 C T ---	---	CATCATGTAGGAGAGCCTTAGTCAAGTGAATGCTGAGGAAGCAGATAAACAGCATGCATCCCCGAA TCTCAGGAAGTCTCTGCTTCCAAAGGTTTGGTCAAGTTGCTGATTACC/C/AGGATTTTCTGACG ATCTTCAACTGCTAGAGCATCTGGTTCCTGTTTAGCATGG
ESTD-NF1	25 A G ---	---	ATTATCCAGATGAATTTACAAAACCT/G/ACCAGATCCCACAGACTGATATGGCTGGT AACATGGACTTGATATTTGTACAAAAAAGTTTTATTTTCTAAAAAAGAAAAAGAGAAA AAATTTAAAGGGGTACTTATATCCACACTGCACACTGCCT/G/GCCCCAAAACGCTTATTGTGGT AGGATCAGCCCTCAATTTGTGCTTTTGTGAACCTTTTGTAGGGGACGAGAAAGATCATTGAAATTCT GAGAAAACCTTCTTTTAAACCTCACCTTTGTGGGGTTTTTGGAGAAGGTTATCA
ESTD- NPPA	45 A G ---	---	TGTCCTTAGGCCAGCCCTGCTTGCTCCCTGGCTGTATCTT/C/AGGTACTGCAAAAGAGAACACA GACAT
ESTD- NPAS	202 C T ---	---	GTGTTTCTTAATCTTTCCAGGAACACAGTGACCATATTTCTTCTGCAGGCATATAGAATTTGGT GGGTTTCTTTTATGTAGGTGATATTGGATACTTTTGTGTGATTATATATAGCAATTTGAGGG ACAAACCCAGATAGGCAGAAATGGGCTTGAATAGTAGTCTTATTTAACCTTGGCAATAGCATTG C/JATTCCCTGTGGTTTTTAATAAAAT
ESTD-PA1	100 A G ---	---	GCCACCACCCACCCACGACACCTCCAACTCAGCCAGACAAAGTTGTTGACACAAAGAGAGCCC TCAGGGGCACAGAGAGAGTCTGGACACGTGGGG/G/G/GTCAGCCGTGTATCATCGGAGGCGCCGGG CACATGGCAGGGATGAGGGAAGACCAAGAGTCTCTGTTGGGCCCAAGTCTCTAGACAGACAAAAAC TAGACAATCAGGTGGCTGGCT

ESTD-PAR	120 A	---	---	CTCTTCAGGAACCAACAGTCTCTTACCAACACGACGTTATGCTGTCGAGAGGTACAAACCCGTAGA
ESTD- Per/RDS	74 A	G	---	ACTTCTTCTTAAGTAATTTAGTTAAAGGAATCGAACTGGCTCTGAAGACATGGAGATACTGGCT
EST68308	29 C	T	---	AATCGACTGGCTTTCATTAGCTCTGTGAGTGTCTTCTTACATTTCTGTGTTCTTAGAACGTTTCTTAG
5				GACTGGCAGTTTAAAGCTTACATTAGGCTTCTGTATACCCATGCC
EST54045	39 A	G	---	ACCTACAGACGCTGGCTGGATGGTGTCCAAACCCGAGGAATCTGAGAGCGAGAGCAGGGCTGGCTG
6				CTGGAGA/GAGAGCGTCCCGGAGACCTGGAAAGGCT
				GGAAGAGATTAAAGAGCTTGAATTGGAGC/TAATTCGTGTTCTTTGAGTGTGGAAGAGTTTCATGTC
				TCTGCCCTGAGTTACAACAGAAATCCTTTAGTACAGCGAGTAATAGATATATTCGACACAGATGGGAAT
				GGAGAAGTAGACTTTAAAGGTAAGAAAGTAGTATTTTTTA
				GGAATTTAAATATTTAAATACCTCCATTTGCTT/GJTCCTTTGTAGTGAAGATGATACCTGCG
				AAAGACATGGCTAAAGTTATGATGTGATGTGGCAATTTGTTTCTTACAAAATCGGATGGGAAA
				TCTGTTAAGTAAGTACTGTTTGGCTTGGAAATGGATTTTAATGTGACTTTATCAT
ESTD- PXMP1	88 A	G	---	ATGAAACATGGTCTTTAAATTTATGATATGTTGTTATAGCTATCTTAAAGGGCTTCTTTTTTTTA
				ATGCAGAAAGAGGGGAAAGAA/GAGCGAGCTGTGGTGACAAAGTGTCTTCTCAAGGCTCATAC
				AGATTTGAAATCATGTCCTCCTAGAACATTTGTAAAGAGTAAAGTCTTATGAAATTTAATCTT
				CCCGAGGAATCTGAGAGCGAGAGCGAGGGCTGGCTGCTGGAGAGAGCGTCCCGGAGACCTGGAAGG
				CCTTCTGGAGAGTGAAGAGCTGGCAAGGGCAAGCAAGGTTGAGGCGAGGCGAGGCGAGACGCGAGG
				CCAGGCCACAGAGGCTGGCTGAGGGCCCTGGGGCCCTCCCTCCCGAACACTGAGAAATAGTGCACT
ESTD-RDS	127 A	---	---	CCAAAGAACGTGGATCTCCCCCTCATCCCACTCCGAAAGTCTGAA
ESTD- s14544	94 G	T	---	TTGGGAAGTTAGAGCTATATTAATACGGAATTAAGGAGGACACAGAGGCTTAATTGAAAAA
EST52908	45 A	C	---	TATCCCAAAGTTGAAATGCTCAGTTCTG/TTCTGTGGGTTAGATGCAGGATTTATATGATCCGTTA
0				ACCTCT
EST19590	55 C	T	---	ATCACAGGTCTCTGGTCTCTGGCCATCATTTCTCTGGGAGAGATGG/CTGGTGGTCTGCAAGCCCTT
EST76136	39 C	T	---	TGGCAATGTGAGATTTGATG
				AGGAGAAGCTGAGGAGGGGAAGAGAGACAAGAAATGACATTGATGAGTGAAGATGTC/TTGGCTCAG
				GATGCCGGAAATGAC
				TGAAGCTTCTGCCAGCTTGCAATGTTTCTAGGAGAACC/CTGGCGTACATCCTTTATCTATAGCCTT
				CCCCTAGTCTT
ESTD- SPTB	176 C	T	---	TGAACACCCCTGTGGTCCGGAGCCAGGTTGTGTTTCTCTCTGGAGCCCTGAGGAGTTTGTGTGTGTG
				CAGTCCCCCGGCCACCTGCTGGTTGAGCCTGGACATACACCTTACCTCTTTGGCCCGGAGAGAC
				ATTTACCCACCTGGCCATGTCCTGGCCTGTTGTGCAAC/CTCTCTGTGAAGACCCCAACCCCTGC
				CTCCCCCAACCAAGCCAGTTTCTCTAGCAAGGGCAGGAC



ESTD-TAT	224 C ---	---	---	AAATGGTCAGGACCCGTATCCACAAGAAGTGTACCATTTTCATCAGGGCCATCAGTTTCATTTCAGCTC CCATGACTGGGATGCTAAGTCAGCAACTGAGTTTCATTCATTTAAATGACTTTGTTGGACAGGATCA ATTTCTCTCACCTAGAACGTTTGTACAACTTTTCTCCAGTATGGATGGGATTTATGATGGGGG GAGAAGCAATTTTAAATAGGACCCATGAGACACATCA
ESTD- THRB	125 A C ---	---	---	TGCGGCTTTCTCCGGCAGGGTAGACTTCTACTTGGCTGTGATTTCCTCAAGAGAAAGAGTCCCAAG CACACGAAACAGAAAGTTGCAGATCCCATGAGGCCAGTCTCAAATCACACAGGATC/A/CJCTTCAT CCACACTGGATTGGCCCAACAAGTCTGAGTGCCAGCCAGGACTCAACGGTCCCTGTAGATGGG TAGTGAAGTTTTCATCTCCTGTGAGCTTCTGGATTCTTGTCCACCCGCAACAAGAGAGTCTATGC CAAGGCAGAAAGCTGGTCTTCATGGGCAAAATCAATGTCTCTCCAGATTTCAGTATCCCCAA GCAGTGCATCCATTGACACATAATAATGCATCCAGACAAGAGGTCATAAATATTGATGTCGTAA CATGGGTGTGATCCATTTTCATTTGGCCATAGGTCCTATGGGGATGACA
ESTD-TYR	122 GT ---	---	---	AGTAGTGGATGAAGCTAACAGCCTCTCCTCACTGATCAGTATCAATGCTATGCTGAAGAATATGAA AAACTCCAGAAATCCTAATCAGTCTGTGGTCTAACAAATGCCCTACTCTTATGCATTAGTATCACA AACCACCTGGTGAATATAATAGATTGAGTTAATTAACGTATTTCTTTCACITTTATACCTTCTTCT AATACAAGCATATGTTAG/A/CJATTAAGTTCTAGGCATACTT
ESTD- TYRP1	222 A C ---	---	---	AGTAGTGGATGAAGCTAACAGCCTCTCCTCACTGATCAGTATCAATGCTATGCTGAAGAATATGAA AAACTCCAGAAATCCTAATCAGTCTGTGGTCTAACAAATGCCCTACTCTTATGCATTAGTATCACA AACCACCTGGTGAATATAATAGATTGAGTTAATTAACGTATTTCTTTCACITTTATACCTTCTTCT AATACAAGCATATGTTAG/A/CJATTAAGTTCTAGGCATACTT
ESTD- TYRP1	222 A C ---	---	---	TTCCCAAGGCCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGCTGTGTTTCTTCTATTACA GGACACATGGATGCTGGAATCACCAGAGCCCCAAGACACAAGGTTCACAGAGACAGGAACACCCAGTG ACTCTGAGATGTCA/C/TJGAGACTGAGAACCACCGTTATATGTACTGGTATCGACAAGACCCCGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12	148 C T ---	---	---	TTCCCAAGGCCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGCTGTGTTTCTTCTATTACA GGACACATGGATGCTGGAATCACCAGAGCCCCAAGACACAAGGTTCACAGAGACAGGAACACCCAGTG ACTCTGAGATGTCA/C/TJGAGACTGAGAACCACCGTTATATGTACTGGTATCGACAAGACCCCGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12b	148 C T ---	---	---	TTCCCAAGGCCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGCTGTGTTTCTTCTATTACA GGACAC/A/GJGGATGCTGGAATCACCAGAGCCCCAAGACACAAGGTTCACAGAGACAGGAACACCA GTGACTCTGAGATGTCA/C/TJGAGACTGAGAACCACCGTTATATGTACTGGTATCGACAAGACCCCGGGC ATGGGCTGAGGCTGATCCATTACTCATAT
ESTD- VB12a	74 A G ---	---	---	ATGGGCTGAGGCTGATCCATTACTCATAT

EST58607 0	105 A G ---	---	CTCTGGATGGGTTACAGGTGGCAGGCACAGCCAGTCCATCCTGTAGTCATCATAGTTGTTGGCTCC CAAGTTGCTCTCCTCACTGGAGAACAGGACAGCCAC/GJTGCGCGGGATGGCGCGGGAGTTTC TGGTTGGCGCCACGGCTGTGGCCTCGTTGTGAACGGTAGCCTTTGGGGTTCGATGCCTAAACCTTTGT TTCTTGCCAAAGGAGGGCGGGGTGCCATGCCCTGAGATGTAGATGGGCGC
ESTD-VWF	36 G ---	---	AGGTAGGAAAGCAAGAGTTGATTAGTGAAGGAGAGAATGGACCTACCTTCCACACTGTCTTTGG TCCCTAGAGTCTG
EST71770 6	189 C G ---	---	AGCACCACTCTCACGTCAAGCCTCAGCACCCAGATGCTGTTCTATAAGGATGACGTGCTGTTTACAA CATCTCTCCATGAAGAGCACAGAGATTATTTATCTCTGAAGTCCGGATCTATGACTCAGGGACAT ATAAATGTACTGTGATTGTGAACAACAAGAGAAACCACTGCAGAGTACCAG[C/G]TGTGGTGGA AGGAGTGCCAGTCCAGGGTGACACTGGACAAGAAAGAGGCCATCCAAAG
ESTD- TNFα	152 A G ---	---	TTCTGTCATCCTGTCTGGAAGTTAGAAGGAAACAGACCACAGACCTGGTCCCCAAAAGAAATGGAGG CAATAGGTTTTGAGGGGCATGAGGACGGGTTTCAAGCTCCAGGGTCTACACACAATCAGTCAGTG GCCAGAAAGACCCCTC/GJGAATCGGAGCAGGAGGATGGGAGTGTGAGGGGTATCCTTTGATG CTTGTGTCCCCAACTTCCAAATCCCCCGCCCCGGGATGG
ESTD- TNFα	88 A ---	---	TTCTGTCATCCTGTCTGGAAGTTAGAAGGAAACAGACCACAGACCTGGTCCCCAAAAGAAATGGAGG CAATAGGTTTTGAGGGGCATGAGGACGGGTTTCAAGCTCCAGGGTCTACACACAATCAGTCAGTG GCCAGAAAGACCCCTCAGAAATCGGAGCAGGAGGATGGGAGTGTGAGGGGTATCCTTTGATGCTT GTGTGCCCAACTTCCAAATCCCCCGCCCCGGGATGG
EST52418 6	113 A G ---	---	CAAAATACAGGGTCAACTGCTATGATGTTTGGAGCCCGATCACCTTTGGTGGCTACAAGATGTCG GGGAGTGGCGGGAGTTGGCGAGTACGGGCTGCAGGCATACACTA/GJAAGTGAAAACGTGTGAGTG TGG
EST13586 3	89 A G ---	---	CCCACTCTATTGCCAGCCCCAGGGACAGAGCTGATCCTTGAACCTTAAGTCCACATTGCCAGGA CCAGTGAGCAAGCAACAGGGCC/GJGGGCTGGCTTATCAGCCTCCAGCCCGAGACCCCTGGCTGCAGA CATAAATAGGOCCTGCAAGAGCTGGCTGTTAGAGACTGCGAGAAGGAGGTGCGTCTGCTGCCTGGCC CCGGTCACTC
EST51976 7	123 A T ---	---	AGGCAGAACTGGGCCCCCATGGGGGGACGTGGGAAGGCCACTTGAGCTTCTGGAGAAGGACCTGA GGGACAAGGTCAACTCTTCTCAGCACCTTCAAGGAGAAAGAGAGCCAGGACAAG[A/T]CTCTCTC CTCCCTGAGCTGGAGCAACAGCAAGGAACAGCAGCAGGAGCAGCAGGAGCAGCAGGAGCAGGTGCAGATGCTG GCCCTTTGGAGAGCTGAGCTGCCCTGGTGC
EST11458 6	140 A G ---	---	CCACTTTGGTAGTGCCAGTGTGACTCATCCACAATGATTCTCCAGTGCCTCATCTTGTCTCGAGTTT CTCTGCCATGTTGCTATTGCAAGGACGGACCTGTCCCAAGCAGATGATTACCATTTTCCACAGTGGT CCC/GJTTAAACAATCTATGAGCCAGGAGAAAGATTACGTATTCCTGCAAGCCCGGCTATGTG TCCCGAGGAGGGATGAGAAAGTTTATCTGCOCTCTCACAGGACTGTGGCC

ESTD- AT3aa	60 C T ---	---	AGACCTCAGTTTCTCTTGTAAAGGGAAGTTTGTCTTGGATCTCCATGGGCCAGC/C/TJAGCA CTGGTGCCCTGTGAGTCTGTATCAGGTAGAGGAGTGGACAGGTGGAGAGAAATTTGAAAGGGCA TTGGAATTCAGAGCAAGAGACAGATATTAGAGCTGGGAAATGTGG
EST39852 8	106 C G ---	---	CGGCTCTCTCCAGGTATTGTTGCAGAGGCCGAGATGACCTCTATGTCTCAGATGCATTCCATAAG GCATTTCTTGAGGTGAGTACACCTTCCCACTCTCTTAC/GJGGTACAGAAAGGAGATGCATGAACA GCAGGAACACGTTGAAAGGCCCTGTTTCCAGTGTTAAGGCATGCAAAAGGCCCTCCACAGGCTGCTAT AATACAGCCCT
EST62448 0	112 A G ---	---	ACCTGGTGTGCTGGTGAACCTGGTCTCTTGGCATTGCCGGCCCTCCTGGGGCCCGTGG TCCTCCTGGTGTGCTGGGTAGTCTGGAGTCAACGGTCTCTT/GJTGAGCTGGTCTGATGGCA ACCTGGGAACGATGTGTCCTCCAGGTGCGGATGGTCAACCCGGACACAAGGAGAGCGCGGTTACCC TGGCAATAT
EST36027 2	120 A C ---	---	AGTGACTTCCAAGGAATGGCTACCCAACTTGCCTTCATGCGCCTGCTGGCCAATATGCCTCTCAGA ACATCACCTACCACTGCAAGAACAGCATTGCATACATGATGAGGAGACTGG/CJAACTTGAAAA AGGCTGTCTTCTACAGGGCTCTAATGATGTTGAACCTTGTGCTGAGGGCAACAGCAGGTTCACTTAC ACTGTTCTGTAGATGGCTGCTCTAAAAAGACAAATGAATGGGAAAGACAA
ESTD- COL2A1cc	112 A G ---	---	AGAATGTATATAGTCTCAAACTGGCCATCTCCATTTTCAGTCCAAAAGTTATACAGCTAGACAACA GTGGTGACATACGTTGCTATTATGCTCTCTTCTCTGCTCACTTTC/JGJGGGTTCAGAGGTGAAAA GGTGAACAGGTCCTCGCTGCTCCAGGCTTCCAGGTAACTCACTCAAGCATATACAATACTGCCT TTGGTCAGCCTATTGAGCTGTAAATCACCATACCGTACCT
ESTD- COL2A1dd	97 C T ---	---	TGAGAGAACACCTAGTCTCCATCCTTCTCTCAATGGCAAGAAAGTTAAGTGACCTATCTAGGGC AATAGACTGAGTTTGTCTGGACCTGGAACA/C/JTGGACTTCTTCTACTGCGAGGACAGAACTTA CCCAAGAGAGATTAAATGGCAAGATATACAATACAATTTTATTTGACCAAACTATCATGGAACA GCATT
ESTD- CPT2	150 A G ---	---	GCCGCAATGCCCGGGAGTTTCTCCAATGTGTGGAGAAAGCCCTTGAAGACATGTTTGATGCTTAGAA GGCAATCCATCAAAAGTTAACTTCTGGGCAGATGAAAAGCTACCATCACTTCTCTCATCATGAAAAAC TGGGAGGCCGGGCAT/JGJGTGCTCATGCCTGTAATCCAGCATTTTGAGAGGCTGAGGCGGGTGGAT CACTTGAGGTCAGGAGTTTGAGACCAACCTGGCCAAACAT
EST12274 0	135 A G ---	---	CCCCAGTTGACAGCCACTGCTCTAGACTAAGTTTCTTGCTTCCAAATAGAGCCTTACCAAAGTGAT TACATAAAGAAAGTCAAGTGGTTTACTCTCTCATGACCAATATCTTCCCTCCTTAGGATGAGGTG A/GJTAGTAAATGACCCGATGGGGTCAGAACTGTTCTGTCACTGAGGAGTACTATAACTGTGAAGA TAAATTCAGCCACAGAGCTTGCCAGATC
EST76807	91 G ---	---	ATGCTAAGGGGATCGGACATGAAAGGACCTGTGAGCCGATTGCTCTATCTCCAGGGCCCTGTCATC CAGCTCACTCATCAATGGGGCCAGTCAGGCCAGGCACTGGGCTCCGGAGGACTCACCAGCTGCCCCCT GCTGCCATGTGGACTGGTGCAAGTTGAGGACTTCTTG

ESTD-SSA1	111	C T	---	TTACATTTGTGGATTGTTCTTTGCTGTGCAGCACCTTTTCAACATGATGTGATCCCATTTGTCCAAAG TTTGTCTTGGCTGCTGCTTGTGGGATATTTGAAGAGATGCT/TTTGGCAGTCCAATGTCTCCTAGA GAGTTTCCCAATGTTTCTTGTAATAGTTTCATAGTTTGAGGCCCTAGATTTAAGTCTTTAATCCATT TTGATTGATTTCGTGA
ESTD-RYR1	109	A G	---	CTTGTGACGGGAGGTCACGTCCTCGGCTCTTTTCATGGACATATGGATGAGTGTCTGACCATTTCC CTGCTGACAGTGTACACGCGCAGACTTGCTACTATAGAG/GGGGGAGCTGTGTGCACCTCATGGC CGCTCCCTCTGGAGGCTGGAGCCACTGAGAAATCAGCTGGAGTGGAGCCACCTGCGCTGGGGCAGCC ACTCCGAGTCGGCATGTCACTACCGGGCAGTACCTAGCGCTCACGGAGG
ESTD-WT1	70	A G	---	AAGCCTACGTGAATGTTACATGTGCTTAAAGCCTCCCTTCTCTTACTCTCTGCTGCAGGATGTG CGA/GCGTGTGCTGGAGTAGCCCCGACTTTGTACGGTCGGCATCTGAGACCAGTGAAGAAACGCC CTTCATGTGTCTTACCCAGGCTGCAA
ESTD-F2 EST4438 7	100	C	---	GATAAGTACACTGAGGCCCCAGGAGTTATTGCTAGTAGCCCAACTGTGCATGCACGCTTAACCTCT GCACCAATGGCTCCAAGGCCCCGTAGGGGAACCTGGGGGATCTAGGGGATGGGTGAGGAATGGCCC AGCCAGTCCCGGCCGTGCTGGGTCCCAACAGAGGAGGCCGTGGAGGAGACAGAGGAGATGGGC TGGATGAG
ESTD-PBDA	103	A G	---	GCAGCCAGGAGCCGCTGCACCATGCCCGCATAGATCGGACCTCAAGCTCGACTTCAAGGA[C/T]G TCCTGCTCCGACCTAAGCGGAGCAGCCTCAAGAGCCGAGCCGAGGTGGG
EST12839 3	122	A G	---	CCCTTCATGCCAGATGGAATTCAGTCCCTTCAGGATCTGCCCTAACCTGTGCACAGTCTAAAGAGT CTGAGCCGTGGCTGGGAAGGGCAGGACTAATCCA/GJCTCTACCCGCAGCTTGTCTGCATACAG ACGGACAGTGTGGTGCAACATTGAAAGCCTCGTACC
ESTD-CTLA-4	48	A G	---	TGCAAAACACACAAATCTTCCAGATGCCCTATGGCTGTGGAGAGCAGAAATATGGTCTCTTTGCT CCTAACATCTATGACTGGATTATCTAAATGAACACAGCAGCTTACTCCAGAG/GJTCAGATCCA AGCCATTGGCTATCTCAACACTGGTGAGTGATTACTTGAGTAAGGGAACCTTGAATGTTATTCAAC TGGATTTCCAGTAGGTTTCAGTTACTTATGAATATTATGATACTTAGTTAG
ESTD-ACE	96	C T	---	ATGGCTTGCCTTGGATTTACGGGGCACAAAGGCTCAGCTGAACCTGGCT/GJCCAGGACCTGGCCCTG CACTCTCTGTTTTTCTCTCTTCATCCCTGCTCTCTGCAAGCAATGCACGTGGCCCCAGCCTGCTGT GGTACTGGCCAGCAGCCGAGGCATCGCCAGCTTTGTGTGAGTATGCATCTCCAGGCAAGCCAC
EST54419 8	88	A G	---	GATCAAGCAGTGCACACGGTCCAGTGGACAGCTCTCCACAGTGCACCATGAGATGGGCCATATA CAGTACTACCTGCAGTACAAGGATCTGCC/C/TGCTCCCTGCGTCGGGGGCCAACCCCGCTTCCA TGAGGCCATTGGGGAGCTGCTGGCGCTCTCGGCTCTCCACTCTGAACATCTGCACAAATGGCCCTGC CTTCTGCCTAATTTGAATGATATTGTTGCTGTGGGACCTGAGCACTTTTATGGCACAAATGATCACTA TTTTCTTGACCCCTACTTAC/GJATCCTGGGAGATGTAATTTGGGTTTAGCGTGGTCTGTTGTCTA CTATAGTCCAAGTGAA

ESTD-PS-1	99 A G ---	---	GGGGAGTAAAACTTGGATTGGGAGATTTCAATTTCTACAGTGTCTGGTTGGTAAAGCCTCAGCAACA GCCAGTGGAGACTGGAACACACCAAGCCTAGCTTTCGTAGCCATATTAATGGTTTGTGCTTAC ATTATTACTCCTTGCCATTTTCAAGAAAGCATTGCCAGCTCTTCCAATCTCCATCACCTTTGGGCTTGT TTTCTACTTTGCCACAGATTATCTTGTA
ESTD- B3AR	104 C T ---	---	GSCCTGCCAGGGTTCCGTGGAGGGCCCTAGCCGGGGCCCTGCTGGGCTGGGGTCTGGCCACC GTGGAGGCAACCTGCTGGTACATCGTGGCCATCGCCCTGGGACTCCGAGACTCCAGACCATTGACCAA CGTGTTCGTGACTTCGCTGGCCGCGACCCGACCTGGTGATGGACTCCTGGTGGTCCGCGCGGGGCCA OCTTGGGC
WI-567b	48 A G ---	---	TCTCACACTGACCCCTTACCTTCATCCTCACCTCTGCTGCCTTGGTTCAGAGCCCTCATCTCTTTTA CAGGATCCGCCACAGCATCCCAACTGATCTGGCCTTAGGCTCTTCTTCCAAATCCATTCTTCAAAG GCTGCCACTGTGATCTCCCAAAGGTGATCTGATGCTACCATCTTGTCTTCAAGCC
WI-801c	58 G T ---	---	ATGGAACATTTCTTCCATAATGAATGAGGTTCTCAATCCATTCACACATCCCTTCTGTGATGAG TATTGGAGAAGTAGACAGAGAAGAAATTAAGTAGGCAATGCATGTTTCAGGGGTGGGGCTGTGC ATCTGTGATGTTAGTTACATGGGCACATATACGCTCATGTTTGTCTCAGCCACCAGAGAGTTAA CATTCTGCCACCCCTC
WI-801b	58 G T ---	---	ATGGAACATTTCTTCCATAATGAATGAGGTTCTCAATCCATTCACACATCCCTTCTGTGATGAG TATTGGAGAAGTAGACAGAGAAGAAATTAAGTAGGCAATGCATGTTTCAGGGGTGGGGCTGTGC ATCTGTGATGTTAGTTACATGGGCACATATACGCTCATGTTTGTCTCAGCCACCAGAGAGTTAA CATTCTGCCACCCCTC
WI-1099b	76 A G ---	---	GAAATTCACCTATACAAGAACTATTTCTCTAATTTACATTAGTCTCATTATCTGAAATATTAT TTTTACAAGTACCCCTTGTATTTTGTATTCATTTGTAAAGGAGATTACAATATCAGTAACGC TGTTCAATTGATAGTGTATCACAATGTCTAAATACITTTGGGTCAACATCAAAATTAGAAAGAAA CTTACAAAGTTTATTTGCTTTAIGGTTTA
WI-2529	71 C T ---	---	AGGAAATGGCTGATACCTCCTGGTGGCTTCATTATAGTAAAGGAGATGTAATTGCTGATGACCTCT CAA[C/T]TCTTAACCTGCTGCCCTCAGTCAGTGAACATTTAATGAAGTCTACACAAATTAATTAGTGT AAGTTGTAATGCTGAATAAGCTTGAATAAAGTGAAGAGGTAAAGAGGAGACAACTGTGCTTT TTAAGAAATAGAAGAGTCACTTTTATTAGAAATGGCTTTGGGGATGACAAGTA
WI-10088	205 C G ---	---	TAAGGCCCTGTCTTCCCCAGAGGCCCGGACGAGAGAAAGCATCTTGATACCCAGGGCCACAAA TGAGCAATCCATAGATACTACATATAAGAGAGACCTGTACCTTATGAGGTAACTGAGGATGAAGGA GTGAGTCATATTGGTGGCAATTAATGACCCAGCCTCTCTCTCAAGAAGACTTTTACATTTTAGAC AGG[C/G]AGCAGAAAGCAGCAAGGAGAGAAAGGAAGT

WI-2625	98 G A ---			GGG CAG TCG TGG CTG TAG TGG TAG A CAG CACT G AAG GAT G GAG G AAG A G A G A A A C A G G C A G A A G C A C T G T G G T A G T T A C A A G G C T T A T T T A G G A [G/A] C A A A T T G A T G A T A C T C C C T G A G G A C T C G C A G A A A T T A C C A G C A G T G G A C A G G G T T A T C T G T G G T G A A T T C A G T T A T T C C A C T T G C A G G A G G A A A G C C A G C C A G C A A A G
WI-2924	54 G A TAGG	TGACCTTCCTA GTCTCTCTTA	GCCTAAGTGT AATCAGAGGG	TCT GTT GTC A T A T T C C C T C T T T G A C T C T G A C C T T C C T A G T C T T C T T A T A G G [G/A] A C C C T G T G A T T A C A C T T A G G C C T A C C T G G A T T A T T T A G A C A A T C
WI-2939	72 G T GTGCCTTT	GGCTTGCTCA	CTTGTGAGGG AAGGTCTTG	CC A T T G T G A G G T T G G G T G C A C T T G T C A T T C C C T G C A C T C A A C A A A G T G G C T T G T C T C A G T G C C T T T [G/T] C A A G A C C T T C C C T C A A C A A G A T G T C T T T C C A T G C T C C G T G T T C T T T G A A A A T T C G A C T T T A T C C T G A A A A A C T C A G C T G C A G T G T T A T C T C C G G T A T A A A G C C A C T C C T G
WI-3203	99 G A AGACGAG	GGTTATGCCG	TCAAGTATTG CTTGTGTG	C T T G T A C C A T G C A T T T C A C A G C A T A C A C C C T C A G T G A A T G C C G T A A C C C C A T T A T A A A A C A T C T T G C C A T C G A A G G G T T A T G C C G C A G A C G A G [G/A] C C A C A C A A G G C A A T A C T T G A A G T G A C T T G G A G A T A A A G A T T T G G A T G G A T G A A A G C A G A G A G A G A T G C T A A A A G T G A
WI-3473	101 A G GCCCTAGGGA	AAGCATTTTA	CCTGATGTCAC CAACATTTCT	G G A A A A G A A A C C T G A A G G A T G A G T A G A A G T T A T T G G G A G A T A G T T G G T A G A G C C C T G T T T G G A G A T T G C A G A G A A G A A G C A T T T A G C C C T A G G G A [G/T] A G A A A A T G T T G G T G A C A C A G G G C T A C A C A C T T T C T G T A T G C T C T T C A T C A A A [A/G] T G C A G G C G T C A T T C T G C A C A T G G T G A T A T T T A A G C A G G A G A G C A T T G C T T G G C T C C C C
WI-1796b	29 A G ---		---	A C A C A C T T T T C T G T A T G C T C T T C A T C A A A [A/G] T G C A G G C G T C A T T T C T G C A C A T G G T G A T A T T T A A G C A G G A G A G C A T T G C T T G G C T C C C C
WI-1796	29 A G ---		---	A G T C G T C C A C T T C A G G G T C T A A C T C T G G A T C T G G C C T G C A G A G T A G G A A A G A A G A T G G G T G A G T A G T C A C A T T A G G T A T T T C C A A A T A A [C/T] A A A A T G C C T C T G A A A A A T A T C T C C C A T G T C C C T G T C T A A T A T A C A T T T T C C C C
WI-4360	93 C T A A A T A A	GTAGTCACAT AGGTATTTCC	GAGAGATATT TTCAGAGGCAT TTT	G C T G A G C T T T G T G C A G A G C C A G G G A C A A T T C A G C T G C C G G A T T T A T A G A T T C T G C A G C A C T G C A A C A G G A C C A A A A T C A G T C [C/T] G G G T A A C T G A G A G T G G T T T C A C A C C C A A A
WI-1959b	87 C T ---		---	G T T G T G C C T G T A G C A G A C A C A G A G G C A [A/G] A G A G G A A A A A G C C T T T T G G T C C A G G G C T T A C A C T G A A T C C C T C A A A C A A T G C A A G A T G A G C T A A T G G T C T A G A G G T A T A A T C T A A G T G T G A G A A A A C A A A G G T A T A G G G T T G
WI-1973b	28 A G ---		---	C T T G A G A T G C G T G G A T T T G T A T A C A C A G A A A T G G G A G A G C T G G A A C T A A T C C C C C C A T A T A C C A A G G G A C A A A T T G A T C T G T T C T A C A A T T A C A G T A G G A G A C A T A T G T T C C A T G A C A A T G G T A A T T T T T A A [C/T] G A C A G T T T T A A T T G A G T G A A A T T A C C A T A A A A A T A A T A A T A G T A G C A G C T A A T A T T T A C T G A G C T G T T A C T A G G T G C C T A T A A A T A G C
WI-1980b	140 C T ---		---	

WI-2015b	190	A G ---	---	---	TGTCAGATAGTCGGTCTACCTAGGTGCAGTAGCATGCTAGGAGCTATTAAAGTACACAATTATGCT ATATATTTATACAATATACAATTACTTGCAGATAGCATGACCATGCTAGTAGTGAACCCACACAAGACTAT GTGTGAATCGTCTATTAGGGTTTCTATAAAGTCTACATGGTGCCTTTTCCAACTA/GCATATACCTT CTAATACCATAGAG
WI-754b	49	C T ---	---	---	GAAGGCACAGGAGAGATGGCTGTCTATCTACCAGCCAGGAGAGAAAGC/CTACATTTTATTGGTAA TCCTATAAAGTGCACTCTTTAAATTTGTATTACTTTIAGA
WI-754	22	T C ---	---	---	GAAGGCACAGGAGAGATGGCT/CJGTCTATCTACAGCCAGGAGAGAGAAAGCCACATTTATTGGTAA TCCTATAAAGTGCACTCTTTAAATTTGTATTACTTTIAGA
WIR-1b	56	A G ---	---	---	AGGCAATCAGACCTACAGAAGGAAACCCCAATAAAAACTCTGTATGTCGTACATCC/A/GJTGCGCTG GAGGTGATGCTCCTGAGGACATGGAGCTTCATGTTGGAGCCCTCCCTG
WIR-1	56	A G ---	---	---	AGGCAATCAGACCTACAGAAGGAAACCCCAATAAAAACTCTGTATGTCGTACATCC/A/GJTGCGCTG GAGGTGATGCTCCTGAGGACATGGAGCTTCATGTTGGAGCCCTCCCTG
WIR-3b	72	A G ---	---	---	TAATTTTAAATGGGGCCAATAACACAGTACTTATCTCACAGCATTTCTCTAAAGGCTAAATAAGAA GAAGT/A/GJCTATAAAGTTATTAGTCTCAGAGCCCTACACATTTCTCAGTGACTGATAAACAATAAGCA AAGCTGGGTGCTGAGATAAGA
WIR-3a	69	A T ---	---	---	TAATTTTAAATGGGGCCAATAACACAGTACTTATCTCACAGCATTTCTCTAAAGGCTAAATAAGAA GA/TJGTATCTATAAAGTTATTAGTCTCAGAGCCCTACACATTTCTCAGTGACTGATAAACAATAAGCA AAGCTGGGTGCTGAGATAAGA
WIR-4	47	T ---	---	---	GAGCCTTTCTAAAAATAAGGATTGTGACTAGCAACCTCCTGTACAGATTCCCTGCTCACACATGTGCA AGGCAGCAGCAAAATTTGCCAGCTGCC
WIR-5g	209	C ---	---	---	CGGGACAGAGAGACAGAGAGAGAGTTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCACAGCCCTGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGTCCGTGGCTCTATGGAAACACACAGG TTTTACGTCCAG
WIR-5f	196	C ---	---	---	CGGGACAGAGAGACAGAGAGAGTTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCACAGCCCTGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGTCCGTGGCTCTATGGAAACACACAGG TTTTACGTCCAG
WIR-5e	194	C ---	---	---	CGGGACAGAGAGACAGAGAGAGTTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCACAGCCCTGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAAAAAGACACAGAGAGTCCGTGGCTCTATGGAAACACACAGG TTTTACGTCCAG

WIR-5d	191 A ---	---	CGGGACAGAGACAGAGAGAGAGTTCTGCAGCATTCAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAACACACAGG TTTACGTCAG
WIR-5c	177 C ---	---	CGGGACAGAGACAGAGAGAGAGTTCTGCAGCATTCAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAACACACAGG TTTACGTCAG
WIR-5b	159 A ---	---	CGGGACAGAGACAGAGAGAGAGTTCTGCAGCATTCAAGAGGTTATTAGGACTCAGTTCTGCTG CTGTGAGNCATCCACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACTGTT AGGTTTGAAGGGAAGGCAAGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAACACAC AGTTTACGTCAG
WIR-5a	37 A G ---	---	CGGGACAGAGACAGAGAGAGAGTTCTGCAGCATTCAAGAGGTTATTAGGACTCAGTTCTGCTG CTGTGAGNCATCCACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACTGTT AGGTTTGAAGGGAAGGCAAGGTTAAAAAAGACACAGAGAGAGTCGGTGGCTCTATGGAACACAC AGTTTACGTCAG
WIR-6	63 A C ---	---	TAACCCGTGAACCTTTGCTCTCTCTCATCTCAGGGAGAACACAGACTTCATGTTAAGACCCAGAA[A/C] CGCAGCTTGGGGTGGGGCAG
WIR-7	12 C T ---	---	TTGCTGACTATT[C]TAAAGCATCTGTAGAATATTGAATACATAGTCTTGAGATTGATC
WIR-8	46 C T ---	---	GGCGTCTATGACTATCCTGGTGCATTGATTTGACTAATGATTCTG[C]TGGCCCTTG
WIR-2	56 C G ---	---	AAACAGAAAAATAGAGGTTATAAGGATGGAACTAAAGTTGTCAGAAGAGGTATGA[C]GJCTGAAG AAAGAACTTACTCTCTTTGACCAATAAATACAATTGGGAAACACTGGAAACCCATGGCTTGATTACT GACAAC
WI-7069	93 G A ---	---	TGTCCTTGCTTATGCCCTGCCTCTTTGCTTGGCAGGATGATGCTGTCATTAGTATTTCACAAGAAGTA GCTTCAGAGGGGTAACTTAACAGAGT[G]A]TCAGATCTATCTTGTCATCCCAACGTTTACATAAAA TAAGAGATCCTTTAGTGCAACCCAGTACTGACATTAGCAGCATCTTTAACACAGCCGTGTGTTCAAT GTACAGTGGTCTTTTCAGAGTGGACTTCTAGACTCACCTGTTCTCACTC
WI-18694	41 A T ---	---	GGTCATTCTCTTTTATCTGTCAGGAGCCAGCTGCTGACTTATCTCTGTTCTGTCATCTCTCCC CCACATACCAACTCTTCCACCATGATGATTATACCAATAATACAGTTCCTTATATGAGGGGCTCTGGA AAATTAGACAGTGAAG
WI-18612	37 A G TGC	CCTATATTCA AGTTTGAAA	CACACTGTTACACCTATATTTCAAGTTTGGAAATGC[A/G]TATTTGCAAGCAGCAATACAAAAAGTA TTCATGAAGMATGCATAATCTCTGAAAAATTAAGAAACATCCCT



WI-18517	87 C T	CAGGAATCAG CAGGCTGA	TGTTTGGACAA GTGCAACA	TTAAAAATCAACTAGGGCTCACCCCTCAACACCCCTCCATTTGTCAACCTCTACAGCCTGCATGCC ACAGGAATCAGCAGCCTGA[C/T]TGTGCACTTGTCCAAACACAACACTGACTGC
WI-18668	76 C T	GGCGAAAAAC TAGGCAAAAA	GCTAAATTAAA CTGCACITTTT GC	CGATTGACAACCTTTTATTTTCAACCTTAGGTAAACAGTCCAAAATCAGGTAGATTGGCGAAAACT AGGCAAAA[C/T]AGCAAAAAGTGCAGTTTAAATTTAGCAAAAGGCTCAAGACAGTATGTGGAAAGGAA GGTGAGATTTCCTCCTACT
WI-18680	75 T C A	GCTGTCACTCT AGCATCTGGA	CCTCCTGAATA TACAACGGAGC	TAAACATACGAGTACTGTACACGCAAGCATGCATCCCTGAGTCTGAGTGAGGCTGTCACTCTAGC ATCTGGAAT[C/G]CTCCGTTGTATATTCAGGAGGGA
WI-18704	99 A C	GGGTTCTCCGA GGGGTAC	TGAAGGCCCTG CTGG	CACCCAGGCTGTACCCAGGCTTTCTGTGCGAGACACACACCAAGGCGAGGTTGGGTTGAAGGAGCC CTTGAGGAAACACGGGTTCTCCGAGGGGTAC[C/G]CCAGCAGGGCCTTCAGCTTAAAGTCG
WI-18673	29 A G ---		---	TGTGGGCAACCTTGTTTAAATGCAAAAC[A/G]ACTTAAATTTACAGCACATTCAATAATGAACCAAC AGGAGAGTTGCTGACTTTGTAAACATATGAATATATAAAAAATCCCTTGCAATTCAGGTAGTCAAGGTA AAAGCGCATACAAGGAAG
WI-18640	121 T C	GTCGTGGGTG GCGG	GCAAATACCAC TGAAGAGGAC A	ACCAGTCATGTTTATTTGGAGGTTAATCCTATTAGGATATGAAAGGATTCAGCAACGATTGAGATT GTGTTCTCACGGAGGGCTCGGGCCAAAGTCTGGGGTGGGGGTGCAGAGT[C/G]GTCTCTCTC AGTGGATTTCGGGACC
WI-18533b	91 T C ---		---	GGGAGAGGAGGTAGATTGCCAAATTGAGGCAATTTTAACTCCCGAGATTTCTCTTTATTT TATATTTTCATTTTTCATCCTAA[C/T]TACTGAAGCCATTTCTTTGGTTAACTTTAGA
WI-18533a	59 T G ---		---	GGGAGAGGAGGTAGATTGCCAAATTGAGGCAATTTTAACTCCCGAGATTTCTTTGCTTTA TTTTATTTTCAATTTTCATCCTAAATTTACTGAAGCCATTTCTTTGGTTAACTTTAGA
D11734	83 A C TTC	TCATCTGATAC CTTGTTCAGAT	AACCAGGATA AGGCTACAAC ATT	GAGCATATGCTGCATGAGGACCCTTTCTATCTTACATTATGGCTGGGAATCTTACTTTTCATCTGATA CCTTGTTCAGATTT[C/A]AAATAGTTGTAGCCTTATCTGGTTTACAGATGTGAAACTTT
D49493	159 A T	CCTGAAGGAA TCTGGGAATT	ACTTTCAGGCC AGGGC	CAGGACTTGTGGTGCAGCTGCAGACACAGACACAGCTCATGGGCAACATCATCTGGGGCCAGAGAG AGCTGTCGGCCAGTGCATCATTAGGGGTCTTTCAATTGCTAGTACTAGCCCTTAAATGCCAGCCTG AGTACCTGAAGGAATCTGGGAATTT[A/T]GCCCTGGCCTGAAAGTGGCCCATCATACCCACTGTT CT
EST10030 7	98 T C	CATTTTGTTC TCTCAAGTCCC	GCAGTGGTGGT ATGGATGA	TATTTCATAGAGGAGACCTAGGAGGAGGTTGACACAGCACACTGCTCAGCAGATGACTTAAATTTT CCCTTAGCCATTTTGTCTCTCAAGTCCC[C/T]CTCATCCATACCACCCTGCTGATTG
EST10052 2	24 G A	GCTCACTTCTG GAGGCTG	TGTGGAACCTC AATCTTAGACT TC	TATTTGGCTCACTTCTGGAGGCTG[A/G]AAGTCTAAGATTGAGGTTCCACATCTTGTGAGGGCCTTC CTGTTGAGTCAATAACCTGGTGGGAAGTCAATCATGTGGCAAGAGAGAGGGCTACAGAGAGCAAGAGGAA A

EST10605 2	118 C G	---	---	CTCTCAAGTAG ATAAGAGGCA TAATCT	---	---	CTTGGCGTAATCACAGTTCTGTATTATACAAAAACITTTGTTTTCTCTGACAAACTGTACACATAGA AACAAATTTCCAAATGGACAGGAACCTTAAATTTGTGGAGATGCCCATGTC[G]TTGTGAGACTTAA AAAAAGAAAAAGATCCC
EST11048 0	61 T G	---	---	CTCTCAAGTAG ATAAGAGGCA TAATCT	---	---	CATGTGTCATCCCATGATTGAAAGACATGTTGCTCTCAAGTAGATAAGAGGCAATAATCTTT/GJAA ACAAATCTTTCTGAAATTTAGCTTATGAACTCATTACACTGCAAAACCCAGAGAAGGAGCAC
EST11260 8	101 G T	---	---	---	---	---	TATGGAGGCCAGAGGAAGTGACACTATATGTGGAAGTGTGAAAGAAATGAAGTGTCAACACAAAA TTCTATATCCAGCTAAATATCATTTAAGAAATGAAG[G]TTGGAAATGAAGGCAATATCAGATAAA
EST11349 9	109 C T	---	---	---	---	---	TTTGATGGAGAAATCCGAGGCCCTGCCAGCATCCCCACCAGTAGATTCTTTGGACGAAGAAAAATCCT TCTGTGGAATCAGCTTTACCGCCTTTCTCATCTGCTGGTGT[C]TTTCTCTCAGAGCTTTAATGTCCGT CCTGCTCTCCGAGTCAG
WI- 16632a	71 A G	---	---	CCAACTACTT TGGAGCCCT	---	---	GAATTCCTGGGTATTAAATAGCGGGTCCACAGGACACATAGGAAGAGCATCCAACTACTTTGGAG CCCT[A/G]AGGAGTTTATAGAGAAAGCTGGAGCCCGAAGACCAGTAGTAGGAGGTAGCCAGACCAA AAGGGAGGAAGGAGTGGAA
EST11772 6	74 A G	---	---	---	---	---	CCAGGAATAAAAGAAAAAGAGTCAGAGGAAACAGCTTTTGATGTTATGAGGCTGAGACACTACTC TTCTTCA[A/G]GACTATTTCATTCTGACTATAAGTGAATAAATACATTGAAGACTTCAGGAGCTCA
EST11795 3	82 G A	---	---	---	---	---	CTTGCCATTATTTTGTGCATGTTGTTCTTAAAGGCTTGAAAGATAAATTTGGAATGTGGGAAAC ACATAGATCCCAGA[G/A]TATTAAAGGGGCTGGAAAAAGTAGCCCTTAAGAC
WI-16644	42 G A	---	---	CAATAAGCAG CTCATTTTGAT TAC	---	---	AGAGCAATGGTGCATCTCAATAAGCAGCTCATTGATTAG[G/A]GGTATACATGAAGTAAATTC ATGAAGTAAATTCATTATACCAAAAAGCCCTCCACAGAACTTCATGCACCCTGAGCTATGTGAAC TGAAAAGTAACAGTGGGAT
EST12005 9	56 A G	---	---	TTGTATAATA ACACTCAGTA CAAAGTCTGT	---	---	GCCTAGTAATTCCAAAGGAACATGTTTGATAATAACACTCAGTACAAAGTCTGT[G/A]ATCCAGG AAGTGACCAGCCCCGACGTTGTGCTATGACCCCTCTGAACCTCCCATTTCCATAGTTTTTGAATC
EST12055 9	32 T C	---	---	---	---	---	GTGGAAATTTTTTATCTGTACGCTTTCC[T/C]ATTATATTATCTTGCTTGTATTTTCAGCACCC CACCCGATTTCAGGAGCTGCTTTCTAAACTGTGCCCTGTAGCTGTAAAAAGTCTTCT
EST12492 1b	95 A G	---	---	---	---	---	CCCCTAGCAAAATGACTTGGAGTTGTGTCCAAATACCAAGTTACATACTGTTGCCAAAAATTAAGCTCTC TTCCCCAGAGGCATTAACTGAGATTAT[A/G]GGAAACGCACAGCAAAATTGACGATGCAGCTTTTAA CCTTTTTA
EST12492 4	25 A G	---	---	---	---	---	ATCTTGAGGTTTCTGGGCCCTGTCTAG[A/G]AAGTGACATCTTTTACTTACCACAGGTGAGGAACCCCTAT AAAGAAACTGTGTAGAAAAAGATATCAGGTGAGACTTTTTTAAAGGGCTTCTTATCAGCTCAATAAA

EST12502 2	52 C G ---			ATACTAGGGAGAAAAACCAAACTGGAGGCAAGTCCACAGGTCACACTTGTCA[C/G]CAGCAAGTAT AAACAAAGTGGGTTTCGATGAAGAGAAAAATGCTCAGGGGAAATGACCATTTTTAAGGGCCATGTG GTCGTCAGGCGAGTTAGAGG
EST12619 8	105 T C ---			CCAGAGAAAAATTAGATGTATCGGTAAAGAAATAGGAATGCATATTTCAACTCACTGTCACAAA CAGGTGTTTATATCCCAAATGACAGTGTGCTGAGAT[C/G]GATGCATGTGGCAGACGAG
EST12620 0	67 A G ---			TTTTCTCTCTCCTTCATTATTCATTGTTCAAACACTGTCTAGTACCAACATTGTCCACCGGGC[A /G]TTGAGAATACAATATTGAAGAAGAGTCACTGCTGCCCTCTGGAAAAATCAGAGTATTGA
EST12817 9a	22 C A ---			TTGGGTTCTCCAGGATCCAG[C/A]CTCGTAGCTGATGTCATGAGGTTCTCATCCATGCTCCACGG GTTCTTGGGAGTGACCGGGATGGGAATCCATGTTGCTTTCGCTACTCCATCAGGTCATTGGC
EST12941 8	23 T A ---			TCTCAGCTTCCACCTGACCTGCA[T/A]CAACAGCCCAAGTTATTCACCAGAAATTTGTTTGGGTTTCA ATGATGTTTAGCTTTAATACACTGCACCTTGTTTG
EST12949 2a	52 A G ATACTGTT	GGCTTTAATCA TAACCTAATA	TGTGCTCCTGT GGGTCTC	AGGATTTTCATGAGGCTTTAATCATAACCTAATAACTGTAAAAACAACAC[A/G]TCTGTCACTTG CAGAGACCCACAGGGACACACATTCTCTCTCTCCTCCTCACATAGACTCTGAGGTAGGAGGTACACTGGCT AAGGAATAA
EST13067 4	104 C T ---			ATTTTTGTTTTCTTAAATGAAGCATAATAACAGTTAAAAATTTTAAATCGCTTTATACAATTGACACCAAAATGCACTA GTGTAAACCTCCCTAAATCAGTCTTCTAGGGCCACA[C/T]GGAGCAGAGCAGCTTCCCACCCAAAG CACCTCTGAAT
EST13117 6	66 A G ---			TGCTGTCTGCATCAGTCCCTTTTAAAAATTTAATCGCTTTATACAATTGACACCAAAATGCACTA [G/T]ATTTAAAGTTTACAATTTGAGAAGCTGACACGTTCCATACAGACACACCTCATTTTACTGTGC TTTACTG
EST13121 6	44 C T ---			TCTGCTTTTAAAGATTCTTCATAGCTGCTTAGGTTTGTCTTC[C/T]AGCATATTCAGCTATAATCA CCTACATTCCCTCCACAAATATTTCTGTGTGTGCGCAGGCGCAGTCTCCTCACTGCCCCATGAATAGCC AGTCTATTTCACACT
EST13226 6	74 T G ---			AACTGTTTACTAACAAAGGTGCTTTAATTTGAAAAGCATTGAGGAAATAAATTAATGAATAGTCT GGCCATT[T/G]GACTAACAGTTCTACAAATTCACATATCCGTCACCTCAGATGAGCATATACCAAG TCAGAGGAACAAAACATG
EST13230 6	72 G A AGAGACGC	GCTCAGATGTG ACAGAGA	CCGGCTCCTGT ACAGAGA	GCATCATCAGCGGCTTTTACTGAACCTTACAACTTCCGCTCAATATGCAGCTCAGATGTGAGAG ACGC[G/A]TCTCTGTACAGGAGCGGTACTGTCTCAATCCCTTGCATGCAGGTGTTTACCACAGGCA AACAGTTTACTCCACAT
EST13236 9a	70 T C TCTCAGGCT	ACAAGAGGGTT TGACAAAAGA	G	AAAGATATAAAAAACAACCTCCCATCAGTAGCAATAAAGGTTATACATTTTAAACCAGATTTTCTCAGG CCTT[C/T]TTTGGATACCTTTAGTAGTTAACTCTCTTTTGTCAAACCCCTCTTGTATATAACCA

EST13278 2a	51	A G G	CTTCACCGAA CAATATTTAG	CATATCTTGG GTGGTGAGAA	TTCCGAGAACGTTTTACAAGCTCCAAACCTTTTCACCGAACAAATATTTTAGG[A/G]ATTTGAAATTTAT TTCTGTAGTTCTCACCACCCCAAGAATATGACAGCTTG
EST13282 0	99	A T	CCACACATTTG AGTCCAAGA	GATGGAAAATTT TGAGGAAGGTT	GCTCAGTAGATGAGCAATTGACCAAAATATTTAGATAATACCTGTGGGAAAGTGCTGAAATTAAGCC TGCCTGAGAAATCCACACACATTTTCAAGTCCAAAG[A/T]AACCTTCTCCTCAAAATTTTCCATCTCCCATCAGA
EST13290 9	39	A G CTT	CAATTTTGA AGTTGGGTT	AAATCACTTCA TGGAATTTCA	AGCTCATCTGCAAGCAATTTTGAAGTTTGGGTTCTT[A/G]CTGAAATTTCCATGAAGTGATTTT TTTTCTGTGCTTAACCTCAGTTACTTAAAGACCTAAAGAGACAAAGTGATATCACATCACATATTTTGT
EST13518 2	45	C G ---	---	---	ATGTGTTGGCTTTTGG GAAACATCTCCAGTAGTATTGAGGTTAAATGATTACAGCATTTA[C/G]ACTTTTAAAAATTAACCTCA
EST13522 8a	66	A G ---	---	---	ATGTTCTCGGAGTCGTCATAGTTTAAATGACTTCTGCACCTTCTCTATAACCTTGATTG CAGGTTGGTGATTTCAACTAGGAGCTATTTTGGCCCCCATCCCCACCCGCGAGTGCTGGAGAC[A/
EST13568 6	69	T C ---	---	---	G[GT]TTTGAATTGTCACAACTGCGAGAGGTGGTGCTACTTGGAAATCACTGGGTAGAGGCCA CTTTAAGGAAGTGAGCCAGATGAATCCAAATGACCAACCTGGTTGAGAGCCATTGGTCTAGGAGTAGA
EST13785 0	101	C G ---	---	---	AA[T/C]GCACACAAAGGAATAAGGGAGAGGAGGTTTCGGTTAGTTGAGGGAGAGAAAGTTGGAAGCA TTTCAAGCTAAGTAAATGGT
EST14038 1	25	A G ---	---	---	AAGATTACGGACCATAAGAACTGCCCCCGACCCACCCATACACACACAAATTTATAGCAGGTAAACCAA CTGAAAGGAACAAAGTAATGACTTTCTTTGAACAA[A/C]GTGATTACGAAAGTGAAAGGCTACAGGG
EST14083 7	23	A G ---	---	---	TGATTACTA CCTCAACCATCTGTACCCGAGCC[C/G]CAGTGACCCGGGACTTGTGCTTCCCCATCCAGGCCCTCT
EST14221 5	42	T C	GCATGCTAGA CAGAGGCATT	AAATATTTTT AAAAGA	CCTATCAGCATCCGCTAAGGTCAGTCAGCAGGTG CAATGGTGTCATGTGAACATATA[G]ACCTATTTCATAAAAGTTAAAAATAATCCCTTCTTGCATCA
EST14812 2	50	A G ATA	CAAGTCAGCTT CTACATTCTGA	TAAAGATTTAC TTAAATCCCAT TATGTACT	CAGTGCAAAAGGCATGAGGGTGAAAGTCATCTGTCTAAATGACCCGAACAGGAGGTAGGAGG AATATCAATGCATTCTTGTGGCATGCTAGACAGAGGCATT[A/T]TTTGAAGATCTTTTAAAAAT
EST14815 3	128	A T	CATACCCACC ATACTGGTT	CGGGAANAACA GTACCGGAA	ATTTTGACTTGTCCCCCTTCACACTCATTTTAAATTTGT TTCACITTAGTACCAAGGATGCCCTTCAAGTCAGCTTCTACATTTCTGAATA[G]AGTACATAATGGG ATTTAAGTAAATCTTTAGAAAGTCCCGGAGTTTGCCTTTTCTAACATTTTTCATATCAGGTGAAAAACAAT
					TTTTTCATATGGGTGATT TTTGTCTGGCAATACATAGTGGCAATGCAGCGTGAGTTGGCGCGCTCTCCCCACTGAACCCAGTAAT
					TCACCAGACAATGGCGCACCACCTTAAATAAACTTGGCCGTCATCACCCACCACCTACTGGTT[A/T]TTCG
					GGTACTGTTTCCCGTA

EST15420 6	109 C A ---			---	TTTAAACCCAAAGACATTGTAGATGTCAGGACTCCGATCATTTTCTCTGCCTATAGCTTGGATATCTTA ATCTCTCCCTTTTGTCATATAATCATATAGCCAAAGGACTC/A/GGAATTTTGGCTGCTTCAAGTCA TTCCAAACCTCTCAGG
EST15700 6	48 G C GGA	GAAGACAA AGACAACAGA	GGATAGCTGA AACAGAGATA TTATTCTC		GTCACCAGCACATTTTATTAGACGTGAAAAGACAAAGACACAGAGGA/GC/AGACAGAGAAATAA TCTCTGTTTCAGCTATTCCAGGATGTTATGCCAATTATCCAGAGTCTTGATCTGATGTAGTA
WI-16739	57 G A CACAAGC	GGTTTGCCAT G A CACAAGC	GATAGTTGATG TTCATTATCC CTATAA		AAGGATTGAAAACATACCTAGATCATATAAAATTTGTGAAGGTTTGCCATCACAAAGC/G/ATTTATAG GGAATAATGAACATCAACTATCTACAGCTAAACCTAATGAAGACCAAAATTCCTCCAAAGGT
WI-16782	96 C T CACTGTAAGG TC	GGTGGAGTCT CACTGTAAGG TC	CTTCTATCTTT CTGTTCTCTCA TC		CTTCTCTCTCTAGACGTGGAATACACACGGATACAGTATCTGGAGATGTAGCAGCTGGCTCTTGAC CATAATGGTGGGAGTCTCACTGTAAAGG/C/T/GATGGAGGAACAGAAAGATAGAAGAAGTTTGGGGT GCTGATGAAATGTGGGG
WI-16783	64 A G G	TCCTGAGATGT CTTTACCTGA	CTGCTTGGTTC AATCCTTATTA G		AAAAATGTAAACCTTAGAGGTTGCTCTTTTGTGTACATTTTCTCTGAGATGCTTTTACCTGAG/A/G/ CTAATAAGGATTGAACCAAGCAGTATTTTTTAAATGGCAAAAGTCCAGATGTAACTCGAGT
EST15948 2	58 T C ---			---	CAGGACTTAAGGTCAATTTTGCCTGGAAAGACTTAACTAAAGGTGAGGGCAACATAGGAT/C/TGTGA CAGCACACTGGACCAAGGAGTGTGAAATCGTCACACTAGCGTGCCAGCCCTTTTTCCTGGC TGCTCGCTCCAGAGC
EST16088 8	89 G C ---			---	GGTTTGAAGACGCAGCTTATCTCCACCTGCCACTGGGATCTCATTTTGAGAGCTGTTTGTGACGOC TTTTCCAGAAAGGCCGCTC/G/C/GGGTTTTCTGAACCTCTATGGGCATTTTAGAAT
EST16089 9	96 C T ---			---	CGTCTGAAGTTTTTCTTTATCACAAGTCAATCAATCCCTCGGGCCCTGCTCAATGCCACCTCTTC CTGAAAGCCATCCCTAAGTAGTCTC/C/T/AAAGAGCCATCCCTGCCCTTCTTTGCT
EST16100 1	24 C G ---			---	ATCCAGCTGTGAAGGGACAGAGAG/C/G/GTAAACACAGTCCATTATAAGGGGTGTGCACATTCCCA GGGGCTCCAAATATGCAACATTGTTTCACTCGTCCATGCTGCTGATAGTTTCATAGTAAAAAAGTC ACTCCAGACAGGTGGCTC
EST16104 9a	83 A G ---			---	TTCTTTAAATAACCCACAGACACCCATGACACTTCCAAATTTACAGAGCAAAAAAGTGATTGTCAG CTGGTCTCCAGGGA/G/TTGGCCCCGAAGCTGGCTCAGTTCACCTCCAGGACCTCAGTC
EST16118 0b	119 T C ---			---	ATGGTAAACAAATCAGTTCAGGTTTTTTCTGAACAAATGATCCTTTGGCTTTCCCGTGGCATG CTCCTAAACAACTAAACAAACCCCTCTACGTCTAATCAGTCAACCTAAGATA/T/C/CGAGTGGCAAGT CTTTCACA
EST16118 0a	32 C G ---			---	ATGGTAAACAAATCAGTTCAGGTTTTTTT/C/G/TTGAACAAATGATCCTTTGGTCTTTCCCGTGGC ATGCTCCTAAACAACTAAACAAACCCCTCTACGTCTAATCAGTCAACCTAAGATATCGAGTGGCAAGT CTTTCACA

EST16151 2	53 C T ---			AGCCAAATCAAACGAACCTCTATCAAAACACACAAAGGCCTAGAGGAGAGATTAC/TAATGAACGT AAATAATTCAAGGCAATTTTGTATCTAAAGCATTTTGTCTAGCTCTACAAAGGCATGAATGAGGTGT GGTCACGTTTTGTATAGGA
EST16182 6	54 G A ---			CATTGGTTGGTAGGGAAGATAGTAGTGCAATAAAATGTTAAACAGCAG/G/AJAATGGAA TTATAGCTTTCTTTTCATATAGGAATTGAAATTTATTACTGAGGTGATAGGCAGAGTAGTA
EST16183 2b	59 A G ---			GCAGGTAACACTGTGGTTCACACAGTATTGTTCTTTTCATAAAGAAAGAAATATCTAGTTG/A/GJTAG AGGAAGGCACCTGTCTCTGCGCCCTCTCTGTTTCATATTTTATGTCACTGTCTCAACGTGGGCCGTGT GCAAGAGATCTTTGAGA
EST16198 4a	28 G A ---			AATCTTAGGCTCTTGGCTTTCAAATCA/G/ATTACAGACAGATAAGAGCTTTAAGTATTTCCGCAATTT CCCCAGAGGAAAAGTCAGCATCATAAACACATGGTCCACATGCTCACGCACATGGTGTGTC
EST16229 2c	52 T C ---			TGTGAACCTCGAATTCGCTTGTCCAAAGTCTGAGTCACAGTTTCA/TTT/JTGGAGTCCCTGTGCAGCC CTTGCCAGTTTCCACGAGGAGGAGGATCTCCACTAGCTGATTTCAGACAGGCAGAGGCTGCA
EST16229 2b	45 T C ---			TGTGAACCTCGAATTCGCTTGTCCAAAGTCTGAGTCACAGTTTCA/TTT/JTGGAGTCCCTGTGCAGCC CTTGCCAGTTTCCACGAGGAGGAGGATCTCCACTAGCTGATTTCAGACAGGCAGAGGCTGCA
WI-16816	124 A G TGGGGTTA	GGAGCCATTGT	GCCTAGATTTT GTTCAGGACAG	CAGACTTTCTCACAACCTCATTGGCTGGAAGTGGTGCACATGCGTCACTATTCATTTGAGCA AGGGAATGGTGCATCAAAATGCTTAAGGCCAAGCAGGAGCCATTGTTGGGTTA/A/GJACTGTCC TGAACAAATCTAGGCTC
EST16269 5b	49 G A ---			GCCACTCTCTGTGGCTGTCTCTGTCCAGCTGCTGCCAGTGCACAG/G/ATGGTCTAGCCTCATGG CAGAAAGCATTTTAGCCAACTCTGTGGTCTGCTCCACTCTCTTCTTCCGCCGCTGGGGCTCACCACC TCTTCTCTCTCAATC
WI-16824b	83 G A ---			GTCACCCAGCCCAATGCTTCAGGAATAAATGATGGTGTGCAGCTGTTGTTTATGAAGAAGTCAG AAGCTGATAAACGTGG/G/AJCTTACACCTTTAGCACGGATAGTTTCTGTTCCCAAGTGGGTGTGGA GCCTTCCATTATGGGAATA
WI-16824a	47 T C CAGCTGT	TGATGGTGGCTG	CAGCTTCTGAC TTCTTTCATAAG AA	GTCACCCAGCCCAATGCTTCAGGAATAAATGATGGTGTGCAGCTGTTGTTTATGAAGAAGTC AGAAAGCTGATAAACGTGGGCTTACACCTTTAGCACGGATAGTTTCTGTTCCCAAGTGGGTGTGAGC CTTCCATTATGGGAATA
EST16445 3	96 T C ---			TTGCTTTTATTAATCCAGAACGGCATGTACAGATACTGTACAGCATGAACATTTTATTATTACAAA AATGGCTTCCAAACCATTAATAATGAACTTT/CJGGAAATAGAGCATAAACGGAACAGTAACATCA
WI-16857	47 G A A	CAAATAAGCA GCTAATGGCA	TGTGAATTGGG AAGACCCT	TATAATCCATCCTCCAAACACACACAAATAAGCAGCTAATGGCAAT/G/AJCTAGTGGTCTTCCCAA TTCAAGACCTGTGCTTCAATTTTCTGATAAATGAGGAGAAATCTGCTCTTTATGTA

WI-16879	79	C T	GATACAGCC ATATTTCCCA	CAAGGCTTCT AGAACTAGAGT CC	AGACAGGTCAAACTCCTAGGGATAAAGATATAAATCCAGCACAGCATATTTCAGATACAG GCCATATTTCCCA/C/TATAGGACTCTAGTTCTAGAAAGCCTTGGGAGAACAGGCCACCCAG
WI-16882	99	A G	GAAATGCCA CGTCTCTGAC	GACACATGTCA GGTAAATCGC	ACATGAATGGCAACCTCTAGGTGGGAGAACAAATCTCCCCCTTTACCCCAAGGTTACTCTGAC AAGGCTATGAATGAAATGCCACGTCTCTGAC/A/GGCGATTTACCTGACATGTGTCATCTCCCT
WI-16888	70	G A	GCTAACTTTGG GCAGGTTT	AATGTTCTGAA TTGACCAAAAT TAA	GTAGTAAATGTTTCATCACTACCCGGGGAGAGCAAGAACCATGGAACGGTAGCTAACTTTGGGCAGG TTC[G/A]TTAAATTTGGTCAATTCAGAACATTTCCAAAT
WI-16905	75	C T	ACTTGGCTGT GTTGTTCA	GTCTACTCT TCTAGGCAGTG GG	TTTGTGTTGTTATTTGGCTCCCAACATCAGAACATAAAGTTCCATGAAAACAGGAACCTTGGCCTGTG TTGTTCA/C/TCCCACTGCCTAGAGAGATAGACA
WI-16910	74	G A	AAGAGTAAAG ATGGCGCTAG	CAAAATGAAG TATCGTTTCTA TAACAGA	AGTTTCAGTATGTGCTTAAGGAGGTTATATTCGCTATGACTTTTCATCTCAGAAAGATAAGATGGCG CTAGAA[G/A]GTATCTGTTATAGAAACGATACTTCAATTTGGGCTGAACCACTGAAGGT
WI-16918	93	C T	CAGCCATTAA CACCAGCAC	TCCTGATACAG AAGTGGCATC	GGAAAGAAAAATAAACTACCACCATTTCTCTGCTACACAGAGCACTAAATCTAGGAATTTGAC TTTACTGCAGCCATTAAACACAGCAC/C/TGATGCCACTTCTGTATCAGGAACCTTAACTGACAAACC ATGAAAGGTCCTCTGAAAG
WI-16947b	127	A C	GGAAAGCAGA CCTGGGG	ATGTGATTGCC CGTGG	TGAGTCAAAACGATCTTGACGGGAAGCTGTTAGAGGTTCTCATGGAAATAGGCCTGGAGCACAGGATT TGGCTGAGGCTTTCAACTGACATCAGACAAGACTGCAATCAAGGGAAAGCAGACCTGGGG/A/C/CCA CGGGCAATCACATGAGATG
WI-16947a	58	C G	CATGGAATA GGCCTGGAG	GCCTCAGCCAA ATCCTGT	TGAGTCAAAACGATCTTGACGGGAAGCTGTTAGAGGTTCTCATGGAAATAGGCCTGGAG/C/GJACAGG ATTTGGCTGAGGCTTTCAACTGACATCAGACAAGACTGCAATCAAGGGAAAGCAGACCTGGGGACCA CGGGCAATCACATGAGATG
WI-16966	43	T C	AAATGCACAC TACATAACAA CCTAA	TGCAAGTTATC AGTATAAAAA CTCATATT	CATTTGTTTACTTTAAATGCACACTACATAACAACCTAATA/T/CJTTAACTTGGTCCAATTTT AGTATAACTAATATGAGTTTTTATACGTATACTTGCAATGGCAATGCAATTTAA
WI-16995	55	T C	GAGCAGTAGA GACTGAGGTA	CATGTTGATTT CCAGCGGT	TTGAGTGCCAGACATCAAGCATAGAAGAGCAGTAGAGACTGAGGTAATAGTATT/CJACGGCTGG AAATCAACATGCCTCTTCTGTGAAGTTGTGAGCTGAGGCTGAGAGGCTGAGTCAATCT
WI-16992b	60	T G	---	---	AAATACATGGTGTCAACCTCAGCTAAGCAGCCAGAAAGTACACTGT/CJCCCTCATCTGAGATGTG TAGGACTGTAAAGGAATGTGTTTGGGGTTTAGGAA
WI-16992a	46	G A	AAGCACCAG AAGTACACTG TC	CACATTCCTT ACAGTCTACA C	AAATACATGGTGTCAACCTCAGCTAAGCAGCCAGAAAGTACACTGT/CJCCCTCATCTGAGATGTG TAGGACTGTAAAGGAATGTGTTTGGGGTTTAGGAA

WI-17010	23	T C	TTCAACAGGA	AATAACGGT	ATGTTTCAACAGGAAAGCCATGTC/JATGACATTCAAACACCCGTAATTATTAGAAAGCTCATTTAAT
EST17127	74	C T	AAAGCCATG	CA	GGTIOCCAGC
9b			CACTCGGCAC	GGGAGGCGAGG	ATTCCGCTCTCAACAGCATCCAGGCCGGGCATCTCCCCACGATTTTATAATACACTCGGCACAGA
			AGACAGAGT	GGTG	CAGAGTTC/JTJGGGAGCCATGGGGCACCCCTGCCCTCCCCAGGCTTCCCTAAGTAACAACCT
			AATTCCTTAT	GGACTATGGCT	CACGCGTTTCATTAATTTGGTACAAAGCATGAACACTCAGGACAGATTGGCACAATACATGCAGTTC
WI-17040	94	T C A	CATCTCAAGCC	TATTCAGTGAT	GAGAAATCTCTTATCATCTCAAGCCAGTTC/JCATCACTGAATAAGCCCATAGTCCAGTCTCGTTTCC
			G	G	AAATCTTTCATATGT
			GCCAAGGGAT		TTGTTTGGTTTGGTTTCTCCTCCTGCCAAGGGATTAAAGTATAGGTC/JTCTTAAACAAGGGGATC
			TAACGTATAG	GGGATCCCT	CCCCACTTATAGCTGACAGCAGCAGCTGCAACCACTGACTCTCCTGCAGAATGGCAGGGAATCGAAT
WI-17044	47	G T G		TGTTTAAGA	CAAAAGAAAGCAAGTG
			TGGACTTGTCA		GCATGTGTGGAGCAGATCTCCATGGTAAGCCAAAAGTGGACTTGTGAGCCTATAACTACTCT/JA/G
WI-17021	62	T A ACTC	GCCTATAACT	TGTAGAGTTAG	CAGCTGCCACTAACTCTACAGGCACAGTAACACTTTATACAGGAGCACATGCCAAAGTGCCTGG
			ACTC	TGGCAGCTGC	GAGGTGCCAATAAAATCAA
			CCAGAAAGGA		
WI-17065	90	T C CTT	AAAGCATAAA	CCCAAGAGAG	TGTAAAAATGTAGACATGGGGAAAAAACATTCGTAAATCAACATGTGCTGTTTCTACTTCCGGTA
			CTT	AATGAATCCT	CCAGAAAGGAAAGCATAAACTTTC/JAGGATTTCATTGCTCTGGGT
			TGTACAGCCA	GAGATGTTGAA	
			ACATCACTGTT	AATGTTCTGGA	TTCATAAGGTTGTACAGCCCAACATCACTGTTT/JCJATCCAGAACATTTTCAACATCTCAAAAAGA
WI-17066	32	A C T		A	AACTCTGCACCCATTAGCAGTCACTCCCTGTAGCTTCCCTCATAGGCAATGGCAACTGCTGATC
WI-17074	86	T G ---		---	TGCTGACTGTCATGACTTAGTAAGGCCATCACAGTTGCCAGAACATCTACTCAACTGTTCCAGCAT
WI-					AACTCTCTACACAGGCCJTT/JCTACATAGGAGTATATTTGGCCAAAGACTCACTAGGAGTGATT
17104b	108	T C ---		---	CAGATGAGAACTCATGCTGGCTCATCTGCAAGCTTCTGATGCTTTGCGAGCTTTCCCATTCATTCCA
					AAATCAGAAAGCAGTCAGTGGCCCCGGTTCAGACGGCTTC/JTCTCTTTGTTAAGAAATTA
WI-					AGCGTCCAACAGATGTTCCATCAAGGACTTTGTTTTC/JGTCTCTCTCACTCTGCTATTTATAATAC
17114a	37	T C	TTCCATCAAG	ATAGCAGATG	AAGTACCTCCCAAGGCCAGATGCTCTAAGTGCTAAAGAAAGACTGCAGCCACAATCAGAGTTACAT
			GACTTTGTTT	AAGAGAC	GGGA
			GATGAAATTC	TTCTCAGAATC	
			AGATAGTCTTC	CTGGAAGATAT	CGTGGCTGGACTAAGTGCTCTTTCCATGTGGACACATCTCCACTGAACAGGATGAATTCAGATAGTC
WI-17150	76	T G CTCIT	CTCIT	G	TTCTCTTT/JGICATATCTCCAGGATCTGAGAAAGGCCCTCTTTGCTGCTCTAATTT
			CATTTCITTTGT		GAAATCGAATACGTCCATTTCTTTGTAATAACAATAACGTTT/JGJAGGCAAAAAGCAAGATTCTG
			AAAATAACAA	CAGAATCTTGC	TAAACCAACATTGGAAAGGGGACACAGGGGAGGGGAGGAAAGGCCAGATTTCACCGTTT
WI-17163	43	A/G TAACGTT		TTTGCCTT	CCTCCACATCTGCAGACAAA



WI-17178	127	T C	GGACTCCTCA TGAGGAGC	CCCTCAATTTT CAACTGCTTC	AGCAATGTCCCTCCCAATTCATTAGCTATGATGGAGTTATCAGTTTCATTTTCAGAGCGAATTACTGG GGCAGGGGGTTTAATATCCTGTGGGTTTAATTCAGTGAGGACTCCCTCATGAGGAGCT/CJAGAA GCAGTTGAAATGAGGG
WI-17180b	81	C G	---	---	TCATGGACATCCTGAAGCAGACACAAAAATATAGAGAAATCCTGCACIT/CJCCCAAGTCTCGTCGCA GCITCAACAAATTAC/CJ/AACATCTTGCCCAATTTGTTTCATTATCCGCACCCACACTGACAGATGAG GGAGTC
WI-17180a	47	T C	CACAAAAATA TAGAGAATCC TGCA	TGGACGAGAC TTGGG	TCATGGACATCCTGAAGCAGACACAAAAATATAGAGAAATCCTGCACIT/CJCCCAAGTCTCGTCGCA CAGGCTTCAACAATTACCAACATCTTGCCCAATTTGTTTCATTATCCGCACCCACACTGACAGATGAG GGAGTC
WI-17156	54	G C	TGTTCTCTAAA CTTTAGATATC TCCCA	CAAGAAATAT ATATTTGATTC TGTGGAA	TGAGGTAGCAGGGCATTCTTAAGAAATGTTCTCTAAACTTAGATATCTCCCAT/CJTTCCACAGA ATCAAAATATATATTTCTTGTTGGAAATTTAAATGTTCTTAACATCTGCCTACCATCCACCTCAAT TAATATCTTG
WI-17149b	79	T C	---	---	CAGGCAGTTAATGTGCTGACATAGTAACAAGGTTTGAAGGAGGAACATCTCATGCACGTGCGTGGAA ACCCAAATGTCAIT/CJGTGTATGAACACAAAAGGATGGGAAAGAACACATTTCTCACA
WI-17149a	48	C G	CAAGTTTGA AGGAGGAACA	CCACGACGTG CATGA	CAGGCAGTTAATGTGCTGACATAGTAACAAGGTTTGAAGGAGGAACAT/CJTCATGCACGTGCGTG GAAACCAATGTCAITGIGTGAACACTACAAAAGGATGGGAAAGAACACATTTCTCACA
WI-17197	67	G A	GCAGAAAGTAG CTGGGGCTAC	GGTGAGTGGT GCATACC	ATTTGCTATGTTGCCTGGCTGGACTCCAGCAATCCTCCTGCCTCAGCAGAAGTAGTGGGGTAC/G /AJGATGACACCACTCACCTGCTATCAGTTTCGTTTAAAGAAATTTAGATTTTGTAGATGGCA
WI-17198	38	A C	TCCCCTTTGTC CCTAGTTT	TCCATTTGTC ACTGAGAAAT	TGATTTTCAGTAGCTTTCTCCTCCCTGTCCTAGTTT/CJTAATTTCTCAGTGGACAAATGGACAA ACCATCTCTGTTTGAATTTGAATACACAGATACATGCAAGATATCTTACAAGAAACAATGCACATCC TTC
EST18753	27	C T	CTACCCAGGCT GGTCTCAT	GGATCGCATGA GCCTGA	TCGCTATGCTACCCAGGCTGGTCTCAT/CJTCAGGCTCATGCGATCCTCCTGCCTCTGCAGTGGCTGG GATAAGACACAACCTGCCACCGGCTGCCCTAGGAGTAGTCTTAATGCCTGATGGTGGG
WI-17108b	74	C T	GCCATTCAGTC TCAAAAGTAAA CA	AACATCGATTT ATCATATGCTC CC	TTATTTTAAACATAACCAAGATGCACCTTGGTTTTTACATTTCTGTTGCCATTCAGTCTCAAGT AAACAC/CJ/JGGGAGCATATGATAAATCGTAGTTTAAAGGAAGCCATAGCATTACAGAGT
EST19067	41	A G	---	---	ACACAAAATTTACCATCGTGACCATTTAAGGGTATAGTTCA/JG/JGTGGCATTAAGTACATTCAACT TTTTGAGCAACCCGCCCATCCATTTCATCATCTCCGTT
EST19067	40	A C	CGTGACCATTT AAGGGTATAG TTC	AAAAATTGAA TGTAATTAATG OCA	ACACAAAATTTACCATCGTGACCATTTAAGGGTATAGTTTC/JC/JAGTGGCATTAAGTACATTCAACT TTTTGAGCAACCCGCCCATCCATTTCATCATCTCCGTT
EST19125	28	A G	---	---	CTGTTTCTCAGAGATGACACTGCCAACAJ/JG/JTCACAGATTTGCATACAATACAGTTATGTATTGGC TATTCACAAATTACAGTAGTGTTTTTCTCTGAAAAA

EST20824 8	115	T G	AGTCGGGAGT GCTGATTG	AAGATTTTATC TTGGACCCGA	GTGTGAAGCGGAGTTTATTATTCAATCAGTCTCTCTGAAAACTCAGGGATTGAGGTTTTTA AGGATAACTTGGTGAGTAGAGGGCCAGTAAGTCGGGAGTGCTGATTGTTGTTCTCGGGTCCAGATAAA ATCTTAGG
WI-17347	50	A G	ATCCTCAGAA CTTCTCAGCCT	TCAAGCATCCA CTTGTGCTA	TTGGTTAAATGATGCCAGATGGGTGCACATCTCTCAGAACTTCTCAGCCTAGTGTAGCACAAGTGG ATGCTTGAAGAACTCAGTCTTGGAACTCAGACAGCAATGGAGCGGATGTGAGTGGGACCA
EST21904 b	128	G A	TTCATATGGCC ATTTTAATAA GTG	GGCAGGTGTTT AGAAAGCAT	TGATTGTGGTCTGGGAGCAGGTGGGCGAGTTTCTAGTGAGGAGCAGAGGAAAGTAGACGCAGTAGAAAT GAGACTGGAATCAATAGAACAGAAAAATGTACTAGGCTTTCATATGGCCATTTTATAAAGTG[G/A]TA TGCTTTCTGAACACCTGCC
EST22111 3	82	T C	GAAGATCTGT CTGGCAATCTT	TGGAAAAACA GCCCCAC	CAAAACAATGTAGACATAAGGGAACAAATTCAGAGAGCTCAAGTCACCATGTTTGTCTAAGAGAAGAT CTGCTGGCAATCTTTTTCGTGGGCTGTTTTCGAAGGCACA
EST22197 2	78	T C	AATTATCTGC TATTCCTGCCA	ACCATGAAGG ATGCGGT	GTTTAAATGATCACTCACCAAAATCCACAGGAGAACTCTTAAATGTTTACAAGCACCAATTTATCTGCT ATTCTGCGCAATTCAGCCGCATCCTTCATGGTAGAGTATCACAAAGTAAAAGTTTCTGGTTGTTTCATC TACTTAAACCA
EST22311 9c	92	T C	---	---	TTTTTCCATGGATTAGATCATCTTTTATTGAGTTATAATATACATAAAAAATCCACCACCTGTAAACAG TAGCAATTCATGGTTTTTACTCTATTCGTCAAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACTTCATCATCCAG
EST22311 9b	54	A G	---	---	TTTTTCCATGGATTAGATCATCTTTTATTGAGTTATAATATACATAAAAAATCCACCACCTGTAAACAG CAGTAGCAATTCATGGTTTTTACTCTATTCGTCAAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACTTCATCATCCAG
EST22311 9a	41	T C	GGATTAGATC ATCTTTTATT GAGTTATAA	TTGAATGCTAC TGTTTACAGTG G	TTTTTCCATGGATTAGATCATCTTTTATTGAGTTATAATTCACATAAAAAATCCACCACCTGTAAACAG CAGTAGCAATTCATGGTTTTTACTCTATTCGTCAAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACTTCATCATCCAG
EST22319	19	A C	---	---	TCGAGGAGCTCTGAGGAGGACACCAAGGGACGTGTGTCCAGGGCCACCGTGCAGGCAAGTGTG GTCCAACTCCTCCTCCCTTTACAAAACCTCCAGCCTCACCCACACAAAACACTGGCTGACAGGCCCTCT TAAGCCTTTTAACTGT
EST22433 c	103	A G	AAGACATGTT CACCAAGTGA AA	CAGCTTCAGCT TAAGTGACAGA AGTTTCAGTTT	GATGTTAATGACTTTCTTTGAGATATGATGGAAAAATATTCCAGGTACACATGGAAAAAGACATGTT CACCAAGTGAACCAATCTAACCAAGAAAGCTTTACCAGTTCTGTGAGTTAAGCTGAAGCTGAAAT CTGGGAGCTTGACATGCTG
EST22657 9	71	A G	AAATGGATCC TTATCTGCACA	GCATGAATTTT T	TATCCATTTCAAGAAAAAAATGACCTAAAAAATACAAATCTATCCAGAAATGGATCCTTATCTG CACAAGCTTGAAGAAAAAAATTCATGCAAACTGAAACTATGCTTT

EST22993 5b	71 T C	ATCCTTTTGT TCTACCC	TTGCTGTAA TTTGACTGAA TG	GCCTTTTATGCTCCTTTTAAACATCAAAATGTTTATAACACACACTTGATCCTTTTGTCTACCCCCA ATT/C/CATTACAGTCAAAATTACAGGCAATATAATAGGTCTAACAGAAATGCTTGCAATTT
EST23021 0	108 T A	---	---	TTATTTCTCAGCTTACCATTGCTGACTTATATCTGTACAAGGTTGTTTTCTCCATGGAGAAATG TTAAATCTTTGTGAGGTTAATTTTATTAATCTTTGCCTT/AJATGGTTTTGACAGTTTGTGCTTTCT T
WI-17387	55 C G	CCTTGCAGAT TGAAGAAAAA	GCCTTTGCCTA AGATTAATAGT AACTACT	ACAGAAATTTAACATGCAAGTTTCATTACATTACCTTTGCAGATTGAAGAAAAA[C/G]AATATTAG TAGTTACTATTAACTTAGGCAAAAAGCCATTTCTTTG
EST23669 1	101 A C	AATGTAAGCT CCAGAGGCAG	CTTCCCTCC TGTAAGC	TTTTTGGCTGTCTGCAGATAGATGAAAAGAGAAAATATACCCAGATACTTTGCTCACTCTCCCA AGTGACACACTAGGCAATGTAAAGCTCCAGAGGCAG[C/G]CTTACAGAGGGGAAGGACGCTGAGGC CAAGAGTGTGGCTCACTG
EST23733 9	31 T G	GGCTGTAGTT TTGTTTTGTT	TGCACCTTTAA TCCCATCAAT	AAAGGCTGTAGTTTGTGTTTTTCTTTTCTT/GJTATTGATGGGATTTAAAGTGCAATATAACTGAAG GCAAAGTCCAAAGGCTAGAGAAAGATATGAGGCCGAGAGAGAGGCTCAGAGATTCTAGAGGGCGC TGAAGAATACCCACCTAAA
WI-17470	83 A G	GTCCCGTCCG CCAG	CCAGTGACGAG GOOGA	CTGACACGTCCTGTGTGCGGGGTGCTCCATGTGCGTGTGTGAGTGAGACTTTTTTACTGCGTCCC GTCCCGCCAGCCCTT/GJTCGGCCTCGTCACTGGCCTTGGTCACTTTGTATTCTGTCTTGGTTGGAAA TACCATCAGCCTTCC
WI-17519	55 T C A	GTGTCTAGC TAATGAATGC	AATTATTATT TGCAGGCAATA CTC	TTTTTAAACGAAATCTCACTACTGCAAAATGCATTTGTCTCTAGCTAAATGAATGCAIT/CJAGAGTATTG CCTGCAAAATAATAATTGAGATTCTATTTTAAAGAGCTTAGAACAGTACATGGTGCAATAG
EST25356 3b	95 C G	---	---	TCTTTGATACAGGTAAACCAGTTTGTGTAACATTATTCAGAACTTCACTGTATCTTCAAGTTTTTGTAT CAGCATCTCTGTGGAGAAAGCAGTGTG[C/G]TATAATGICAAACATCAGGATTTCTTTTT
EST25356 3a	26 A C	---	---	TCTTTGATACAGGTAAACCAGTTTGTGTAACATTATTCAGAACTTCACTGTATCTTCAAGTTTTTGA TATCAGCATCTCTGTGGAGAAAGCAGTGTGCTATAATGTCAACATCAGGATTTCTTTTT
WI-17581c	99 C T	---	---	GGGTGACGCTCCAGAAATGGGAGACAAAGCCAAATTTGGAGCAGATTGGATCCAGCTTCATCAACATT ACTACCAGTTATTGATAATGATAGAACCCAA[C/T]TAGGCGCAATTTACATTGACGCGTCATGC
WI-17581b	86 T C	ATTCAACATT ACTACCAGTT ATTGATAA	CGTCAATGTAA ATTGCGCT	GGGTGACGCTCCAGAAATGGGAGACAAAGCCAAATTTGGGAGCAGATTGGATCCAGCTTCATCAACATT ACTACCAGTTATTGATAATGATAGAACCCAACTAGGCGCAATTTACATTGACGCGTCATGC
WI-17596	86 A G C	ACTTCCCTGTG TAAACACTCG	CATTCCTATAG CTAGAAATCGA CAATAT	GTGTGCTGGTAAATGGATAATAGCAGTCTCTCATCTCTGAAAGGGTGGGAAGTAGGAGAAAGGCCCTACT TCCCTGTGTAACACTCCCA[G]ATATTGTGATTTCTAGCTATAAGAAATGGGCGCCACTAAGTGGGTC

WI-17623	46 T C ...			---	TGTGGTTTAAATTTCCCATATAATTAATGTTGGGCACATT/CJGCATGTGCTTACTGGGTC ATTATATATCTTTTGTGAAGCATCTGCTCCATCTTTTGCCTGACTTTGGAGTTTTTGGT
EST26419 1b				---	ATTTATACAGAGATACAAAGGCAACTATGTGCAGCAACAATCTGAT/CJGGGCAGTCCAAACTTCT TGGGAGGAAGTAAATTCATGTTAAATGTCTATGATGGCTGGTTCGAGGAGAGGTTCAAAGGAGGTAG AGAGAGGAGACAGAGAATG
EST26419 1a		ATACAAAGGC AACTATGTGC		CAAGAAGTTTG GACTGOC	ATTTATACAGAGATACAAAGGCAACTATGTGCAG/CJAAACAATCTGATGGCAGTCCAAACTTCT TGGGAGGAAGTAAATTCATGTTAAATGTCTATGATGGCTGGTTCGAGGAGAGGTTCAAAGGAGGTAG AGAGAGGAGACAGAGAATG
EST26780				---	TCAGCTTTAATTTAAGGGACATGTAAATAAAAGATGCATTTGACAGGACAGCAGACTAGTTCAAGC AG/CJAGGTTAGACCAGTAACAACAACCAAGAAAGCAAGTCTGCTTCCATCTTTGGCTTTACCA CACTTACAACTGATACCC
EST26900 7				---	TACTCAGTTTAAGGCAAAATCCACACAGAGACTGTCTCJAGJGAGACGGGCACAGAACACACACC GTAGAAACACCACCACCATGTCATGACGGGGAAGCAGAG
EST27152 1				---	CAAAGGATTTTATTTTTCCTTAAAGTAAATCTAGAAAATAGCAACCCACTGCAGAGAGAGTT CTATACTAAACATTTTCAATCATCTCTCTTCT/CJTTTACATGGTGTACTCTTTTCATGTACACAT CATCGAAACACAGACTGA
EST27504 0a		GCACCTTGCAA CAATTTAATA ATT		GCTGGTGTGAT GCTACTGTAT G	TTTTGCACCTTGCAACAATTTAATAATTTATC/GJAJCATTACAGTAGCATCACACCAGCAGTCAAT AATGCCACTTTAGGCAAAAGTCTTTTCAGTATTTCTGTTACACATCTGTTAAACAAGAACCCATACATT GGTAAATTCATCT
EST27662 4		CACATTCTGTT CTCCAGTCTTG		TTATGGAATG GCTTATGTAAC C	ATCTTAAAGGACCATAGAAAAGGCCAGTCACATTTCTGTTCTCCAGTCTTG/CJTAGGTTACATAAG CCATTTCCATAAATCTATAGCCTTCTTCTTAGAGTAACACACACTCTTGTTTAGGAATGTTG
EST27788 3				---	ATTTTATTAGCGGTACAAATTCOAAGGTGGTAAGGTGAAAGGAAAGGCGAGGCGCAAAATACAT TATTGAGCTGAAAACAACTTTACATTTCAAGGACJAGJGCTTCCAGACAAGCCATGTAGAACCAGCAT GCCTTGGGACTGTGTGGAT
EST27828 4		GGAAGTCATC AGAACCCAC		GTGCAGAGAGG TACTCCAAGTA C	TCCTCTAAACTTTCTTCTGTGGATCCCAGTGACGTGGAGAGTCATCAGAACCCACJGJAGTACTT GGAGTACCTCTCTGCACCAAGATAGCTGGCTGATTTTCTGCTCAGTCACAATTTTACTTGAA
WI-18369		AATAAAATTC AATCTGTCAC ACAATC		TCAAGAAGGCC TTATCCATT	TAAAAATTTGAGATACATTTCCCAATGTAAACAATAAATTTCAATCTGTACACAATCJGAJAAATG GATAAGGCTTCTTGACAAATTTCTGCCACCTCCGTTTAAACGCATCAGAACTCAATCTTATCTC
EST28036 4				---	TCCCGCTCCAAAGCTTTATTGGCAATATGCTCTAT/CJAAAAAAGATGATCAATCTGTTGCCCTCT AAGTCAATGGAATGAAGAGCTGTGTCCAGGGACACACCACCGCTGCTGAAGGAGACTGCTGTTGTG TCCACCTTTATTCATAG

EST28483 7	31 T A	GGAGTAAAG GTGTTCTTCT TAAAA	TTTCTGCATT TATTTTATAC CA	CATTTGGAGTAAAGGTGTTCTTCTTTAAATTAATGATGGTATAAAATAATGCGAGAAACATTAAC GGAGATGTACAGACAACAGACGAGACATGAGTTGTTTCTGACTGTGACACATTTGGTGAAA
WI-17724	50 T C	TGGGOCCTOOC TGTC	TGGGTTGGCAG TGTOC	AGAAATGGTCTAGTAATCGTTACAGATTTCGGTGATGGCCCTCCCTGCTGTC/CJGGGACACTGCCAACCC CACAGCTGGAGGGGCACTTAAGGCACGTCATTTTGATTAGA
WI-17730b	68 T C	---	---	TGAGCCTGGGAGAAAGACACAGAGTGAAGTGCTATTAGTTACATCATACCAAGTGATACATACTG TTT/CJACATGATTTATGGCTGTTGATGTTGACCTCAATAACCTGGCTGATGTAGTATGTGCA
WI-17730a	39 A C	GACCACAGAA GTGAAGTGCT ATT	TCAACAGCCAT AAATCATGTG	TGAGCCTGGGAGAAAGACACAGAAAGTGAAGTGCTATT/CJGTTACATCATACCAAGTGATACATA CTGTTACATGATTTATGGCTGTTGATGTTGACCTCAATAACCTGGCTGATGTAGTATGTGCA
EST29041 5b	53 G A	GGAACAAACA CATTAAAGCAT CA	GGTATTGTTGA TTTGAGGAGTT AGC	TACTCAGAAATGTGAGTTTCATGAGGAACAAACACATTAAGCATCATTTGTCACCTG/AJGCTAACTCCT CAAATCAACAATACCCCTTATTTTAGCCATGAAAAAC
EST29128 4	58 A G	---	---	CTTTTAGAAGGACACACAGCTCTGTTGGACTTAGGGCTACCCCTATTCACGAGGTGCCJAGJTATTT TCACITGGTTACGCTGTGAAGGACCGTTTCCAAATGAGGTTACAGTCACAGGTTCTGAGCAGACATGA GTTTTGCTGGGGACACT
EST29912 3	103 C T	TCTGCCAGCTT ACAGGCT	GCGTAAGTGTC TCATTTCTCTG T	ATTTATTAGGTATCTGCTGTTGGGGTGGGGAGGATTGTTGAGATACTGCAACAGACACAAA AGCAAAGAAAGAAACATTTCTGCCAGCTTACAGGCT/CJACAGAAAGATGAGACACTTACGCATG GCCATGATACACAGCAGTGA
EST29936 8	121 G C	---	---	TATTTGGTATGCTTAGGGAAGATCTGATTTAGAGATATTAAATCTTTAAAGTTAACTCACCATGAAA TTTAACTTCTGACTGGCTTCACTGATGAGGCACTAACTACATAGGGATAAAJG/CJAGCTCAGTA TCTGGAATCATGCTTCCTG
EST30223 2	99 A G	---	---	AAATAAATACATCATGGGGAATGGGATATCCATCCCTCAAGCATTTATCTTTGAGTTACAAGCAA TCCAATTAACACTCTAAGTTATTTTAAATTTCCJAGJGGATTTAATTTCTTCTAGTTCAATCTTGGGA GG
WI-16260b	86 G A	---	---	CTTTTCCATTGGTATTAACCTGCTAGAGGTTCTTTTGAGGTGGATTCAAGAAAGAAAGACCCAGA GTTTCACAATATAGGTAGC/GJATAACCAAGGCTCACTTTCCCTCCGTGAGAACTTCGTGGGAC
WI-16260a	59 G T	TGAGGTGGATT CAAGAAGAAA A	CTACCTATATT GTGAAACTCTG GGT	CTTTTCCATTGGTATTAACCTGCTAGAGGTTCTTTTGAGGTGGATTCAAGAAAGAAAGJG/JACCC AGAGITTCACAATATAGGTAGCGATAACCAAGGCTCACTTTCCCTTCGGTGGAGAACTTCGTGGGAC
WI-17835	30 G A	ACAGGAAATA TTGTGCTTTCT TG	TGGGGTATAGG AAACAGGC	AAGAGAAACAGGAAATATTGCTTTCTTG/GJAGCCTGTTTCTTACCCCAATATCATAGAAAT GTTGTTGCTTCTATAATGTTGAGCTTCAAAATCTTTTGTCTTAATCAATCCAAATGAATTACCTGAAT TTCTCCTCTTGTTCAAAA

EST31951 4	87 C T	GGGTGTCCAG CCAACA	CCCAACAAAAT CACCTCC	ACAGCCATTATTATGTTTACTTGGTAATATCAGAGACTGAAACATTTTCACTCTTTTAGCAATGACA TCGGGTGTCCAGCCAACA/C/TGGAGGTGATTTGGTGGGAATTTCTTATCACAAATATTCT
EST31968 8b	95 T G	---	---	CGAATTTGCTCTCTTATTGTTGATTCTAGTAATCCTAAAGATTTGGGGGGCGGGTTACTATAAGT GCATTTTATAATGGGATTTCTGCTT/GJAACCTGCCCACTGATCTTACATGGGAAAGGTGCAAG ACAGTGGTACTGCTCCC
EST31968 8a	75 T C T	GCGGTTACTA TAAGTGCATTT T	TGTAAGAAATCA GTGGGCAGTT	CGAATTTGCTCTCTTATTGTTGATTCTAGTAATCCTAAAGATTTGGGGGGCGGGTTACTATAAGT GCATTTT/CJATAATGGGATTTTCTGCTTAACCTGCCCACTGATCTTACATGGGAAAGGTGCAAG ACAGTGGTACTGCTCCC
EST32063 2	103 C T	---	---	TCCATGGATGAACAGACGCTACCATGCCACATCCCACTCCCACTCCCGACCAAGATGCTGGGCCAGAGC TGGCTTCCCTTCCAGACCTAGCTGGCTTTGTAGT/C/TGTTCCAGGCCCACTGAAATAGCAAAACGCAC AGTCATGTAGCACTCGG
WI-16303	65 A G	---	---	AAGGCTTTCCAAGCATTCAAAGGCACTTGGGTGTTGTGCTCTAAGTTTCTGGTCACTGCAGCCCCC[A/G TCTGTATTAGGGAGCACCCCAAGCCCAAGTAACTATGTTCTTGCAAG
WI-17800	29 C G	GGGAGCAAA GAGAACTCA	TTTCCTACAAT TAATCCAGTC TT	TGGACATGGGAGCACAAAGAGAACTCACT/C/GJAAGACTGGGATTAATTGTAGGAATATTTACACAG TTTCCACAAGTCAGAAAGAGACTAATCCCAACCCTCTGTATCTGGAACATACACTGCTGCCATTTTCTGC CCATGAAGGGAAATAGCC
WI-17857	34 T G C	CCTAAAGTCTG GGATGACTTTC G C	TGGCTTAGGT TCTACTTTGATG T	AAACTGTCACTTCTAAAGTCTGGGATGACTTTCC/T/GIATCTACATCAAGTAGAAGCACTAAGCCAA TCAGAATCAGAATCCTTTTGTCCATCAAAATCCAGCTAACTCCCAAGCTGAATTAATGTTCAATCT GTATCTGATGTAGTTAACCATGGCCTGTCATGATTATATTGCTATAAGGAAGGGAAACAAAATCTTTA TAGTGTCCAAAGATAATTAAATCTTGTTTAAATCTTTGCCAGCAAGCAATA/T/AJCCGACTGAC TGCTCCTTAGTCTGTGATC
WI-17860	121 T A	TTTGCAGCAA AGCAAATA	ACTAAGGAGC AGTCAGTCGG	CAGCAACCTTTTTTTTGTATAGCCTACTCTCAAAATTTGT/T/AJTTTGTGATTAGTGACAACG GGGGAATCTACAATGCTCAGATCAGAGTAACTACCA
WI-17866	43 A T	TTTATAGCCT ACTTCTCAA ATTGTT	CCGTTGTCCT AATCACAAA A	GAAAAAAAAGTCAAATGTGTTCCCTTTATGGGTGATGCCACCATGATTGCCTCACACAAGCATGATC AATGCCACGAGA/G/AJACTGGATGCCAAAGAGATGG
EST33301 4c	80 G A	---	---	GAAAAAAAAGTCAAATGTGTTCCCTTTATGGGTGATGCCACCATGATTGCCTCACACAAGCAT[G/A] ATCAATCGCCACGAGAGACTGGATGCCAAAGAGATGG
EST33301 4b	63 G A	---	---	CTATCCAAAGATATTTATGCAGCGTGGTTTTCAATACTAAACA[G/AJGTAAACAATGCAANTATT TAACAATAATACAGTGATTAATAAGCCATGGCATATCCAGTTGATGTAATACTTTTGCAA
EST33460 1	44 G A C A	AGCGTGGTTTT CAATACTAAA CA	CTGTATTTATT GTTAAATATTT GCATTGTT	

WI-17904	50 A	AAAGCATGAC AATAAAATGA ACAC	CGCTTATGTTA ATAGTAATTCC CG	CAAGTGAATATTGATACATGGCTGACAAAGCATGACAATAAAATGAACACAGTACGGGAATTAC TATTAACATAAGCGATAACATCAAAACATCTGGTAAATGCAGTTAAACACAACACAAATGA
EST34149 5	69 A	TGCCAAATAC TCAAGTGTGA GAT	AACTACTAGCG AGAACAACTA ATAAAATC	GTTTTTCTTTGAGTGACACAAGCTTGTTCATTTTGAGAAAATGTGCGCAATACTCAAGTGTGAA TJAGJGATTTTATTAGTTGTTCTCGCTAGTAGTTTGGTATTCTATGAAAAAAGCAGCTAGTTTCAGC TTACAAATCACACAAGT
EST34343 8	95 C	---	---	TGGGAAACATAAGTTAACTCAAGAATAATTCAGTCTTTATGTTACTAAACATTGTAATAGTGT TTTTATCAATGATGCCGAGGTCACTGCTCJAJTACAAAGATTAAAGAAACTTACCATCAACACACTTC CAGTGCATCAA
WI-17982	98 C	GGACCATATG ATATATAACT CCTAAAGC	CAGAAATTATG TGATAATAACT CCTTCC	GGTACACAAATTTTAAATGGAAGGAACACACAGGTATGTTGAAAGAACATCAGTACAGCTGGAGACAGG GAGGGACCATATGATATATAACTCCTAAAGCJCTJGGAAGGAGTTATTATCACATAAATTTCTGGGC GCTACAGAAGTTTTTCATCA
WI-17993	118 A	---	---	CTCAGTAACCTCGGTGTTAATCTGCCATTTATTGATTTATTATGATAAAACAACTCTCATTTGTA AAACAGCTAAGGTGACATCTCCAGACCCCACTGTCCTGTATGJAJCJCTGCTGAGAGTCC ACATTTTGGAAATCCAAAT
WI-17996	84 A	GTAGAGGCGA AGGGAACAG	AGGCACATGGG CAGC	CCCATCCAGAAACCCAGTGTGATGTTGGAGGAGCATGAAACACATCTCCCAGGCCCTCGCAGT AGAGGGAAGGGAACAGJAGJGCTGCCCATGTGCTGTCTCTAAAGACGCCACCTCAGGTTGATGT CACCTGTGGAGACCGGGT
WI-17136	33 C	---	---	ATTCTTTATAAAACACCATGTCCCTAAATGTJGJATTCAACATATATGCACACCTTCGATGTAT AGGACACTGATCAAAAAGACAGAGAAATGTGTCCT
WI-18041	24 A	---	---	GCCACTGAAAAAGGTGCTCTTCCJAJCJGTTTCTAACTCCCTGGACTCCCTCATTTGGAACGAAAGCTC ACAGATGTTTCAGCTGGACTAGTTTAGACTTTGCTGTATTTTAAAGGCAGTGTGATGCTCCAGGAT TCAAACTACTTAATCA
EST35164 8a	57 A	CACAGCCCTGC OCC	CCCTCTGGATT CTGAATCTCAA	TTGAACCAAGGCCCTAACAGATGACTCAGCAGGGCCCTTCAAGCACAGCCCTGCCCCQJAJGJCTTGA GATTCAGAAATCCAGAGGGTGCAGTCCCTGGTTAGGTGCTTCTGTGACATTTCTCTTG
WI-18052b	67 A	---	---	AGCGAATGAAAAATGCTACATAGGCTCCCTGAGTCTTTTATGTACGAATCTTGGTTACACATCTTAGJ AJACAGCAGAGCTGCCTGAGGGAGGGTGTGTTTAAATGTCGTATGCTATGCTCAGCACAGTGTGCTGGC ATGGCCCATCCATGCTTT
WI-18052a	50 T	CCTGAGTTCTT TCATGTACGA ATC	CTCAGGCAGCT CTGCTGT	AGCGAATGAAAAATGCTACATAGGCTCCCTGAGTCTTTTATGTACGAATCTTCTGGTTACACATCTT AGAACAGCAGAGCTGCCTGAGGGAGGGTGTGTTTAAATGTCGTATGCTATGCTCAGCACAGTGTGCTGGC ATGGCCCATCCATGCTTT
WI-18054	46 G	GGGAGTGGGG A.GAGTAAAA	CGTCACCCCTGC TTCCA	CTGTTGTGCTGAGAACAGAGGGGTCAAGGGAGTGGGGAGTAAAJAJTGGAAAGCAGGGTGAAGC CATGCAGGAGTCCAGACAAAAGACGGGTGATTTTGCTCAGGTTGGTAGCAACAGAGGTAATG

WI-18064	54	G A	GTAGCTGCTA AGCTGTATTTC	CCAGTGGTATG ATTGTGACATT C	CAGCTGCCAATCATCTCTCAACCCCTGTGGTAGCTGCTAAGCTGTATTTTCAGA[G/A]GAATGTACAC AATCATACCACCTGGGAGAAAGAGTAAGCACAGTGTCTATTAGGTGCCAACTGGGGTACCTGGGAG GCAGAAA
EST35347 2	97	T C A A	GCATAAAATT TTCCAGTTGGT	CCCTCGGCAAC TGCT	TTTAGCACCATTCTTAGTGGAGCAGGATCTTGATCATGGGTGGAATTTTGTATCTGGGCTTCAT GGGATGCATAAAATTTCCAGTTGGTAAGT[C/J]AGCAGGTGCCGAGGTCTGGATCAGAAAAAAGG CAGGCA
WI-18070	28	A C	AACCCACTAC TTACTCAGAGT GTGTAT	AAAACTAATA AGAACTGGA GGTTTT	AAACCCACTACTACTCAGAGTGTGTAT[C/J]ATATTACACATGAAAGATATAATCTTAGAAAAA ACCTCCAGTTCTTATTAGTTTGTATTTTCTGTACTCAGAAGCATTTTAGGTTGCAAGGATATAA
WI-18080c	80	C T	---	---	TGGCATAAAGTTTGCAATATCAATATCAAACTAGTCTCTCTTTGTAATTAATCTACTATGCCGTG TTTGACTTTTAT[C/J]TCTTATGTAAATTGAAGCCAAATGCATGTTAATCCTTCTCCTTTGGTGAT
WI-18080b	65	G A	---	---	TGGCATAAAGTTTGCAATATCAATATCAAACTAGTCTCTCTTTGTAATTAATCTACTATGCC[G/ A]TGTGTGACTTTTATCTCTTATGTAAATTGAAGCCAAATGCATGTTAATCCTTCTCCTTTGGTGAT
WI-18080a	41	T C	GCAAATATCA ATATCAAACT AGTCTCTC	CAATTTACATA AGAGATAAAA GTCAAACA	TGGCATAAAGTTTGCAATATCAATATCAAACTAGTCTCT[C/J]TTGTAATTAATCTACTATATGC CGTGTGACTTTTATCTCTTATGTAAATTGAAGCCAAATGCATGTTAATCCTTCTCCTTTGGTGAT
WI-18086	63	G A	---	---	GTGGGCATCCTATAAAGCAGCCATGTGTTGAACAAATGATATGCACAGAAAGCATACTCT[G/A] TGGCTTTGTTACACGGGTTTCTTTCAAGAGGAAGATGACTCAGCCCTCCAGCTTCTGCAGTCTAGC TTAGGAGAGGTGTTTGA
WI-18115b	71	C T	---	---	AACTACATAGTATGGTGGCTTAGAATCAATGGGTAAAGCCCTTTAGTGACCTTTGGTATCCC TT[C/J]TTTGGTATGAAAGACAGACCTCTGCTGGAGGACTCATTAACAATGTAAGAAAGGGTGAG TCAGT
WI-18115a	70	C T	TTAGTGTAACCT TTGGTATCCC TT	AGAGGTCTGTC TTTCATACCAA A	AACTACATAGTATGGTGGCTTAGAATCAATGGGTAAAGCCCTTTAGTGACCTTTGGTATCCC TT[C/J]TTTGGTATGAAAGACAGACCTCTGCTGGAGGACTCATTAACAATGTAAGAAAGGGTGAG TCAGT
WI-18136	78	A G	---	---	TTTTGAGAAGCACTCTGTAAAGCAAGGATGCATTCAAAAATGGCTTTGAGGATTAATCTTCTCTTA GGTAATTTTGC[J/A]GTAAGAACATAAAAGCATTTTAAAGTCCACTGCCGCTTAGAAACT
WI-18169	115	A G	CCATCTTCCG	GAGTCTGCTT	GGCAAAATATTTTACATCACACCTGGAATCTGCCCAAGTCTTCCACTATGAAGGCAATCGTAGAG TGTGCAGGAGGAAAGGTATTATCCAAAGCAGCCATCTTCCGGAAGCTC[J/A]JTTGGAGCACAAAGCAGA ACTCGTGGGTAGTGA
WI-18190b	26	G A	GAAGCTC	GTGCTCCA	TGAAAGAGTCGACACAGCGGACACT[G/A]JTCATAAGTGGAAACAAAGGATGAAGCTAATCATGGAG GCAAGCTCCCTGGAGAGACAGGGACAAAATCAAGNAATGAGCTGGAGACATTAATCTCTGGCGA



WI-18190	62 G A	---	---	TGAAAGAGTCGACACAGCGGACACTGTCAATAGTGGAAACAAAGGATGAAGTAATCATGGA[G/A] GCAAGCTCCCTGGAGAGACAGGGACAAAATCAAGATGAGCTGGAGACATTAACTCCTGGCGA
WI-18181	100 A C	AAATATATAC AACACTCCCTT CAGATC	CGTTTACCAT TTGTTAAGCTT TTG	GACAGTGAACACATTGAAACACACAAATACAAACAAACATTAGGAACAAGAAATGTGTAATCCAA TGTGTGAAACAAATATATACACACTCCCTTCAGATC[A/C]CAAAAGCTTAAACAAATGGTAAACCGTA TGTTCTCTTGAAC
WI-18215	78 G A	AGCAGAGTTC CTGCCCTC	CCTCCCTCTCT OCCCC	ATTACATCAAGCATTTCTGAGTACAACTAGGGACAGGTATTTACAAAAACAATAGAGCAGA GTTCTGCCCTC[G/A]GTGTGCGGGGGAGAGAGGGGATTACGCAATTTGGTGGAGTATGTTAATT CCCTCAAGTTAATTCCTC
WI-18232	60 T A	TGTTGTTGATT GTGATACACTT	AAATAAAGGT TTTCAGGGGTT C	CATTTCCGAAATCTGATAGTTAAATATCCCGTCTGGTGTGATTGTGATACACTTAAGT[A]GAA CCCTGAAACCTTTATTTTGAATGAAGTTTTGCTCAGAAACTGGGCAGAACTTTTCACATTCTG AC
WI-17892	76 T C	GGAAACTTG AGTTTGAGATC ACA	CACAGAAGTG AATAGACTAGT GAGACA	TTAAAAATGCTTAGATTTCTCTCAGTATTTATCAATAGTGTGAAGCTGGAAAACTTGAGTTTGAG ATCACATA[T/C]CTGTCTCACTAGTCTATTCACTTCTGTGGCATTTCCGGCAGAAAGTGGC
WI-18242	30 G A	CCCCAAATGTT AATCGTAACA	GCTAACACTTC TACTGTAACAG CTTTC	AATATCCCCAAATGTTAATCGTAACATACT[G/A]GAAAGCTGTTACAGTAGAAGTGTAGCAAAAAT TGGATGCCACAACCTATCTCACCATTCTTCAAGCAAGTGGGGTCAAGTATGTTCTTGCCTATATC TGCAAAAGATCGAACAAAG
WI-18266c	119 C T	---	---	GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAGAAATGAAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACTGCACAAATGATGCATGAATCCACAT[T/C]TGAGAC CCGCAACTCCGAGGTACCT
WI-18266b	124 T C	---	---	GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAGAAATGAAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACTGCACAAATGATGCATGAATCCACAT[T/C]TGAGAC CCGCAACTCCGAGGTACCT
WI-18266a	97 C T	AAATAGGAAA TATGGACTATC TTCAAA	TTTCATGCATCA TTTGTGCA	GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAGAAATGAAAAAGTGTGCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACTGCACAAATGATGCATGAATCCACATTTGAGAC CCGCAACTCCGAGGTACCT
WI-18312	73 A G	GCTGTCAGCTA TTGTTATTTC	GGAGAAAAGG GAGCAGAAGA	CTGAGCCTCTGGATATGTGTTAGTGTCTATCATTAATTTGGAAAGCTGTACGCTATTGTTATTC AAAT[A/G]TATCTCTGCTCCCTTTCTCCTTTCTGGGATTCATTCIGCATGTTTATA
WI-18330b	66 A G	---	---	AAACATCTACAGCTGTCTTAGGCCATCCTGTAAAGAAATCAGGATAAGAGCTGAGGAACAAGAGGGI A/GTATGTAGGCAGTGAGTCAGGACTATGCAAAACCATAAAATAAAGAACATAATTTTTTTGTTGAT TCACA

WI-18330a	49	G A A A G A	TCCTGTAAAG AATCAGGGAT	AGTCTGACTC ACTGCTACA	AAACATCTACAGCTGTCTTAGGCCATCCTGTAGAAATCAGGGATAAGA[G/A]CTGAGGAAACAAGA GGGATATGTAGGCAGTGAGTCAGGACTATGCAAAACCATAAATAAAGAACATAATTTTTTTTGTGAT TCACA
EST37564 5	85	T C A G A	AAATTC AAGC CATCTACAAA	CTATGGAGGC TCAATGAGA	AAATTAGTTAGCCATAACAGGCTGGAAATGCTGGTTAGATACTGCATGTTATTTAAGCTAAAATTC AAGCCATCTACAAAAGAT[C/T]CTCATTTAGGCTCCATAGGCTGCAAAACACATCAAAGGCATTAC TGTACTGGAGAGGACTGAG
WI-18327	104	G A T T	AACAGCTTT CGTTAGGCTAG	CGCATACAATG GCTCAGC	CAAAGGGATTTTATTACCTACAACAAGTAAGGAGGACAGCTGGGGCAGTTTCCCAAAGCAGTACCTC CCAAACAATGGTGAACACAGCTTCGTTAGGCTAGTT[G/A]GCTGAGCCATTGTATGCGGAGGCAGA GT
EST37624 6b	102	G A ---		---	GTGGCAAGAGCAGCTAAACACACACTCATTTTGCATGAACCTCCAAATACGAACAGTGCA[C/Γ]GCTGA TGGCTGCAGTCCTCTGCGGTGCTTGGCTCTCTGGACGGTTCACTTACATGGCTGCTTTGCGTCC TCTGACCTCCCCATTCC
EST37624 6a	58	C T ---		---	GTGGCAAGAGCAGCTAAACACACACTCATTTTGCATGAACCTCCAAATACGAACAGTGCA[C/Γ]GCTGA TGGCTGCAGTCCTCTGCGGTGCTTGGCTCTCTGGACGGTTCACTTACATGGCTGCTTTGCGTCC TCTGACCTCCCCATTCC
WI-18357	89	C G	CCAGCCCTTA GCATCAA	AAGACTCAA AGACTGAAGAT GA	AATGTTTTAAAGTCCTACCGTGCAGGTGGCCATGAAGCCCAAGCCCATGGAGAGACATTTTCA TAATCCAGCCCTTAGCATAA[C/G]TCATCTTCAGTCTTTGAGTCTTCCAGCCAGGTCCAAAGCTT GTGACCAAGAGACAAGCC
WI-18012g	117	A G ---		---	TTTTATCTGGGTCAAGCTCCTCTTAATGGCCTGAAGGTCACTCCTTTCAACTTTCCAGACTTGGAAAG ATCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGGCCCTTC[G/A]TGAAGTGTTCCTGATACA CGCTGACGTTTCGAGGG
WI-18012f	113	G A ---		---	TTTTATCTGGGTCAAGCTCCTCTTAATGGCCTGAAGGTCACTCCTTTCAACTTTCCAGACTTGGAAAG ATCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGGCCCTTC[G/A]TGAAGTGTTCCTGATACA CGCTGACGTTTCGAGGG
WI-18012e	112	C T C C C T T	GCCACTTTTGC CCCTT	TCAGCGTGTAT CAGGAAACA	TTTTATCTGGGTCAAGCTCCTCTTAATGGCCTGAAGGTCACTCCTTTCAACTTTCCAGACTTGGAAAG ATCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGGCCCTTC[G/Γ]GTGAAGTGTTCCTGATACA CGCTGACGTTTCGAGGG
WI-18012b	46	T C ---		---	TTTTATCTGGGTCAAGCTCCTCTTAATGGCCTGAAGGTCACTCCTTTCAACTTTCCAGACTTGGAAAG AGATCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGGCCCTTCGTGAAGTGTTCCTGATACAC GCTGACGTTTCGAGGG
EST38390 4	75	A G C T C T G C A T T G	GCAAAAAGGA GCTCTGCATTG	GCTAAAGTCAG CTGATTAATAA ACTTAA	CATATCATAGCCAGATCTACACCCACAGAGTAATCCCATGGTTATGTTACATGGCAAAAAGGACTC TGCAATTGTA/G/ATTAAGTTTATTAATCAGCTGACTTTAGCATTTGGGAGATTATCTGGAT

EST38512 7	91 T	TGACGATGCC AATACTTCG	CACTGCACTCT GGGAAGC	TAATAAAACTGACCCCAATTGGTAAACTGTGCTGGACTGAGAGAAACAATGAAAAATCTGTAAAT ACCTGATGACGATGCCAATACCTCGT/G/GCTTCCAGAGTGCAGTGATAACTGTTATAGCC
EST38519 0	24 C T T	CCTGCACCTCC TAAAAGATCT	TCTGTTAGGAC TTGGGGA	CCTGCACCTCCTAAAGATCTTTT/C/TTCCTCCCAAGTCTAACAGAATGGTATATCTCTCGAAAA AGATGAACGTCATCAATGGATTGCTGCTCTCTGCTTTGAGTTTTTTTGTCTTGAGAACCTTG TCCTCCCTGCTGATTT
EST38575 1	66 T C A A	GAACATCCCA TGTTTCTGTTT	AGGGAAGGTA GTATAACACAT	AGTGGTCAAAATGTAATAACTAATGGGACACCAAGCCTCAGGAAGAACATCCCATGTTTCTGTTTAA T/CJTCTCTTATGTGTATATACTACCTTCCCTTTCTCTTTCTTATACACATAGATTTCCCTTAATTGCAGC CCA
EST38616 9	101 C G C T T C	CCTGCTCCGCC CTTC	GAGGAATGGAT GGTGGC	CCATCTAGGAGGCTACCTGAGCTCTCTGTGCTCCAGAGTGGTGCCTACGCCGGGGCCCCGTGG AGTCTCCGGGGCCCCGCCCTGCTCCGCCCTT/C/G/GCCACCATCCATTCCTCCAGGGG
EST38652 8	59 T C C A T T T C A A	TCTGAACCTGGG C A T T T C A A	TTGCAAAAATG AAAGGAAAAA	TATAGTAGGTACTTTCTTGTCTGCAGCAGGAATATTACGTCTGAACTGGGCATTTCAA/T/CJGCGTG GTATTTTTTCTCTTCATTTTGCAAGTAAAAAATCAT
EST38654 5	42 T C G T T T T A C A	AATGGTCAATTT TAATATATCA	CAGTGATGGTC CTTAATCTTCT	CTCAAGCTGAGAATGGTCATTTTAAATATATCAGTTTTACATA/T/CJAGATAGAAGATTAAAGGACCAT CACTGAGGTACATAGCTCAGAGGCAGAGTTAAGATTGGACCCAGGAGTTGGTTCAGCATATA
EST38707 9	75 A G ---		ATC	GGATCCTCACTCACCTGGGACAGCCTGAGAAGGGACATCCACCAAGACCTACTGATCTGGAGTCCCA CGTTCCCC/A/GJAGGCCAGCGGGATGTGTGCCCTCTCTCCCAACTCATCTTTTCAGGAACACGAGG ATCTTGCTTTCTGGAAA
EST38759 2	86 A G G G T A T G G	TGCTCCCTGA GGTGATATGG	TCACCATCGTG GACTTAAGG	TGACCTTGATTTCTCACTAGAGGGGAGAAGATCACCTACCTTTTGGATGCCCTCCCACTCTACTTGT CTCCCTGAGGTGATAGG/A/GJCTTAAGTCCACGATGGTGACCTAAACTCAGTTTAAAAATTTTGCC TAGCAGCACC
EST38775 1	40 T A C	AATCAATAGG AGAGGATTGG	GGCTTTGCTCT GAATTCAAA	GACTCTCAACCAAGAGAAAAATCAATAGGAGAGGATTGGC/T/AJTTGAATTCAGAGCAAAAGCCCT CTTACTGAGAGGTGAGCCCAAGCCCTCCAAATGCCCTTTTCATGAGTTAGGATCTCCTAAGTGGTAC AAACAAACCAACATGGTGG
EST38815 4	91 C A C A	TGTTTATGAGA ACCCATTACA	GCTGACTGGCA CATGCTTT	CACCCCATATTTGACCAAGGGATGAAGCCTAGCCATGCTCTTTCACTTATGTGTCTTCAACAAG TGTTTATGAGAACCATTACACA/C/A/AAAGCATGTGCCAGTCAGCAGATTCTGTAATAA
EST38858 4	98 C T T G A C	CACGAGTAAA AAGAAAAC TCA	GGAGCGAGTCC AAGGAGAA	TCCTTACTGTGCTTACAACCTTCTCCCAAGTTTGGGGTGTTCATATTTGTTATTGTTATTATTA TTCAACACGAGTAAAAAGAAACTCATGAC/C/TJTTCTCCTTGACTCGCTCCTCTCCCCCAATCTCGAT ACCGACTGCACTGTG
EST38865 2	72 T C T G T G T G A T T	GCTGTAGAATT TGTGTGATGC	GGAAGGACGG AGGACACAG	CCTTAATGGATTTTACAGCTCATCTGAGTCTCTGCTGTGTTCTCTGAGGAGCTGTAGAATTTGTGTG ATGCT/CJCTGTGCTCTCCGTCCTTCCCCAAATGAGCACATATGAGGGCAGGCAAGAGCATGCTGGA TTTGCTTAGTTGTTAA

EST38878 9	47 T C	AAACATCATT ACTAGCCTAG ATCCTAA	CCTTCAATAAA TCTCATGTCCT CA	CCAAATGAGAACCAAGTAATTAACATCATTACTAGCCTAGATCCCTAAAT/CITGAGGACATGAGATTT ATTGAAGGGAAATCCTCAATTAATATGAACATTTCTTGAGAAATGGGAAATTTGAAACATTCCTCC TTATTCATGTCAATCTCACACATTCCTTTATTTATTTGTTTACATTTCTCAAAATATCGGATTTGTC TCATGAGAATAATGGCTGAGGGAGCTGGCAGGCAGTCTTCTCA/GC/GCTCCCTGGATAGCTAAAT TTA
EST38882 6b	113 G C	---	---	TTATTCATGTCAATCTCACACATTCCTTTATTTATTTATTTGTTTACATTTCTCAAAATATCGGATTTG TGCTCATGAGAATAATGGCTGAGGGAGCTGGCAGGCAGTCTTCTCAGGCTCCTGGATAGCTAAAT TA
EST38882 6a	35 T C	TGTCATCTCAC ACATTCCTTAT TTTT	CGATATTTGAG AAAGTGAAAA CAA	TTATTCATGTCAATCTCACACATTCCTTTATTTATTTATTTGTTTACATTTCTCAAAATATCGGATTTG TGCTCATGAGAATAATGGCTGAGGGAGCTGGCAGGCAGTCTTCTCAGGCTCCTGGATAGCTAAAT TA
EST38909 5	47 A G	GCACAGCATG GCTAAAACG	GGTATTTGTG ATTCCCATCTT T	GCACATAACTAATCTTTCATTTGTGGATTGCACAGCATGGCTAAAACG/A/GTTAAAGATGGGAATCAA CAAATACCATTGAAGATATGGAGCAAGAGAACTCTCACATACTGCTGGAGGGAATATAAAT AACTGAATGGCAGTGAAACACTACACATCAAACTTAGGAAATGTGGTTAGTGTGGTACGTTGAG GGAACTTTATAACCTCAC/A/GC/GCTTTGTTTCACAAAACAAACAGCAGACACAGAGATTTCCAACTC CAGCAATGACAGGCTAGGG
EST38911 9	85 A G	GTTGAGGGAA ACTTATAACCT CAC	TGTTGTTTTGT GAAACAAGCG	TAAACATTCCTTGAATCCCTTGGTGGG/GC/GGGGGGGGGTGGATTGAGATTCAGTGTCAAGATAAA TATCACAATAATATCAAAACCTTCAAATTTGCTATGCTATGCAATTCACACACTGACATGAGCCACAACAT CCTTCACAGGGACTGTAC
EST38955 5	30 G C	TGAATTCCTT GGTGG	CACGTGCAATCT CACCCC	CCTGCTATGATGCTGGGAGATCCCGGACCTTCGGTGAC/G/A/CAGGCTCCCTGCCAGGGCTTGG CCCCGACCGGGCTCCCCAGCTCGGCCCTGACTGTGGAGGAGCTGAAATACGCTGACATCCGCAACCT C
EST39002 0	42 G A	GGACCTTCGG TGACC	CTGGCAGGGAG CTG	CACGTGGCCCTAAGTTTCGGGTCTTCCTCAGTCTGGATGGCTGTGGAAAAAGCTTGGTGGTAAG GCCTAAGGAAT/GAGGGGCGAGGGGCGATGCCGCCAGCCGAGATGGTCTGTAAAGCCTGTGGGTC AAAGACCTAACTTCTGGA
EST39004 8	79 T G	GGTGGTAAGG CCTAAGGAAT	ATCTCGGCTGG CGC	AAAGATAATGTGCATCACACGCAACATATAGAAACATAAAAGAAAAATAAGTATCCACCCTAAAA CCCTATTATTCCATGATATTTTCA/T/C/JAGCAACTAGTATATATCAATATATATTTTTCACAAACCAT TCAGTTACAC
WI-16398	90 T C	TCCCTATTATT CCATGATATTT TCA	GAATGGTTGT GAAAAATATA TTGATAT	GGTTGTCTTTTCATGATTTTCTCATTTCTCATCAGGTTTCTGGTCTTTGTCCTCAATTTTAAACACTT T/C/CTTTTATATAGGGAATAGCCCTTAACTGTGGTACATGCTGCCAAAAATTTCTCCCGATT
WI-16403	69 T C	ACT	AAAG	GCTTTAATGGC TACAGAAAGA AGG
WI-16406	24 C T	AGG	AA	GCTTTAATGGCTACAGAAAGAGG/C/TGGTTTTATTTCTTTTAAACACATCTGGTTCTGGCAGC AAGTTATATTGCAATTAGAGCAATAGGTGCCCTGAA

EST39236 0b	57	C G G C T	TCATCTGAGA ATAAACTTCCT	CATTATAGGTA CTGAGTCATAC ATTAAACA	TCCTTTTATTCATGATTGTTTCATCTGAGAATAAACTTCCTGTCTAATTTCCAA[C/G]ACTATGTT TAATGTATGACTCAGTACCTATAATGAGACTGGAAATATATTACCTGGCAAATGAATGAGGTGCTC TTT
EST39294 4	63	G T G G A T G C C	CCTGAAACAG GGATGCC	GCACAATTAA ACATAGTACCG AGAA	CAACAGACCTTTGGTTGAGCTCACCTGGTGACAGGAGACTCTACCTGAACAGGGATGCC[G/T] TTCTCGTACTATGTTTAAATGTGCTGAGCCAGCAACCCTCGAGTTACCCGGCCTTTTACCCCCAGCC AGCTGCTGCTGCTGCAT
EST39366 2	72	T C ---		---	AGAAACATTCTGCTGATCAGAGGAAGATGTATGTAGAAAATCAGAATCTGACTGAATTCTCTAAA ATCTATT[C/J]ACACTGAGAGGAAAATGAAAAAGAAAATGTTTGCAATAAGCTTTTCCCTGACTCTCA GAGGGGTTGAGA
EST39371 9	86	A G C G T G A G A G G	CATTGGATTA GCGTGAGAGG	TGATTTGAGAC ATTTACATTT TT	AAAAAGCTGAGCTGGCAAGTCAAGTTTATTTATGTGTAAATCCCAGTTGAGCATTTTTTCAT TTGGATTAGCGTGAGAGG[A/G]AAAAATGTGAAATGTCTCAAAATCAAATGCTTCTCTAAAGATTA GACATTGCCCAACCCTGC
WI-17177	23	A G ---		---	ACAAAGTACATATCCAAACCAACC[A/G]TCCATCCCCACCTGTGGCCCTATTCTTCCCTGTGTTCTTT AGAGCCTTTTCAGCTATTCTCTGTGAAGCAAACTGCACGAAGGCCCTCCCCGTACTCTCCCTGGAA G
EST39428 8	31	C T A T T T G A T T	GCTCCCCACA ATTTTGATT	GGTCCCTTATG AAGCCACC	AGGTTCTGGTTGCTCCCAAAATTTTGATT[C/T]GGTGGCTTCAAGGGACCCAGGATTCTGCATT TTCTGGTGGGCTAGGTAATCTGTGCTTTGGTCCACAGAGCAACAATTAAGAGATCAGGTCT GGCTGTGC
EST39430 2	45	A C C	GGCAGAGGAA TAACTGATGTT	CAGGGGTGGG GTATTG	AATTTAGCAGAAACAATGAAGTTGGCAGAGGAATAACTGATGTT[C/A]CAATACCCCGACCCCTGA CCAGTACCTTTCCCTCAGGCCAGGCTCCGGTGGAGGATGTCCTGGG
EST39446 7b	117	C T G A G T A A	CTACTGACAT AGGGACTTCA	TCCTGGAAAC TGACATAAACCC	AAAGCCCTGTAAACTGAAGCTAGACAACGTCAACTTTGGAGAAAATAACAGGAACCTATTTATAT ACGTAATACATTTTCATACCTGCCTACTGACATAGGACTTCAGAGTAATA[C/T]GGTTTATGTCAGT TTCCAGGATTGTTCTCC
EST39465 2	80	A G G T G C C	AATGCAGGAG GGTGGC	CAATCTCGGC CCTCT	ATGGTGTCAATTAGAGGGCCACAGGGGATGGGGAGTAAAAATAACATAAAACGAACCTGAACAGAAA TGCAGGAGGTGGC[A/G]AGAGGGCCGAGATTGGGTGTTTCAGGGCAGAGAGGTGGAAGACCAG
EST39501 0	81	A G A A C A T T A G	AAAGATTCTCT GTAGACATCT	CACATTGCAATT CTGAAGGCT	TGCTTACAACCCATAACCATAGGCCCATGTGTTTCAGACATTCTTGACCAGCCTAAAGATTCCTGTAG ACATCTAACATTAG[A/G]TAGCCTTCAGAAATGCAAGTGCAAGTTCAAGTCAAAACCAATTC
WI-18387b	84	A C ---		---	CACAAAATGGGACTGCTGAAGAGTGGACAGTTGGACCTTACTTTGGTGACCCCATACATTTGTGTGTC CATGCTTTAGCCATAC[A/C]CATGTTGAACATTGACTATGGAGTCTTGTAAGAGTGTAAATGTGCGATG GCTATGTAGACATAAGA

WI-18387a	57	A	G	CC	CTTACTTTGG	GCTAAAGCATG	CACAAATGGGACTGCTGAAGAGTGGACAGTTGGACCTTACTTTGGTGAACCCCATACACATG
EST40601				GA	CGTACCCCAT	TGACCACAAA	GTCACATGCTTTAGCCATACACATGGTAACATTGACTATGGAGCTTGTGAAAGTGAATGTGGGATG
9	78	A	G	GA	CGTGGAAACCT	TTCTTGGAGA	GCTATGTAGACATAAAGA
				AA	GAACAC	AAGCGTC	TCCAGATGGTTTATCCAAAGCTGTGGACGTTGAACATTAAAGACAAAGAGGTGACTCGCGTGGA
					AGTATACAC		ACCTGAACACAG/GAGCGCTTCTTCCAAAGAGGGCTGTGGCGATTGAGGCACTCAAGG
EST41935	32	A	G	AG	ATCTTCAGGAT	GCACACCCTTC	TCCATTGAGTGTATCACATCTTCAGGATAGGTAG/JATAACAGTGTGAAGGGTGTGCTCATTTCTTC
				AG	AGGT	ACACTGTTA	AGCTGTGAGTAGAGGAGTCTTCCCGAGAGTAGCAGTTGTGA
EST43091	28	C	T	CA	CATTCTGGTCT	AAACTGATTT	ATGTCATTCTGGTCTTTATTTTGGACA/C/TGTAGCATGTTTAAACAAATCAGTTTTTCATAGGCAA
				TT	TTTTTTTGA	GTAAACATG	CCTTTGAAACATCAAAAGAAATACAATATATTTTCAAAATTTCTCATCTACTGTAAATCA
WI-18420c	108	T	C	C	TTCCATTAAAC	AAATTCAGC	AGAGAGACAACAAGAAATAAGGAAATGGGAAGAACAGAGTGAATTAAGCAAAATCTTGA
				AG	GAAGTTTC	ATTGCTATAAG	TTCCAGATTCCATTAAACAGGAGTTTCTCAAAAAAATCAAAT/C/GCTTATAGCAATGCTGAGAA
				GA	TAAGGGA	C	TTTCATAGGTACTTTCATGGGA
WI-18420a	38	C	T	AA	GAATAAGGGA	CCAAGATTGC	AGAGAGACAACAAGAAATAAGGAAAAATGGGAAGAA/C/TJAGAGTGAAATTAAGCAAAATCTT
				AA	ATGGGAAG	TTTAATTTAC	GGATTGAGATTCCATTAAACAGGAGTTTCTCAAAAAAATCAAATGCTTATAGCAATGCTGAGAA
				TT	AA	TC	TTTCATAGGTACTTTCATGGGA
WI-18425b	101	T	C	---		---	AGCTGATCAGCTGCTGTTACTGTGTTTATGTGTGGCCAGGGAAGCCAAAGATCAGACACCCCTGTC
				CA	CCCTGTCTCT		CTAGACAGATTCA/C/TGCACACAACAACAGGAGGT/C/GGGGGTCAACACGGCGGAGAGCCAAAGAC
				AG	ACAGATTG		TAGGGC
WI-18425	81	A	C	A		CCTCCTGTTGT	AGCTGATCAGCTGCTGTTACTGTGTTTATGTGTGGCCAGGGAAGCCAAAGATCAGACACCCCTGTC
				CA		TGTGTGCA	CTAGACAGATTCA/C/TGCACACAACAACAGGAGGTGGGGTCAACACGGCGGAGAGCCAAAGAC
				CT	CTTTGGCTCT		TAGGGC
WI-18449	129	C	T	A	AAGTGGGACT	CTCCCTGACT	AAATTGAGGTCCGGGTGGAACATAAAAAAGGAAAGAAAGAGAAAGTAATCAAGGGAGGCCAAAGTG
				TT		GTATCCAGA	GGAAGCTGATTGCTGATCTAACGTGCTGTCCAGTTCTTCTTTTGGCTCTAAGTGGGACTA/C/TJTC
				TT			TGGATACAGTCAGGGGAG
WI-18457	120	T	C	---		---	ATCGCTTCATTGAAGCCTGCTTAATTTCTCTCAGTCACTGGTGGCCCCCAAGACATTTTATTCTT
				CC	CAATGGC		AAATGTCCAATATCTGCCTGATGCTGTGTTTGTGCACATTGGGGCCACAG/T/CJAAATAGGCTAAA
				AG	AGAGTGA		AGGCAGTCCACCTGCT
WI-18462	39	A	G			TTTAGGCTTTG	GGTGTATAGCTGCTTGTACACCACATGGCAGAGGTGA/JGTAGAAACCATCTCAAGCCCTAAAA
				GG	GGGGTGC	AGATGGTTCT	TATTTACCATTACATCCCTCACAGCAAAAGTTTGTCTATCTCGGGTTTAGGACTCCATTGAG
WI-18476	60	C	T	GAGG		GCACGATGGGA	TGAGGAGGTGTACAAGCTCCAGCAGGGGTGGGGCGGGCTGAGGGTGGGGTGCAGGG/C/TJGGT
						GTGACC	CACCTCCATCGTGGCCCTGGCGTCCCTCCACTCACCCACACCTGGCCCCAGTCCACGTTGAGGT

WI-18491	109	G A	AACAAATGGT AGGTGGTATT	CGTGTGCATTT TCITGTAATCC	CTAATGAGATGAATACATGAAGGGCGTTTAGCACAGTGCCTAAACACACAGTAAGTAACCAACAAAT GGTAGGTGGTATTAATACTATTATTATTAATCCAGAAATGAC[G/A]GGATTACAAGAAATGCACA OGT
EST50757 b	79	C T	GAGCTGAGG CTGCTTCT	ACCCTTCACCC GGCC	AGCCCCCTCCACTCCACTCTGCTCCACAAAGTCGGCTCCCGAGAGCTCGAGGCTGCTCTCTTTTATAT GTGACGGGC[C/T]GGGGGGTGAAGGGTCAGAGA
WI-17675	103	T C	GGACATTTGG CATGGTGACTT	GGGGAACCAAC CAGG	GATCTTGGAAAGCACTAGAACTAAACATCTTACCAGGTGCTGAAGAAAAGTGTCTTCGTTTTAAT TGCCAAAGCAGGGATGTGGACATTTGGATGGTACTT[C]CCTGGGTGGTTCCTCCCATAGATTCACCAT TGCCCTCTAATGGTGCTA
WI-16543	67	G T	AGATAAACTA CATTTGGGTTT	GATTCATCATT ACAGGGACTT	GATCCATTACCTAGGGTAAATCTCCCTGAATGTCAAACAAAGAGATAAACTACATTTGGGTTTTGG G/TAAAGTCCCTGTATGATGAATCAAGAACTCTCAAGTCTGCTTGCCACCCATTTAATACGTATT TTTGTAAAGGCTGAAGTT
WI-17687	107	C G	GCCAAAAAGG TTGGGGAA	TTACTTTTGT CCGACCAGCA	ATCTGAGATGGAAGAGTTTCATCCCAAAACCATCTCCCTGACCCCCAGTCCATGGAAAAAATTGTC TTCCACAAAACCGTCCCTGGTGCCAAAAAGGTTGGGGA[C/G]TGCTGGTGGGTACAAAAAGTAATT G
WI-17690b	79	A G	AGGCAATTTTC TAGCTGTGTTT	CAAGAGTTATG GGTCTGAATC	ACAACATGTGAAAGAGATATGTGCTTTACTACAGTGGAGGCATTTTCTAGCTGTGTTTGATTT GGCTTCCCTAT[G/G]GATTGAGGACCCATAACTCTTGTTCACATCATCTGCTATGCTGCTG
WI-17690a	63	G A	AGGCAATTTTC TAGCTGTGTTT	CAAGAGTTATG GGTCTGAATC	ACAACATGTGAAAGAGATATGTGCTTTACTACAGTGGAGGCATTTTCTAGCTGTGTTT[G/A]A TTTGGCTTCCCTATAGATTGAGGACCCATAACTCTTGTCTCCTCATCTGCTATGCTGCTG
EST51717 b	128	C T	GCGGAAGACA GTGAGCTGTT	TTGAGGCAATA ATCCAGCTC	GATCCAACTCAGTGTCTAATCATCATCCAGATTATCTGAAGTGGAAACCCCTCCGACCCAA TGGCAACATCACCCACTACCTGGTTTCTGGGAGAGGCGGGAAGACAGTGAAGTGT[C/T]GAG CTGGATTATTGCCTCAA
EST51717 a	39	C T	---	---	GATCCAACTCAGTGTCTAATCATCATCCAGATTAT[C/T]TGAAGTGGAAACCCCTCCGACCC CAATGGCAACATCACCCACTACCTGGTTTCTGGGAGAGGCGGGAAGACAGTGAAGTGTGCTGAG CTGGATTATTGCCTCAA
EST53012	97	C T	TGGTCACTTTG GGGC	GGCTCTGCCCA GGC	TTTCCAGGTTGACAGGTTTATTCCACCCCTTCCATCCCATCCCGAGGAGGAGGAGACAG GTGTGCTGGAGTCTGGTCACTTTGGGGCC[C/T]GGCGTGGCAGAGCCCACTGGGTTTACATCTCTGT GGGCAGGTGTGGACAC
EST53349	96	A G	TGTTGAAAGC AGTCACAATG TAC	CATCTGGATAT CTTGTGCACATT TT	AAACTGCAATAACAAAAACAGAAAGTCCCAAGAGGCTAAAGTCTAAGCTATAATTACACATG AAGTATATGTTGAAAGCAGTCACAATGTAC[G/G]AAATGTGACAAGATATCCAGATGTTTAA
EST53389	74	A/G C A	GGAGACCTGC AGAACTTAA	GGCCTTTCTAA CAATAAATGCT C	TTTCGAAATGTCCTCCATGACTTGACAGACTGAGAGCCAGCCAGCCAGGAGACCTGCAGAACT TAAACAC[G/G]GAGCATTTATTGTTAGAAAGGGCAAGTCTTACACTCAATAGGTTTTAACATGAAC ACATTAAAGGGAGATGGCC

[illegible]



[illegible]

TIGR- A003P30	117 C G ---			...	ACAAGTTCAAAGGAGAACTCCCTTTGTTTAAATGCAGCTGTGCTCAGAAGCCCTGTGATTTCTCCTAGGA AACCATCTGGGTTTAGCCCATTAGAAAAATGCAGTTTAAAGCAGTGTCA[C/G]ACTGGCTGCCTGAA GGTACCCCTGGAGATACT
TIGR- A004S34	156 C T A	CCAAACCTCCT CATTCCATATA		TTAAA	GCTGTCTTTTATGTTAGGTTCCGGGGAAGGAAGGGCTGACAACCCGACACATCTGGACACCAGC AAGGGTCCAGGGGAGGTTTGAGAACCTCTTTGTCTTGGCTAACAGTCTGCTATGTGACAAATAGCCA AACCTCCTCATTCCTATATAA[C/T]CTTTAACAAAAACAGTAGCTGTTTACAAAAACAGTTAGCTGTT TACATG
TIGR- A004T44b	97 A C ---			...	AACAACAGTGAATCTTTAACAGGGGATGTTAAAGGTAAGAAGTCAGGAAGATAAACCCAAAAATGAT TGAGTATGATAAAGAAATTTGCATGGCGATT[C/G]AAATAGAAAAACCTATAAATGTAGAAAAAGCA GGTCTGGACTTAGCAAAGAAACAATATGACTTAGCAAAGAAACAATATAG
TIGR- A004T44a	69 G A TGA	GGAAGATAAA CCAAAATGAT		GCCATGCAAAA TTCCTTATCA	AACAACAGTGAATCTTTAACAGGGGATGTTAAAGGTAAGAAGTCAGGAAGATAAACCCAAAAATGAT TGA[G/A]TATGATAAAGAAATTTGCATGGCGATTAAATAAGAAAAACCTATAAATGTAGAAAAAGCA GGTCTGGACTTAGCAAAGAAACAATATGACTTAGCAAAGAAACAATATAG
TIGR- A004V08	60 T C GGCATTCTCT	CAGGAAAAACA		TCCTTCCCACA AAAGGC	CCTACAATCCTATAATTTGCAAGGGTTGGGAAGGATGCAGGAAAAACAGGCATTCTCTTAT[C/G]GCC TTTTGTGGGAAGGATCAATTTGGGTGCATGCACCTTAGGGGACAATTTGGGCAGTAGCTGTCAAAATTC AGTAGCTGTCAAATTTCAAA
TIGR- A004V26	125 A G ---			...	TCTAGCTATAAGACCAGATTTAAATTTCTAGATATAGAATATCCAGAATAATCTATTGAATTGA CTGATTACAAAATGTTAACAGCTGGATAAACGGTAAATATGCATTATCTTCACATGA[A/G]AAGGT TTCAGTTTATAAATGCTTAAATCTGTATCTATTTGCTTAAATCTGTATCTATTGG
TIGR- A004V28 a	29 A G CGATCTC	TGTTGTGGTG		CGGAGGTTGCA GTGAGC	CCAGGCTATAATGTTGTGGTGCATCT[C/G]GCTCACTGCAACCTCCGCCCTCCAGGTTCAAGCAA TTCTCCTGCCTCAGCCTCTTGAGTAGCCGGGACTACAGGCACCCGCCACCGCACCTAACTAATTTTGTG TATTTTATAGTAGAGACATTGTAATTTTATAGTAGACAGG
TIGR- A004X20	25 T C GA	AAGTTTTCCTT CTCTTCTGTAG		TTTTATAGTTG ACTGTAACATG GAGAC	TAAGTTTTCCTTCTCTCTGTAGGAT[C/G]TCTCCATGTTACAGTCAACTATAAACACATGGCTCATGT TCACTCTGGCTTCGCTTCAGAGGAGTTTGATATTTTGGAAAGTGGTACCTTTGTTCTGTGCTTTTCA GACCAACCGCTTCTTTCATTTCTTCAAGGCTTCTTCCAAAGGAGTTAAATCATCATCATGTCCCAATC ATCATCATGTCTT
TIGR- A004X30	26 T C CCAC	TTTGAATCTT AGAGTAGAAC		TTCTTTATGGA AGTGTTTAAAA CTATTTT	TTTTGAATCTTAGAGTAGAACCCAC[T/C]ACTCTAGTAATACTTGTAAATAAAATAGTTTT AAACACTTCCATAAAGAAATAGGGTGCCACAGCTCCTTGATTTCCCCCTAGGGATAAGATATCCAT GTTAGGGATAAAGATATCCATGTAC
TIGR- A004Z04	102 T G ATGCAAAACT	TTCATTTGGGT		CTTATAATTAG AAATTTTCATGA	CACGGTATATGCCTTATATATAGGTATATATACAGATCGTACACAATATATTTAACAGTTTGACATG GGGTCCACAGTACCTTCATTTGGGTATGCAAAACT[T/G]TTGCTTTTCATGAAATTTCTAATTATAAGG ACTGTTGCTTCTTCATATTCATGGACATTATACAAAAATACAGTCTCTTTAGTGAATTTAAGACGTC TCCTTAGTGATTTAAGACTG

TIGR- A004Z19	85 C T	GAGAACAACT GCAGCATTTT	AAGATGGTCAT CGGGAAGA	TAAGTGGAGACAAGTTTATTGGAGGAGCTTGACACCCCTCTTCTGCGCTAGCTTGAGAGAACAACTGC AGCATTTTTTCTTTTTC/TTCTCCGATGACCATCTTTTGGCTGGCGGCCAGGCCCTGGGTGTC TCCCATATCGCTGCTTTAGTGAGACTGAGGATCTGGTATAAGGAACAGATC
TIGR- A004Z42c	89 C T	TTGGGGGAGGT AGGAGACT	CAGGCTGCGG GTCC	GTCTAGCAGAGAGATACTTTGAGGGACAGCCCCAAGGGCCAGGTAGCCTTCAGGGCGGGCA GGTTGGGGAGGTAGGAGACTCTGGACCGGAGCCCTGGCTCCAGCTTCATCATCTGTGTCTCTT CATCATCTGTGTCTTC
TIGR- A005D17 c	81 T C		---	TATGGACTGTGTAGAAATATGATTTGGACAAGAAGGTATGATCTAATAGTAATAGACTGAGAGGGG AAACCCAGCAAGGC/TCGTCTAGATCTCTTGGCCTCTCTGCGAGGATTCCTTCTCTGGGCAC GGGTGGGACCCCTCTCTGGAATGGGTATCTTACGACAGTCAAACTCTTACGACAGTCAAAACAC
TIGR- A005D17 b	79 G C	GGGAAACCC AGCAAG	GAGAGCCAA GAAGAATCTAG AC	TATGGACTGTGTAGAAATATGATTTGGACAAGAAGGTATGATCTAATAGTAATAGACTGAGAGGGG AAACCCAGCAAG/GC/CTGTCTAGATCTCTTGGCCTCTCTGCGAGGATTCCTTCTCTGGGCAC GGGTGGGACCCCTCTCTGGAATGGGTATCTTACGACAGTCAAACTCTTACGACAGTCAAAACAC
TIGR- A005D44	97 G T	TTAACATTATT GAACTTAAAA CTGTACAC	TTGTCTATTAT TTAAAGCCAA AAAA	CATCAGTAACATATACACAATTGGTCACTCAACTGAACCTTGGCTCCAATATATTTCTATACAATACTT AACATTATTGAACCTTAAACTGTACACTG/TTTGGCTTTAAATAATAGACAATGATTTTG TCTATTACTTATGATAGACAAGGTGATTACTTTGTAGACAAGGTGATTACTTTGTTAC
TIGR- A005E31b	27 G A	---	---	GGAGTTCAAATTTATAACCAAGGCCTCTG/A/CTCACAGCTGTACTGGCTAGGCAAGCTTTCCAGAC ACAAAGCCACCTGCCTGCCATGTGGATAGTACTCTTTGCCTGCTTGGCCCTACAAAGCCACTTCTAT TTCATACCAATACCTTCTATTTCATACCAATAAG
TIGR- A005E39	182 G C	---	---	CTCAGTGTAACAACTTTGTTTAGGGAAAAAATAATCCAAATGGATATATGGGAAGAGAAGTG CCAGGCTGGATGGTGTGAGACAGAATGACCCCTGGCTCTTTATTTGTTCTTTTCAACAGGAC CCACAGATAATTTGCGGTATGTCATGAGGACTGGGATGCTTCTATTG/GC/GGATGCTTCTATTT
TIGR- A005E42a	42 A G	AGTAAGGTTA CTGCACCTTAC AGAG	CCTAAATCAGG GGAAATTGAG	GCTGAGTTTTGTATCTTAGTAAGGTACTGCACCTTACAGAG/G/CTCAATTTCCCTGATTAGGA AGCGATGCTAATGGGTATTGCATAGGTGTAAGTATAAAATGTTGTTATTAAGAGAATCCCAAG CTTGGTATAAGGCAGAAAAATAAATGGTATAAGGCAGAAAAATAAATAG
TIGR- A005E46	76 A G	CACCTGACTCG GTGCTTTAC	COCTGGCTGTG AGGTAATGT	ATGACAATGATGATAGTATTAGCCTACCGTTTGTAAAGCACCTACTGCGTATCAGGCACCTGACTCGG TGCTTTAC/A/G/TACATTACCTCACAGCCAGGGTTGGCAATGGTCAATTTTGACAAATGGTCAATTTTG ACAC
U20979	24 C T A	GCAGGGGTGA CGTATGTAGA	GGGGAGGACAC CCTAAGC	AGAGCAGGGGTGACGTATGTAGAA/CT/GCTTAGGGTGTCTCCCCACAGAGCAGATACTTGAACCG ACTCAATTCCTGTGTAAAGAGCACTTTGTCTGCTTTCACGGACCTCCCCAAAGTGTGCAGAGTTCTAT ATAGGATGCTGGATTAGTCTCTTGTATATTTGTAAAAATTTCCCAAGAGCCGCATATGAATCTGCC

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X57830	106 G C C T	AGTGGAAACA ACGATCATAT	CATTGACAGAA TAAATGAGGC A	GTGGCAACTGTGGAAGGCACACTGAGGAAGTTTTCACCTATCTCGAAAAAATATGAGATTGGA AAAAATTAGACAAGTCTAGTGGAAACCAACGATCATATCTGTCATATGCTCATTTTATCTGTCAAT GAAAAGCGGGTTCAATGCTACAAAATGTGTGCTTGAAAAATGTTCTGACAGCATTTACAGCTGTGAG CTTTC
X74070b	72 T G T G G A T C	CTTTTAAAGAA ATTTTGTTTA TGGATC	GGGCTTAAAAA TATTAGAGATC TAGATT	AACCTGAAGAAGTTACTGGAGCTGCTATTTTATATTATGACTGCTTTTAAAGAAATTTTGTATTG GATCTT/GIGATAAAATCTAGATCTCTAATATTTTAAAGCCCAAGCCCTTGGACACTGCAGCTCTTTT CAGTTTTTGTCTTATACACAATTCATCTTTCAGCTAATTAAGCCGAAGAAGCCTGGGAATCAAGTTT GAA
Z48804	44 C T ---		---	ACTGCCGAAGTGTAGCGGCCCCCAACCTTGTCTCATCACAGTC/TTAGAGCTTCTCCCGAAGGG CCTTTAGGATAGGAGAAAGGGTTCATGCACACACGCTGAGATGGAAGAGCCCCCTCCAGACCACT CTACAGCTGCTTAGCCTTAGTTGCCACTAGGAAGTTTCTGAGGCTGGCTGTAAGTAAGTGTAAAG TCCA
D28513b	133 A G ---		---	ATGACCAAAGCCACCACATTTAGAACTTTGGCTGCCTTTGGAAGTCCAGAGCTGGATCTCTCAGCTCC CGCCCCAGAGGGTCAGCACCTTTGGACATGGCTCACAAGCAGTTTGTATTGACTGCATGAATGC/A GJTGCGGTGCAAGCATGAACCTTGTTTAAATCAAGAGGCTTACATAATTTTAAACCAGTTCTGTCTTC AGCTGTACATA
D29833b	85 A G ---		---	CCACTCCATCCTGATGCCCCAAGTTATCCACAGCCTCCTTCCCGACCAAGACCCCTATCCACCTGGACC TCCATTTTCCCTGTAA/A/GJTTCTCCAACTGATCCTACCCTCCCTACTCCTGCACCCCAATATGAA CAACTGCAGCAGGTGCCACCACCAACCAACAAAGACACCCACTACCCCTTGTAACCTACTGCTTCTGCTAC
D29833a	21 A G ---		---	CCACTCCATCCTGATGCCCCA/A/GJTTATCCACAGCCTCCTTCCCGACCAAGACCCCTATCCACCTGG ACCTCCATTTTCCCTGTAAATTCCTCAACTGATCCTACCCTCCCTACTCCTGCACCCCAATATGAA CAACTGCAGCAGGTGCCACCACCAACCAACAAAGACACCCACTACCCCTTGTAACCTACTGCTTCTGCTAC
D31762	82 G A ---		---	CTCCCTGCCTCCTCCTCCTGCTGCTGATGCTCGTCTCAACAGCGCAACCTGCTTTCATATGGGGG GAGGGGCGGTTT/G/A/JCTTCTCCTTCTGCTTCTGCTTCTTATCTCCACAAACCATTCCTCAATAAA GCCAAAATCTTCTCTTCTCCTCCTCAGGCCACCTCCTGCTCCTACTCCTGCTGCTGCTGCTTTT CTGGA
D37931	64 T C ---		---	ATTATCGGAGTGGTTGACCTTACACTTACTCCTTAAATAGCAGTGAGTAATGCATTTGAGCTG/T/CJ CCCAGGCTGTCTCCTCAGCTCATTTCTACTCTTTTCTCTATATAACTCATTTTATTAATACATT GCACCAAGAGATATGGAGACATAAACCTGTAATGAATGAGGCTGGGCTTTTCTGTAATAAGCTTCC TTT

D63807	101	CT	---			CAGGAGGACTTCAGTGTGATCCCTGCCCTTCAGTCTCTTTAGAAATCACATCTGTGTTCAATCC ATTGTTTAGAGGGAGTGTATTTTCTGTTCCA/C/TJGAAGAGGAGCTTTTGTTCACAAATGGATCAC AATGCAGAGGAGTGTCTCTCCCGCTGGCTCTCTCGGTCTGGGAGGTGACCTGTCCAGATGAC TGGAAACATGCGTGTGACCTC/TJACAGCTACCTCTTCTATGGACTGGTATTGCCAAACAGCCACA CTGTGGGACTCTTCTTAACITTAATTTAAITTTAATTTATTAATACTATTAGTTTTTATAATTTATTTTGAT TTCACAGTGTGTTGTGATTGTTGCTCTGAGAGTCCCGCTGCTCCCTCCACCTTCCCTCACAGTGTG TCTGGTG
D90145	21	TC	---			ATTATCACTCTCAAAAATTTGGTGTGTGTTTAAGTACTTTCTTATTATGAGCCCC/TJ/CJGAGGA CCAGACATGTATTATCAAGCCCCATTATACCATCTAAT
EST14035 1a	59	TC	---			GCATTTTAAATTCACATTGAATCATATTACTATTATGATGTTTACATAACAATTCAGTATCATTT ATG/C/TJGTAGATTTCAGATGTAGTGGTCAATACTGAGCATTATCT
EST16668 5	71	CT	---			ACAGACTATCGGCAACTTATAATGCTTAACTTTATGATCAATAGTAATAAATTACA/C/TJGAGATA TTCACACTTTATTATAAATAGGGTTTGTGAAGATGATTTTCCCACTGTAGGTTAAACAT
EST16904 7	57	CT	---			TTTTAAGTACCAGAGGCTGCTGGAAACAGGATGAAACTGATACACC/JG/JTGTACTACTTACTC TTCACCTTCAAACTGATCCCTAAAGACTTCTACTTAGCAA
EST21863 9	49	AG	---			GGCTGTAAGTAGAATCAAGGTTAAGAACATTTTATGCACTTATCCACAACAATTTACTGAGCATA CTAGGTGCTGGG/JG/JGTGACAGTGAGCAAAAACACAA
EST21885 6	80	GA	---			ATTTAGTGCAATGACAAAGCCCCA/JG/JAGAACAGAGGATCAAAATAGATTGAAATGTATTACC TTCATAGTATACGAAGTTTAAACACAAGTATGGGAGT
EST22623 8a	26	AG	---			AAAATGATTGAATTCAGCAAGTACATTTATGATCTATCTACATTTGTTAAAACAGCACTAAAAATAA AAATTTTAAATGATTATCCATTATTTACAG/JG/JAAATGTGGAAGAGATGGCTTTTAAACCC
EST22644 2	98	AG	---			CCTCATTATTTAAAAGACGGACATAAAA/JT/JATACAAACAAAAACCCCAAGTCACATTTTCAG GAGGTAAACCTAAAAAGTCTGATATGAAAATATGGTGG
EST23587 1	31	TA	---			AAAGATCTGGCATTATTCACATCATTTCTAAATATTTTGTAAATTTTCCATGAGTATTTTTTCA TGTCGAAGCATTTTAACTATCATTTTAGCGTAAATACC/TJ/CJGAATAACCCATAGTTACAGAAATGG GTCTGTGAACCTCAAT
EST24246 7	106	TC	---			TAGTTTAAATTTCTGAACCTTTGGCTTATAAATTTTCTCAACTT/JG/JCATTTAAAAATGTATCAAT GCACCTTCTCAGTAGTACCACATGAAAATATAAACCTCGTTC
EST24308 3	45	AG	---			CTTGAACCTCTGGTCTCAAGTGGTACGTCGCTCAACCTCCCAAAATGATGCGATTACAGGCATAAG CAGCC/G/JGTGCTGACCCACATTTCTTATCCGATCTGTGATGGACATTCAGGTTGTTTC
EST24435 6	73	GA	---			TATTGTGCAATTATCAAAATGGTTA/TJ/CJAGTTTTCAATTTAAACTGTAAITGATTTCTATGTATAA ACAGCTTTGAAGTTGTAATGTAGTTTCCAAATCGTTAGTTAATGCTACATT
EST25089 6	25	TC	---			

EST25476 9	33 G A ---		AATGATCTTTATTTCAGACCTGCTCCTAAA[G]AICTTCTCCTCTCTAAATAAACCAACACA AGAGGTCTCTTGCTGCCTTCCATGGACTGTGGCGGCTGTGGACTTGGACCGTCTGCTGA
EST26183 2	70 T A ---		AGATAATGCATTAGAGCCTGCCCTCATTTGATCTTGATTAACITTTGTAAAGATTGATCTCTAAATAAG ATT/AJACATCTCGGGTACTGGGAGTTAGAACAAG
EST27231 1a	28 T C ---		AGAAATAAGGTGCTACCAGAACTCATGT/CJGATAGCGCTTCTTTAGGCACATATTATAGCAATT CAGATGAAAGTTCTGTAAATCACACACACACTGTGCCTCTAACACAAACACGGTGACTCTGA
EST27816 5a	26 T C ---		CAACTCAAGGTACAAGACAAATTGCAT/JCJAACATTTGTTATAAATAAAGGAACATCAGATCAAT CATTAAAGGGCTCCAGAGTGAACAGCATCTTCATAACTTCCATGTT
EST28588 0	78 A T ---		GTTTAATTGGCGTATGTTCCACAGGCTGTACAGAAAGCATGATGGCTTCTGGGAGGTCTCAGGAA ACTTACAATCA/JTGGTAGAAGGCAAAGAGAGCAGGCATCTCTCCATGACCACAGCAGGAGG AACAGACAGAGGAGGGGGAT
EST30226 5	25 A C ---		TACTCACACCGACATACATATCTCAI/A/CJGTAGAATTAGCTATAGCTACTAACTTCACTTGTAGT AGGGAATATAAACTACTGAACAAGACAGACTTGTCTAACTTAAACAAGACAGACTCACTTCCCTTTGA G
EST30935 9a	59 C G ---		AGCTATGGTAGAGCAAAATCCAGTGGTGGTAAATCAAGAACTCTAAAGATTCAAGTAGAG[C/G]AGGT GTTTTGAATGTCAAGGAAATCACTGAGGTAGATTGGGATTACAATAAGACAGCTGCCCTGTGAGGT CATAAGAGCTTTTGTGAGG
EST32515 7	25 G A ---		CCGAATATAAGGAAAAATGGTGG[C/G]AJTGCCTCTAAAACCTGTGTAATAGAATAATGGCCAAT ATTACAGTTCTCACTTCCATGAACTACTGGCAGTGTATTTTATGTTATATGTGAGTTTCTATGC ATAAAATCCCAGTAAGA
EST33274 4	27 T C ---		TGCTTTGTTCCCTCCAAATCTCTAAA[A/T]/CJGTGTCTTCAAAGAAATTCGTGGAAAGGACTTTGAA TACGAGTTGTACCATATTCAAGTATTCTTGAATACAGGTTTCAGATACTATGGAGATGATACCAATT GGACTAGGTA
EST33352 7b	75 C G ---		TACACATTATCAAGAGACCACCTGACATGCTCTCCCGCAGAAATACATTCGTCCTCTCTTAGAGA AGTTTAA[C/G]GCACATAGTATTATTTTACTAAGAGAAATATCTCTTGGTGCATATCTAGGGG
EST33424 1	126 A C ---		ATTTTCCCACAGCAGAGTATATTTATGTGCTGAAATCAGGTAGCAGGGAATGAATAGCTCTGG GAACCAGTACAGAAATGTTTACAAAAGATTTACAAATCTCAGTCATTACACACTGAGCAAC[A/C]AAA CAAAGGTGTTGAATCTCTT
EST33488 7	90 A G ---		CCTTTGGGGGAGTTTAAAGCCAGAATGTGACAAAAGTCACTTACAGGAAGACTGGAATGTAGCCATAG TTGAACTCTAACATCGTCTATAG[A/G]JACCATTTCCTCCGCTCCAGTTAGGTTCTAGGCATACTAAGCT GCTC
EST33508 1b	45 C T ---		AAAAACATGCTATTTGAACAAACTTTTTTATAAGAATAAGTTGA[C/T]TGAAAAGCAGTTTTTAAAT AACATCAACTCACAATGACTTTTTAGAGGCCAAATAA

EST33508 1a	36 A G ---			AAAAACATGCTATTTGAACAAAACCTTTTTATAAAGA[A/G]TAAGTTGACTGAAAAGCAGTTTTTAAAT AACATCAACTCACAAATGACITTTAGAAGCCAAATAA
EST33863 4	77 C T ---		---	ACAACATAGGACTGGTATTCTTGGTTTTGAAAAATTATGTTGCCACTTCCTATTGTTTTTAAAAATGA TCATTTAAC[C/T]CTTTGAACACAGCCTGAATCCCCC
EST34739 3	97 T A ---		---	GAAGTATCCTTCCCAGTGGCAGGAACCTGAAGACTCCAGACTCAACAGGTGGACCTTTTCGTTGATGA GCTGATAGCTTCTAGGCTGTGGGGAACCTC[T/A]GGTGCCCTTACAACCTCAACTACTGCAGAAATTTCT TGTTGTGCTCATAAACA
EST34792 6b	104 A G ---		---	ACCTGACTGCTTTAAAGCTCTTTGTAAGCTGACCGTAGCAGACAGATCACGTGGCATCCACTATCAATA CTCATAAGCTAATTTATCCTCAGGATGTTCCCTGA[A/G]GTATTCAGGAATCTTAGTCCTATTACA AAGATTTGTGCTGTG
EST34835 9b	93 T G ---		---	GGAAATGTTCCCTTTGCAACAAGGTACGTTTATTCTGCAACTTAGGAGATAAAATGAGATTTCTG TGGGAGTCTATGTTGTGCTTTCTGGT[G/G]GCCCTTAAAGAAACAGACAAAATTTGTCTAAAGAT
EST34835 9a	82 G A ---		---	GGAAATGTTCCCTTTGCAACAAGGTACGTTTATTCTGCAACTTAGGAGATAAAATGAGATTTCTG TGGGAGTCTATGTT[G/A]TGCTTTCTGTGGCCTTAAAGAAACAGACAAAATTTGTCTAAAGAT
EST35230 0	93 G T ---		---	CACAAAGTCCACTTTACTTACATGAAGGAACATAAAGGCATGAGAAACAGTCATCTCAATAAATG CAAGACATGAGCATAAAGAGGTTCT[G/T]GCCCTTCCAGCGTTGTTATTACAGAGAGAAACCT
EST35337 9	33 C T ---		---	TCITTTCAAATTTTGTAGGCATTTAATG[C/T]ATAAAATTTCTGCTTAGGAATGTATCTGCT ATATCTCAGAAGTTTGGGCATGTTGTGTTCCATTTTACTTAGTCAGAACITTTTCAATTTTCATCT
EST35708 9	32 C T ---		---	CTGCCCCAAATTAACTTTTAGGCAATGGAAA[C/T]AGACTTACTGTATGGGACATTTTAAAAAG ACAGCTTAGTAATATGTTTCATATGACGCGTGTGCTTCCCTCTCTGAGGTTGGCACCTTTCTCTGTTG ATGTGCAAGTGTGGCT
EST35747 9	51 C G ---		---	ATCCAGTGCAGAGTTGTAGCTGGAGACATATTTCAACCCCAAAAGGCTCC[A/C]GATGTTAAACGT TTCCCAACATCAACCTAATACAGTGACAGCAACACCTCCCTCCTGCCCCCTCCAGTAGGGTTGAGATT G
EST35751 9	89 C A ---		---	TGGTCCATTATTTAAACCTGAGGGAACAACCGGTGCTGACATGGCAGACATTTATTCAATGGAGA AGTTCCCTCCCATGAAACCAAGA[C/A]CTTGCTCCTCATGATAAAGTGGAGACAATAAGAAAGCCAGGT ATAATAATTAAGCCTGTGA
EST36301 4	93 C T ---		---	CACCTGTTCAATTTGTTCACTGGGCTGCTATCTGTGGGCTGATGCTCTACCAAGTGCCTACGCCTACAGC AGTCAGGAGGCGAGCCATGGCCCTG[C/T]GCTGATGGAGCTTGTAATTTAGCCCCAAACTGATCTTCA GAAAGAGGTACAAACA
EST36519 0a	33 G T ---		---	GCCATCAGCCCCACAAAGACATGACTACCAACGC[G/T]GGCCCCCTTGCAACCATACTGGCCTCAGCAC CTAAGACTGGACAACCTTTGTACCTAATGACCGCCCCACCTGGCATATACTGGCTGGCCTCTTCTCTGT CACAGGGGCTTAGTCGT

EST36620 6	50	G A	---	---	GACITATTAGATAAGGGTTTCGGCTACCCCTCAAAGCTCTCAGGACTGG[G/A]GCTAGGGTTTAAGG AAGGCTTATTTAAATATGGGAAATAAAATACAAAAGGGCCACACCCGATGCAAAAAGACTTT
EST36690 0a	89	C G	---	---	CCGTGATGTGCATGGTGGCTGAGCAGTCGTACTTACTATGCGTCAGACAGCTCAGCTATGTACGGA AAGGAAGTCTGGGATTCTA[C/G]AGGGGACATATCACACATATCTAAGTCACTGTGTGACTCGG CTTGAGCAAGTCATTTCA
EST36729 9	62	C T	---	---	GAGACAGAAGCCATCAGTTAAATGAGGTTAGGCCCTCCTCCTAATATAGTATTGACAATG[C/T]A TATTAGCCAGGTAATGCACCTTTAGCTACCCTGGACAATGCTATCAAGTGTGCTGGGAAGGGAG
EST36823 6	103	A T	---	---	ACTGCTGGCCGATGATTGGAGCTTGAAAAAAACTACCATGCCAGATCTCCACCCAGACCAATTAG GTCAGTATCTCTGGGGTGCTATTCAAGCAACAATT[A/T]TCTTTTATGTTCTTAAGCTCATCATGAG TTAA
EST36987 4	126	C G	---	---	ATGATCGCTTATGTAATTTGAGGGCGACATGGGTAATGGGAGATACCCACAGGACCTGTAAATATT TAAATAATATTTAACAGCTGATCAGAGGCTAAATTACAACCTGACATTTTGATGCAGTTT[C/G]GTTA GGGAATTAAGACAATGCAG
EST37054 3	88	T C	---	---	GGTCTCACTCTCTTGGCCAGGACGGTTTGAACCTCCTGAGCTCAAGTGACCTCCACCTTGGCTTCC GAAAGTGCTAGGATTACAGG[T/C]GTGAGCCACACACCTGGTCTTGTTTAAAGTAACCACTGAA C
EST37269 3b	105	T G	---	---	AATAGTCTATGGTACGGCCCGTGGGATGTTAAAAATTGGGATTTTAAATTAAAGATTGTGAACATG CAAAACCCAGCAAAATTTCTCAGCTTATATTTTGAAGTCT[T/G]CAGGAGAAAAAATGGGTCC
EST37284 2	93	G T	---	---	AAAAGACCTTTCTCAAGCAGTAAACTTTGAGCAGAGACTCAGATGAAGTAAGGGATGAACCAAGAA GCTCTCGGATAATGTCACCTCTAGGAA[G/T]AGTAAACAGGTGTTAAAAACCTGAGATAGCAACCCCT CTTGGCTTGGTTGAGGAATA
EST37315 2a	90	A G	---	---	AGATGGGGTCTTGCTAGCTTGCTCGGGCTGAACCTAAAGATATCCTCCTCAGCCTCCAGGTAGT TGGAACCTATAGTAGGAGTATCT[A/G]CCCTGCCCTGCTAGAACTTCAAGTTTGATGGGCAAAATCCA CCCCAGAGGACAGGACAA
EST37374 1	45	C T	---	---	CCTGCCATGATAATGTTAAACATATCAAGATCCTCCTCAAACCTT[C/T]AAGGGTGAAAAAGCATACC ATTCCATTTTAGTTGAAATATTCCTTCACATAGCCCAACACATTTTTCAGGCACTCTAGCTACTACA CGA
EST37376 8b	101	G C	---	---	GTGACATCATGCTCTTCAATGCCCTTTCAATTAAATAGTAGT[C/G]GCTGCTCCTCAGGCAAGTTGCTGACTTCTCTG CTCTGGGTTCAAATCAGAGTGCTGTCTCTGCA[G/C]GCTGCTCCTCAGGCAAGTTGCTGACTTCTCTG TGTCAGG
EST37376 8a	41	T C	---	---	GTGACATCATGCTCTTCAATGCCCTTTCAATTAAATAGTAGT[C/G]GAGCGCTGGGGGCTGAAAGTCAG ACTCTCTGGGTTCAAATCAGAGTGCTGTCTCTGAGGCTGTCTCCTCAGGCAAGTTGCTGACTTCTCTGT GTCCAGG



EST37378 9	63 T G ---			ACACACAAAAAATGGTGGCAGAAAAATCTGGAAAGATTCTTAATAACCTCAATTTCGTGAAAACT/G JAACATGCCTCAAAAAAGAGGGGAAAAAATTTAACAGAAACACTGTGCTGACATGATTAGCTT
EST37452 4	46 G A ---			AAGACATAAAATCTGCAATGAAATCAGTTATGAATAATTAACCTCTG/AJCTTCTCAGGAGTGACAC TAATCATGGTCTGGAAGCTAGCCTATCGCATTTTAAACACCCCTTAATCATGACGTAGAA
EST37613 6	34 A G ---			CTAGGCATGGGGCTTTACAGTCATTTATTTACCA/GJGTCATGAATTCATTAATAAACCCACAGCGAT ATAGCAATGAGCAAAACAGACCCCTCCCCAAATCACCCCTGCGTTCATGGATCTTCCATCTTAA
EST38025 4	56 T G ---			TTATTGAGTAGCTACACTGTGGCCAGAACTAAGCTTTACATGTTTTATATCACTTAT/GJTTATCTCA ACAATCTTGAAGGTGGTATTATTTCCCGTCTTATAGGTGAAGACTCTGAGGTTTCAGAA
EST38068 6	57 C T ---			TCTACCAGGTCACCAAGTATCTGTATATGCTTTAAGTGGCATTTTCATGTCACTTAC/TJCGCATGG AAGAACGCTCTCCTTTTAAATCCCTAACTCTCTCTTCTGGAAGACAGAACGTGCACAA
EST38420 6a	100 T C ---			TAAATCAAGGCCTCTTTCATTACCAAAACAAACAAAAAAGGGAACAAAAATACGATGGGAGAGG GAAGAGATGATGCCGAAGTGCATCCTGACTGACTGACTGACTGACTGCTCCCTGCAGTGCCTCCCGTGCCT TATTCACTCTCCTCTCTCA
EST38950 5	25 T C ---			TTTATTGCAAAAGTAAGCAGCCGGT/CJTGCTCCCTGGATTGAGGCTGAGGAAGACATTACTTCTCTG CTGGAATACTTGGGACTTACATTTGACACAGGCTAAAGTATGGGATGAGAGAGGAACAAAAGCTT ACAAACAAAGAGCAGCCA
EST39053 6	90 T C ---			TTTTTGTACTCTGTAGCCAGTCATTAATCTGAAGGTTTAAATATATCATTTTATTGGGATGAGATCA TAGCTTTACACAAATGCTATG/TJAAACAAAGTTACTGAATAATTTTACCCTCGTGGAGTTG
EST39331 1	70 G C ---			TCCTTCTGCTCTAGCACTCAGACCACCAAGAAAGCCCTGGAAGACCAGCCATGGAAGGAAAGTA TGCG/CJGTGTTTGGGAGAGCTGGCACCTGGCCTCTAATCTTCCCTCTGCCATTGACCAGATGGGT GCCTTTGGATACATCACT
EST40544 7	31 C A ---			GTCAACATTGACCTTACATAGTGCCTCTAGT/CJAJACCTATGAGGCCTAGAACTCTATTGTACTTCT CACTTTATCACATTAGCTATCGAAGTTTGAAATTT
EST40548 4	37 T C ---			TTCTAATAGCATGCCCCTGTGACAGGGGAAACTAAGCTC/TJCAAAATAACTGAAACTAAATCTGTA AGATAAAATGCTGGAATTTGAGAAGGCACATGCCTTTTGTAGTTTCTCCAGAAGGCTCAAGGTGTTG AATAATCTGTGGGACTCA
EST40549 1	42 A G ---			TGTTTCTAGAGAACCCCTGTGTGATACACTACCGATGCACAG/JATAAAGTCACATCAAGACTAA TAATCTAAATGTAGTTTGTACCACCAATTTCTCACITTTGAACCTAGCTCCCTGCAAAGCACCTTCTA CCCTGCACITTTGGGGAG
EST40579 1	81 A C ---			TGTGAATTACACATCAGTAAGGCAGTTTACAGAATTTTACTCTTACCTAAAGCTGTGCTATCTG AGCTGGTGGAAA/A/CJGGACTTGGAGACAGCGAATTTAAATACGGAACAAGGCTCTCCAGGAAG
EST40584 3	68 A G ---			TTGTATGTTGTAGGAATTTGGGAAGAAATATCTGTGAAGGAAATTTGCCACTGTAAATGCACACCC A/A/GJCTGTACTCCCCACAATATCCTATGTTTTAAGCT

EST51340	51	G A ---					GATCAAACTGTATTGCCAGGCCAGCTCCTGAAGAACTGTGAACATATGAAC[G/A]TCTCAGCCTAGA AGGATAATGTGACCTTCAATTTGCACACCATCCATTGTCTCTTCAAACTAAGAGCCTCTCTAAGCTA GATAGGCCAAGGATTATT
J04162	134	T C ---				---	CATGGAGTAATAAGAGCAGTGGCAGCAGCATCTCTGAACATTTCTCTGGATTTGCAACCCCATCAT CCTCAGGCCCTCTCTACAAGCAGCAGGAACATAGAACTCAGAGCCAGATCCCTTTATCCAACCTCTCGA T/CJTTCCTTGGTCTCCAGTGGAGGGGAAAGCCCATGATCTTCAAGCAGGGAAAGCCCCAGTGAGT AGCTG
K01506	63	T C ---				---	CTGAACTCCAGCTGCCCTACAAACTCCATCTCAGCTTTTCTCTCACTTCATGTGAAAACCTAC/T/CJC CAGTGGCTGACTGAATTGCTGACCCCTTCAAGCTCTGTCTTATCCATTACCTCAAAGCAGTCAATTCCT TAGTAAAGTTTCCAAACAATAGAAATTAATGACACTTTGGTAGCACTAATATGGAGATTATCCTTTC ATTGAGCCTTTTATCCT
L18877	69	T C ---				---	TGAGTCTGAGCAGGAGTTGCAGCAGGGCCAGTGGAGGGAGTCTGGGCCAGTGCACCTTCCAAGGCC C/T/CJATCCATTAGTTCCACTGCCCTGTGTGACATGAGGCCCATCTTCACTCTTTGAAGAGAGCAG TCAGTATTGTTAGTAGTGAGTTTCTGTCTATTGGATGACTTGGAGATTATCTTTGTTTCTGTTGGA ATTGTTCAAATGTT
L31848	36	T C ---				---	GCATTTTACATATCCCAAGCCCTTTAGGGCTACAGT/CJCTCTGTCTCTGGACCCTGTAGGGTGCCA TTTGAGTTTACAGCCTAGAGAAGAAAGGCTTTGGCCCTGGTGGTGGCATAGGCCGTGTAATCGT AGCGCTTTGAGAGGCTGAGGCAGGAAGATAGCTTGAGCTCAGGAAGTTCGAGACAACCTGGGCAAT GT
L38517	137	G C ---				---	GGGTCCAGAAGCCTCTCAGCCAGGAGGAGCTGGCCCTGGAAGGGACCTGAGCTGGGGACACTGGC TCTGCCATCTCCTCTGCCATGAAGATACACCATTTGAGACTTGACTGGCAACACAGCGTCCCCCAG CC[G/C]CGTGGTGTAGTCATAGAGCTGCAAGCTGAGCTGGCAGGGGATGGTTGTTGACCCCTCT CTCCTAGAGACCTTGAG
L39059	123	T G ---				---	ACTTGAGAAGCAGAGCTGCCACCTTCTGGAGGCCACTGTGATGATGAGCCAAGCAATTTGGAGCCA AGTTGAAGGGACAGGGCAACAAAATACAGTAGTTCTTTTGTATTTTGTATTT/GJCGCCTGA AGATCATCCCGCAAGCAGGCTGGAGGTGCCGTGGGCTGTGTTGCTGGGATTTTAGTCTGTGCTGG GAG
L41268d	173	G A ---				---	CAAAGTTGCTCTCTGCCATGAGCACCACAGTCAGGCCCTTGAAGGGATCTTCTAGGGAGACAACAGC CCTGTCTCAAAACTGGGTTGCCAGCTCCATGTACAGCAGCTGGAATCTGAAGCGGTGAGTCTGCAT CTTAGGGCATCGCTCTTCCCTCACACCACAAATCTGAAC[G/A]TGCCTCTCCCTTGCCTTACAAATGTCT AAGGT

L48728b	111	T C ---	---	AAGTGAACAGAAAGCAAAGATGGATTGTGTTCTCTATAAAAGCACATAGTTATGTTTACTGGTATCGT AAGAAGCTGGAAGAAAGAGCTCAAGTTTTTGTTTACTTTTCAGAA[T/C]GAAGAACTTATTTCAGAAAG CAGAAATAATCAATGAGCGATTTTAGCCCAATGCTCCAAAAAAGCTATCCTGTACCTTGGAGATCCA GTC
M18079	52	G A ---	---	GGCACAGTCCAAATACAAATTGGACAGAAGATCTATATTGIACCAGAAGT[G/A]JTATTATTCACG CCATCAAGTATAAGGTTACTGATTGATTGGTCTTTTATAAACATTGGTATATTTCATTTCATGCCAA AGCAAAAGAAAGTAAAAGCTAA
M19169	113	T C ---	---	TAGGGATCTGTCCAGGCCATTGGACACAGCACACCCACTCCACCCCTGTAGTGCTCCCAACCCC TGGACTGGTGGCCCCCACCCCTGGGGAGGCCCTCCCATGTGCTGT[G/C]GCCAAGAGACAGACAGAG AAGGCTGCAGGAGTCTTTTGTGCTCAGCAGGGGCTCCGCCCTCCCTCTCTCTCGCTTCTAATA GC
M21539	114	T G ---	---	TCACTCGTTCCACAGCTCCACCTGCATCTTCTCATCAAGCCATCCAGGGATACACAGGGAGCTTCT TTCCCTTAGCCTGTGATCTGCCATGATGATCCCCGACAGCAAA[T/G]GTTTCTTTCTGAGGCTG CCATGCTGCCACTGTCCAGGTGGAGACTGAGCAAAAGGAAGTCTCAGCTGTACCGGCCCTTCAGAGCT TCTCTTGGGTGC
M26041c	173	A G ---	---	CCTAGCATTATTTCTGGCCCCATTATCATATCCCTTTTCTCTCCAATGTTTCTCTCTCACCTCT TCTGTGGGACTTAAATTGCTATATCTGCTCAGAGCTCACAATGCCCTTTGAATTAATTCCTGACTTC CTGATTTTTTCTTTCTCAAGTGTACCTACTAAG[A/G]GATGCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M26041b	157	A G ---	---	CCTAGCATTATTTCTGGCCCCATTATCATATCCCTTTTCTCTCCAATGTTTCTCTCTCACCTCT TCTGTGGGACTTAAATTGCTATATCTGCTCAGAGCTCACAATGCCCTTTGAATTAATTCCTGACTTC CTGATTTTTTCTTTCTCA[A/G]GTGTTACCTACTAAGAGATGCCCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M26041a	45	C G ---	---	CCTAGCATTATTTCTGGCCCCATTATCATATCCCTTTTCTCTCCAATGTTTCTCTCTCACG TCTTCTGTGGGACTTAAATTGCTATATCTGCTCAGAGCTCACAATGCCCTTTGAATTAATTCCTGAC TTCTGATTTTTTCTTTCTCAAGTGTACCTACTAAGAGATGCCCTGGAGTAAGCCACCCAGCTACC TAATTCCTCAGTAA
M63967	57	G C ---	---	TAAGCAGCTGTCAAGGAGGCCAGTCACAGTCCAGCAATTCACAACCCCTTGAC[G/C]AATGCT TGCCAAGCTGTTTTAAAGCCAAAGAACACCCCTTCTTTGTTCCAAATTAACCTTAGAAGAAACCCCA CAAAATAAGCAATTCAATC
M81695	34	G A ---	---	ACTTACTTACCCCTCACCTGTACGGCTGACGGGA[G/A]GAACCACTGCACCACCGAGAGGCTGGG ATGGCCTGCTCTCTGCTTTGGGAGAAAACGCTTGTCTGGGAAGGGCCCTTGTCTTGTCAAGGTT CAACTGGAAACCCCTAGGACAGGGTCCCTGCTGTGTTCCCCCAAAAGGACTTGACTTGCAATTTCTACG T

U06641d	166 C T ---	---	CTCTCCTTTATTTACGATGGAGGGTTAAATGGAGGATCTCTTTTCTGTGACAAAACATCTTTC ACAACTTACCTTGTAAAGACAAATTTAAAAAAGATCTTTTACAACTTACCTTGTAAAGACAAAT TATTTCCAGGCTATTTAATACGTACTTTAG[C]/JTGGAATTAATCTATGTCAATGATTTTTAAGCTA TGAAATACAAATGGGGGA
U09607	39 T C ---	---	GAGGCCTTATGAGGTCCTCTACTTCAGGAACACCCCTT/CJGACATTCATTTGGGGGGCTCCCG TGGCCTGTAGAAATAGCCTGTGGCCTTTGCAATTTGTTAAGGTTCAAGACAGATGGGCATATGTGTCAG TGGGGCTCTCTGAGTCTGGCCCAAGAAAGCAAGGAACCAATTTAAGACTCTCGCATCTTCCCAAC CCCTTA
U09608	82 T C ---	---	GAGCAGAAGGCAAGAGCGGCAAGATGAGTTTGGCGTTGTATTCAAAGGCTCATCTGGAGCCTC GGGAAAGTCTGGTCC[C]/ACATCTGCCCGCCCTTCCAGCCCTTCCAGCCCCCTCTCTGTTTCTTC ATTCATTCAACAAAATTTGGC
U10694	20 C G ---	---	GTGACATGAGGCCCATTTCTC/GCTCTGTGTTTGAAGAGAGCAATCAGTGTCTCAGTGGCAGTGG GTGGAAGTGAGCACACTGTATGTCATCTCTGGTTCCTTGTCTATTGGGTGATTTGGAGATTTATCCTT GCTCCCTTTTGGAAATGTTCAAATGTTCTTTTAATGGTCAGTTAATGAACCTCACCATCGAAGTTAA TGAATGACAGTA
U13877b	162 T C ---	---	AAAAAGGACTCTGGTTCAAATCCAGGTTCCATTTTGCTATCTTTGTGACCTTGCACAAGTTGTTTAAAC CTCTTTTTCAGAAATTTCTCCATGGAGTAACAATATCTAGTTGGAGGATTAGTGAAGTTACATGT AAAGCACAGAGGAAACAGCCAAAGAGAT[C]/JTTACCGTGGTCTTACTAAAGTACATATCCTAACTTGG GGTTACCTTCAGCA
U15555	187 T C ---	---	TTTCTGTCCACTTTCACCTGGTTTAAAGCCAGCCAGTCATAATAGTAGAGGAATCAGTCAAGCAA AAATGCTTTGGGAAGAAATTAATAGCAATGCTGAACATCAGGAATTTAGATATCCGTACAGAGAGT TCCAGTAAATTTATGAGTCCACGACCCCTTTTCTAAGCAGTCTGGTCCATG[C]/JGGTCTCATAG CTCATATGCAGGATTCATCA
U17077	122 T C ---	---	TCCAATTTATGGTCCCAAAAGCAGCTTCCACGTTTGCCATCTGGATGACAAACGGAAGATCCACT AAAACGTCCACGGGATTAACAGAACGTCCTTGCAGACTGAGCGATGACACCACAC[C]/JTTGTTTGG ACATTTAAATTCACCTCTGCTGAATAGGAGGAAGCTTTTCTTTTCTGGGAAACAACTGTCTCTTGG AATTA
U18543	58 T C ---	---	GCACATGCAGAATAGACTCAGCCTATGTCTGATTCAGCTGGGTAGTTCTAGAACTTT[C]/JAGAAG CTCCATCTTTAATGTTTTATTGTTATGTCCTCCCTCCCGGCTTCCACCTAAATTTAGAGCTTTAAA AGATGCACTGCCCAATAGGACACACGATGGTGTAGCTGAAGTTTGATTAGCAATTAGGCACCTCC AAGGCTTTAGTAGAGAGAGCC

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U25975b	164 C A ---	---	TCAC TGTGTGGCCTCATACTCTTTTCCATTTTCTACAAGAAGCCCTTTAGTATATGAAAAATTATT ACTCTTTTGGGGTTTAAAGAAATGGTCTGCATAACCTGAATGAAGAAGCAATGACTATTCTCTG AAGACAACCAAGAGAAAAATTGCAAAAAGAC[C/A]AAGTATGACTTTTATATGAACCCCTTCTTTAGG GTCCAGAAGGAATTGTGGACTGA
U25975a	143 C G ---	---	TCAC TGTGTGGCCTCATACTCTTTTCCATTTTCTACAAGAAGCCCTTTAGTATATGAAAAATTATT ACTCTTTTGGGGTTTAAAGAAATGGTCTGCATAACCTGAATGAAGAAGCAATGACTATTCTCTG AAGACAAC[C/G]AAGAGAAAAATTGCAAAAAGACAAAGTATGACTTTTATATGAACCCCTTCTTTAGG GTCCAGAAGGAATTGTGGACTGA
U25997	61 A G ---	---	CAGGGAGAGGTTATTACAAACCTCACAAACTAGTATCATTTTAGGGGTGTTGACACACCA[A/G]TT TTGAGTGTACTGTGCCTGGTTGATTTTAAAGTAGTTCTCTATTTCTATCCCTTAAAGAAATTT GCATGAACCTAGGCTTCTGTAATCAATATCCCAACATTTCTGCAATGGCAGCATTCACCAACAAAA TOC
U28413	29 C T ---	---	ATTCTGACAGCTAAATTAGCCCTAAATG[C/T]GGGTAATATTTTCTCATGTTTAAATGAGGTT AATATTGCATAAAATCCTAAACAGACTTCTGTATAGTTTATTTAGTCAAAATGTGTTCTTGATCC CAGATGTTGTGGCCTGGGAAAGCCCTCATTGCTACAGTACAAGTAAACAAAGTCGTTGTACCTCAGTT G
U30884c	89 A G ---	---	TAGGGGTAGCATTTAAGATTCAGGAGTCATTAGCAGTGATGATTTTGGACCTGCCGTATAATCTGTT CTTCTATTCCACGTTAGCCA[A/G]TTGTTCTTGATGAATCTATATGATCATAGAACACAAATCTAT TGACGGAAGTCATTAGAATGGCTTGTGATATCTGATGGCTTGAACCTTGCCACAGTTGAACACAAAGT GCTGTCA
U30884a	34 A G ---	---	TAGGGGTAGCATTTAAGATTCAGGAGTCATTAGC[A/G]GTGATGATTTTGGACCTGCCGTATAATCT GTTCTTCTATTCCACGTTAGCCAATTGTTCTTGATGAATCTATATGATCATAGAACACAAATCTAT TGACGGAAGTCATTAGAATGGCTTGTGATATCTGATGGCTTGAACCTTGCCACAGTTGAACACAAAGT GCTGTCA
U31216b	78 A G ---	---	GGGACAGCATATGTGGCACCCTCTCTGTGCACGTGAAGACCAATGAGACGGCTGCAACCAACA GCCGTCAATCA[A/G]CCCTCACTAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTCAGATA CCAGCACCAGAGCCCTTTACAACGTAGAGGAGGAGGATGCCAGCCGATTGCGTTTAGCCCGCC TGTTAGCCCTTCCAT
U31216a	70 G A ---	---	GGGACAGCATATGTGGCACCCTCTCTGTGCACGTGAAGACCAATGAGACGGCTGCAACCAACA GCC[G/A]TCATCAACCCCTCACTAAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTCAGATA CCAGCACCAGAGCCCTTTACAACGTAGAGGAGGAGGATGCCAGCCGATTGCGTTTAGCCCGCC TGTTAGCCCTTCCAT

U31416c	76	G A ---			AGTTGCCAGCTCCCATGTACACAGCTGGAATCTGAAGGCGTGAGTCTTCATCTTAGGGCATCGCTC CTCCTCAC[G/A]CCACAAATCTGGTGCTCTCTCTTGTCTTACAAATGTCTAGGTCCTCCCACTGCCTGCT GGAAAGAAACACACACTCCTTGTCTTAGCCACAGTCTCCATTTCACCTTGACCCCTGCCACCTCTCC AACCTAACTGGCTTACTTCCT
U31416b	68	C T ---			AGTTGCCAGCTCCCATGTACACAGCTGGAATCTGAAGGCGTGAGTCTTCATCTTAGGGCATCGCTC [C/T]TCTCAGCCACAAATCTGGTGCTCTCTCTTGTCTTACAAATGTCTAGTCCCACTGCCTGCTG GAAAGAAACACACTCCTTGTCTTAGCCACAGTCTCCATTTCACCTTGACCCCTGCCACCTCTCCA ACCTAACTGGCTTACTTCCT
U37519a	78	C T ---			ACGGGTCACACAGAGAAACCTGAGTCTAGCCATGAGGGGCTTATGCTCCCAACTCACATTGTTCTCTCC AGACCGCAGG[C/T]TCCCCAGCCTCAGTTGCTGGAGCTGTCACATGACTGCATCCTGCCTGCCAGG GCTGCAAGCAAGTCTTGTCTTATCTGGGGACGCTGCTCGAGAGAGGCGGAGAGGCGCCGAGAAC ATGCCAGGTGTCC
U37690	54	A G ---			GACACGCTGAAACCCACCCACCCGCTGTGCTGACCATGGGCCCTGAGCGTCTT[G/C]CCCCGAATTC ACGAGGCTGAGGCATCCGGAGCTGGCGTAATGCTGGCCGAGTGTGTGTATCCCATACCCCACT CTGGAGGAACCATCCAGTAAAGTCTTT
V00540	39	T C ---			TGAAACCGTTTCAACATGGAATGATCTGTATTGACTAA[T/C]ACACCAGTCCACACTTCTATGACT TCTGCCATTTCAAAGACTCATTTCTCCTATAACCCAGCATGAGTTGAATCAAAATTTTCAGATCTTT TCAGGAGTGTAGGAAACATCATGTTTACCTGTGCGAGGCACTAGTCTTTACAGATGACCATGCTGAT A
X15943	106	A T ---			TCAAGAAGGTGACTGCCCTTGTATGATGGATGGGAAGATGAATGACTGTTTTTACTGGGGTGTA AACCACTCTGAGCCTCTCTGAGACCCTGTGGTTTTAA[A/T]ATCCATAAGGAAGGTACCCACAC CAGTATCTGAGTTCAGTAGCTAGACCCTAGAAATTTGGATTTCATCTCTGTTTTTTCATGCTCTCCTT GTAAACCTGAGATCATCAG
X52011b	148	C T ---			AGGAAGATCCCAACCGACCTTCTCGCCCTAATCCTTTAGATTAGGTACATTACATTAACTTTAGGA ACCCAGACCGAAAAGTTGCTGAAAGGGAAGGAGACACATTCACAAAGAAAAGTTGCGAAAATTGCG AAATCTGTTGTGCA[C/T]GCTCAATGAAAACGCCCTTTGGCTTTGGGCTTTTATTTTTTGGAACTG CGAGTGGCTTAGGTCTAGCCT
X52011a	118	A C ---			AGGAAGATCCCAACCGACCTTCTCGCCCTAATCCTTTAGATTAGGTACATTACATTAACTTTAGGA ACCCAGACCGAAAAGTTGCTGAAAGGGAAGGAGACACATTACAAAGAAA[A/C]GTTGCGAAAATT GCGAAATCTGTTGTGACGCTCAATGAAAACGCCCTTTGGGCTTTTATTTTTTGGAACTG CGAGTGGCTTAGGTCTAGCCT

X54741	24 A G ---	---	CAGGCCACCTGCTCTCTCCACAG/GJTGACAGCTTCTGAGTACCCCTCTGTCCAGCCAGCTCT GGACAAATGGAACCTCCAGGGCTCCAGGACTGGGGCTTGCCAGGCTTGCAATAGCAAGGCCAG GGCACAGCTGGAGACGATCTTGCTGGCAGGGCTGGCCCTTGTCOCAGCCCACTGGGCCCTTCTOC AGCAAGCAGTGC
X54869	99 A G ---	---	AAGCATTGCGTTACAGTGCATCAGATACATTTATATTCTTAAATAGAAATATTATGATTGCAT AAATCTGAAATGAATATGTTATTTGCTCT/GJATACAAAATCTAAATCAATATTGAAATAG GATGCACACAATTACTAAAGTACAGACATCTAGCATTTGTGCGGGCTCATTTGTCTCAACATGGTA GCCGTGCTGACACCTCAGAACGACGAGGTGCTGGCCCGTTCTGCTGGACCCCGGGAACCTCTC CTGCCGGAAGCCGGACGGGATGGCCCAACTTCGCCCTGCCACTTGACTTCACCAATCCCT TCCTGGAGACTG/AJACCTGGTCTCAGGAGCGAAGGACTGTGAACCTTGCGCTGAAGAGCCAGA GAAATGTGAAGATGTGACAAAGCCTTTAAGCGTTGTACACTTGATTGTATATAAGATAAT/GJT CATACTGGAGAAACTCCAGAGGTGACAAATGTGACAAACATTTAATTAATCTCATACCTTA TTGCACAGGAAAGCATTTATCTTGAGAAAAATGTATAAAGAAATGGAAGATCATTAAATATCTGCT CATATCTTAACATCAGCGAGTT
X66924	147 G A ---	---	CTCAACCCATAACCTCAACCACATCT/GJATCTCCACCCACATCCACACATCCACCTCCATCC CCAAACCATCTCATCCCAACTACAGCCCAACCCAGCCAGCCAGACTAATCCACAGCCATCCCCAA CTCATCTCATCCCAACTGCAGCCCAACCCAAACCCAGGGCCATCCCCAAACCCATCCCCAAGCC AACTCAACACCATCC
X78932	62 T G ---	---	ACCCAACTCAAGTCCAGGCCAGGCATCTTCTGCCCTGCCCTTGCTTGGCCCATCCAGTCCAGG CGCTGGAGCAAGTGTCTAGCTACTTCTCT/GJACITTTGAAGACCCCTCCACTCTTGGCTCA CATTTCTGTGTGATCCCCACTTCTGGGCTCTGCCACCCACAGTGGGAAGGCCACCTAGAAAG ACCCAACTCAAGTCCAGGCCAGGC/GJCTTTCTGCTGCCCTGCCCTTGCTTGGCCATCCAGTCC AGGCGCTGGAGCAAGTGTCTAGCTACTTCTCTGCACTTTGAAGACCCCTCCACTCTGCTGGCTCA CATTTCTGTGTGATCCCCACTTCTGGGCTCTGCCACCCACAGTGGGAAGGCCACCTAGAAAG GGCACCCAGAGTGACCAAGTCCAGGAGGGGCGCCCTGCCGTGCTGCTTTCTTTT CAGCCCGGAGAGGTCTGACCTGGGGCTTCTCAAGCCTACTGGCCACGCTCCCGCCGCTCT CTTTTCTCCCAAGC/GJAAACCAATGGCCCTTCACTCGCTGCCGTGGAGGCGGGGGCTT CTTTCAGAGC
X80026	25 T C ---	---	ACCCAGGACATGGTCTAAGGACATGGATGGGTGCCCCAGACGTGTGCACAGGGACCCCTCTGCC CACTCTGGGCTTTTCAGATACTCTGACCAAAAAGCCTGCTTTAAACCGCAAGATGGGGCT/GJGGG ATGCGCAGGAGGAGCCATCGGGTACTACGCAGCAACACTCACAACTGTCCAGGCTGAGATAATCCC GGGA
X80197b	99 G C ---	---	
X80197a	28 A G ---	---	
X85106	150 G A ---	---	
X87160	128 T G ---	---	





1282	130	C T	---			GTGGATACCACTACAGTCTAATTTTCAGATGTTTTTCATTACCCCTAAAAGAAATCTTGACCCATTA GCAATTATCCCTCATCTGCCCTCACCCCGAGGCCCTACTCTTTATCGCTATAGATTTGCC[C]TACT TGACATATCATACACATGGAGCCATACATATGTGTGCCCTTCATGATTGGCTTCTTTCACTGAGAATA ATGTTTTCAAGGT
6810	68	C T	---			AGTATCACACATACCTTAATATATAGATATACACAATAATAAAATCACTCCCTACCTTGAAAACTTT A[C]TJAGAAAGCATTTTTAATTTTACAAACAAAGCTCAAACGAACCTACAATAAGTCTAGTAGTCTG TTACGTGCCAAGGGATAAGGCTGAACAATAAATTAAACCTTTAAAATGTCTATGAACAAGTACAA TTTTCTTTTGTAGTCTGCAGAGCAATGACCCTAAGAAATATTTTAAAGGC
6817	118	A C	---			CCAAGTACATTGGGTGAACGATGAGCTAGCTGTTCTAGTATTGCTTTTGTATCCAGTTAAGACCA TCAGCATATACAACATCACTAACAATGTAAGCTGAGGGTAAC[A/C]TGTGGATACCCCTG TGTGCTCTACTGGCCTCCAAAGGCATTGAGGGGATCATCAAGATGTTGGACACCTTGTGTTCAATC TTGGTTCAGGTGCGGCCCTGTCAGATCGGCTTTTGGTTTGGTTGCTTAG
6819b	212	C	---			CCATTTATTTTCTCTAAATTTTAAATAGAGACTTTAATGGAAACATTTAGTACCATCATGTCA CCCTGAATGCCAGCAATACCTCGACTTTTACACAGCAGGAAGCCTAGTAAAGCCCGTCAGTAGT ACACATTTCTCTATGGTCTTCAACAGTTTGCATATACAAAATTTCTGCTATTTTGCTTTAGCAAA CAGCAATAACTTTTGTGTTCTCTATATGACACCTAATATCCA
6819a	166	G T	---			CCATTTATTTTCTCTAAATTTTAAATAGAGACTTTAATGGAAACATTTAGTACCATCATGTCA CCCTGAATGCCAGCAATACCTCGACTTTTACACAGCAGGAAGCCTAGTAAAGCCCGTCAGTAGT ACACATTTCTCTATGGTCTTCAACAGTTT[G/]CATATACAAAATTTTCTGCTATTTTGCTTTAGC AAACAGCAATAACTTTTGTGTTCTCTATATGACACCTAATATCCA
681xx	39	A G	---			CTGGTATGTCATAAGCAATCCATAATTGTTATAGCTATT[A/G]TTACTATGGCACCAATTTGGGACA CAGATTATATATGTCAGACACCAAGCAATGCTCTTAAAGATATGCAGCAAGCACAAATCTGTCATGGT TTAACAAGAAATGAACGCTAGG
6972b	149	G T	---			AGGATTCCTCTTTTCTATTGATTGGAATAGTTTCAGAAGGAATGGTACCAGTTCCTCCTGTACCT CTGGTAGAATTGGGCTGTGAATCCATCTGGTCTGGACTCTTTTGGTTGGTAAACTATTGATTATGGC CACAATTCAGA[G/]CTCTGTTATTGGTCTATTTCAGAGATTCAACTTCTCCTGGTTAGTCTTGGGA GAGTGTATGTGTCGAGGAAT
6972a	122	A G	---			AGGATTCCTCTTTTCTATTGATTGGAATAGTTTCAGAAGGAATGGTACCAGTTCCTCCTGTACCT CTGGTAGAATTGGGCTGTGAATCCATCTGGTCTGGACTCTTTTGGTTGGTAA[A/G]CTATTGATTA TTGCCACAATTCAGAGCCTGTTATTGGTCTATTTCAGAGATTCAACTTCTCCTGGTTAGTCTTGGGA GAGTGTATGTGTCGAGGAAT

7598k	210 A C ---				AAAGGTAATCAAAGTTCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCGATTTACCTTGGAGAAATGAAATATTTCTTGAGGATGCCCTTTTA ATATTTGATCCCATATGTGAGAGATTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTTCCT CAATGCAG[A/C]
7598j	208 A T ---				AAAGGTAATCAAAGTTCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCGATTTACCTTGGAGAAATGAAATATTTCTTGAGGATGCCCTTTTA ATATTTGATCCCATATGTGAGAGATTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTTCCT CAATGC[A/T]GA
7598i	192 G T ---				AAAGGTAATCAAAGTTCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCGATTTACCTTGGAGAAATGAAATATTTCTTGAGGATGCCCTTTTA ATATTTGATCCCATATGTGAGAGATTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTTCCT CCTCAATGCAGA
7598h	144 C T ---				AAAGGTAATCAAAGTTCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCGATTTACCTTGGAGAAATGAAATATTTCTTGAGGATGCCCTTTTA ATATTTGATCC[C/T]ATTATGTGAGAGATTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTTCCT CCTCAATGCAGA
7598g	142 C T ---				AAAGGTAATCAAAGTTCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCGATTTACCTTGGAGAAATGAAATATTTCTTGAGGATGCCCTTTTA ATATTTGAT[C/T]CCATTATGTGAGAGATTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTTCCT CCTCAATGCAGA
7598f	120 A G ---				AAAGGTAATCAAAGTTCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTAACCGATTTACCTTGGAGAAATGAAATATTTCTTG[A/G]GGATGCCCTT TTAATATTTGATCCCATATGTGAGAGATTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTTCCT CCTCAATGCAGA
7598e	83 C T ---				AAAGGTAATCAAAGTTCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTA[C/T]CAGATTTACCTTGGAGAAATGAAATATTTCTTGAGGATGCCCTT TTAATATTTGATCCCATATGTGAGAGATTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTTCCT CCTCAATGCAGA
7598d	77 C T ---				AAAGGTAATCAAAGTTCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAAAGGAACTCA ATGAAATAAGCCGCTA[C/T]GCTAACCGATTTACCTTGGAGAAATGAAATATTTCTTGAGGATGCCCTT TTAATATTTGATCCCATATGTGAGAGATTTCCCTGATATGTTATCTTATTTATATTTTCCCGTATTTTCCT CCTCAATGCAGA

7598c	56 A G ---	---	---	AAAGGTAATCAAAGTCCCTCTATAAATTATGATTACAAAAGACACCCAAAGCCAA/GJAGGAAC TCAATGAAATAAGCGCTAACCCAGATTTTACCTTGGAGAAATGAAATATTCTTGAGGATGCCTT TTAATATTTGATCCCATTTATGTGAGAGATTTTCCCTGATATGTTATCTTATTATATTTTCCCGTATTTT CCTCAATGCAGA
7598b	47 C G ---	---	---	AAAGGTAATCAAAGTCCCTCTATAAATTATGATTACAAAAGACAC/GJCCAAAGCCAAAGGAAC TCAATGAAATAAGCGCTAACCCAGATTTTACCTTGGAGAAATGAAATATTCTTGAGGATGCCTT TTAATATTTGATCCCATTTATGTGAGAGATTTTCCCTGATATGTTATCTTATTATATTTTCCCGTATTTT CCTCAATGCAGA
7598a	30 A G ---	---	---	AAAGGTAATCAAAGTCCCTCTATAAATTATGATTACAAAAGACACCCAAAGCCAAAGGAAC TCAATGAAATAAGCGCTAACCCAGATTTTACCTTGGAGAAATGAAATATTCTTGAGGATGCCTT TTAATATTTGATCCCATTTATGTGAGAGATTTTCCCTGATATGTTATCTTATTATATTTTCCCGTATTTT CCTCAATGCAGA
7998c	116 A T ---	---	---	GTGTTGATCTCACTGGGTGCTGAGGCCGGAGCTGTTCTTATTCAGACATCTTGCCAGCTCTCCTGTA ATACITTTAATGAATGGGTGATGCTCTATCTTCAAGGTCCCAATAA/TJCTTGAGGTTCCCT
7998b	94 A C ---	---	---	GTGTTGATCTCACTGGGTGCTGAGGCCGGAGCTGTTCTTATTCAGACATCTTGCCAGCTCTCCTGTA ATACITTTAATGAATGGGTGATGCTCTATCTTCAAGGTCCCAATAA/TJCTTGAGGTTCCCT
7998a	75 A T ---	---	---	GTGTTGATCTCACTGGGTGCTGAGGCCGGAGCTGTTCTTATTCAGACATCTTGCCAGCTCTCCTGTA ATACITTTAATGAATGGGTGATGCTCTATCTTCAAGGTCCCAATAA/TJCTTGAGGTTCCCT
8071	119 A G ---	---	---	AAATACAGAATTTTATTAGAACTGTTTAAAGTAGAAAAAACCCCTGTCAAGAAAGACCAGGTGG AAAATGGGTCCCAATAAATGGAATTTTAGGGCAACAAAAGTCTAAAGGCCA/GJCAAAAAGAGA AATAGCACCACTGTCAATTTGAACAATGGCTAGTTACTTGCAATTTTGGCATTGTTAATCACTGAATC TGGGTTTCCCTCTGAAATCCACACAGAGCATGCACACACATTTTATCAT
8467b	93 C T ---	---	---	AAGGCTTTCCCTCTAAACATCAGTCTACGGAGAACTGGGAAAATCTCGGATATTTGGCTTATCAGTTT TGACGCAAAATCCACTTTGCTGTAA/C/TJGGTCACTCCGAACCTCCCTTCAGAGAGCAAGCAAGCAAAA TTAAGTGTGATACCTGGAGCTTATGCATGCAAAAAGCTTGCAAAAAGTATTAAAGGAAAAATTAATG
8467a	70 A G ---	---	---	AAGGCTTTCCCTCTAAACATCAGTCTACGGAGAACTGGGAAAATCTCGGATATTTGGCTTATCAGTTT TG/JGJGCAAAATCCACTTTGCTGTAAACGGTCATCCGAACCTCCCTTCAGAGAGCAAGCAAGCAAAA TTAAGTGTGATACCTGGAGCTTATGCATGCAAAAAGCTTGCAAAAAGTATTAAAGGAAAAATTAATG
8498	84 C T ---	---	---	AGGGTTACGGGTTTGGTTTAAATCAGGCTGCACACCTTTCAAAATCAATCTGACATCTCTCTATGTCA AACTGGCTTCAGCTAG/C/TJAAATACCTTCAATTAATCGAAAAAGAAAAAATGCTTTAAGGAAAAAA AATCCAGTTTAAAGAACAAATTAACATTAGTCTTTAAATAAAGGAGGGCTAATGTTTTCATGTTGCT TTATACATCTCTCTCTCAATACAGAACCCAGGAATGTAATTTTCTTAACCTCAG

WI-18562	29	G A ---				CTAAGGAAAAATTTAATGATGGAATATC[G/A]JACAAATATTCACATCATTTAAAAACAAAGTAG CTTCTCTATTTCACATAGCTTAGTTTGGGATAGAAATAGAATAATGTTTACAATGATTCCTTACATT TAGCATTAAATCAGAAACGA
WI-18618	51	A C ---				ATAGCAGACTTTTAAATCAATGCCAGAGACAAAGTGAGCCGAGCTAAGAAC[A/C]JGCTCAGCTTCG TTACAATGAAGAAATGGTTTCCTTCGATGCAAAAGTATAATTGTAAACACACAGTGCTCGCACAGTTC AC
WI-18683	22	C T ---				TAAGCTGTTTCAGGACTGGACTC[G/T]GGTCCCTTTATTGAGACTGACAGGCCAGTGGGTCCACCCAAA CAAAATAAATTTCTCTCCAAAGCCTGCCTGCAGT
WI-18520	75	G A ---				GACTTTGGTGATTTAATTGCTTTCCCTTAAATATGAGAAATAGGTGTAATTTCTCCTTTGTTCTTTT ACTACA[G/A]JCCGGAGTGGTAAATAGTACCTACTGCTCAACAAACACGGGCATCCACTCTGTCTTCAA TGCCTCTCCGTGAGAC
WI-18563	94	A G ---				AAATAAGTTTTATTGGCACACAGCCCAAGCCCACTGGGATGACACATTTGCCAGGGCTCATCTTGCAA TACAATAGCAGGGTTCACTAATGTGAC[A/G]GACATGGTGGCTCACAAGCCAAAGATATT
WI-18582b	69	T A ---				GTCTATTCAATTTAGTAGACCCATTTCACTCTGTTTAAATGGCTACATTTGTTTTCATTGTGAGAC T[A/G]TGCCATAATTTAATCAAGTCCATATTGAAAGACATTTGGATCGTTTCCCAG
WI-18723f	94	G A ---				AACTTTATTGATCTGACGATCAGCGATTAGTTCTCATCCACATTCACATTCGCTGTAGATTTTGAAAG TGGTAACAGGTACATAGGTAACCAA[A/G]ATATATAGCTTATTGGTGAATCTTCATCCT
WI-18723e	71	T C ---				AACTTTATTGATCTGACGATCAGCGATTAGTTCTCATCCACATTCACATTCGCTGTAGATTTTGAAAG TGGT[C/A]ACAGGTACATAGGTAACCAAAGTATATAGCTTATTGGTGAATCTTCATCCT
WI-18723c	96	A G ---				AACTTTATTGATCTGACGATCAGCGATTAGTTCTCATCCACATTCACATTCGCTGTAGATTTTGAAAG TGGTAACAGGTACATAGGTAACCAAAGT[A/G]TATAGCTTATTGGTGAATCTTCATCCT
WI-18619	44	G A ---				TTTATTACAATATTAGGTGGCACAAATAACTAACAGCTTCTG[A/G]ACAGGAGGTAAACATTCTCA TAGACTTTGCAACTCAGCCAGAAAGTAAACTCGAAATA
WI-18715	76	G A ---				TTATTCAAAAAAGTGATATTGCAGAGGTCTGGGGCTGTACATGGGCAGGGCTTGGTGAGCTTTG TACATGGG[G/A]JCTGGGAGACAAGGGAGCCTCCAGGTGGAAGGTATTTTAAATAAAAAAATAA TGGAGCTACAACACCCCC
WI-18535	107	G A ---				GTAATAAAGTTTTATTGGCACGCCACGCTCGTTTCATTTCATATGCCATTGACATCTGCTGTGCCCT ACACAGCAGGTGGGACCTGCTCTTCACGGGAGAGCTA[G/A]JTGTGTTAAAGCAGTGGTCCCAAC CTTCTGTGTOOCCGIG
D17525	107	C T ---				AGAGTGGTCAGAACACAGGCCGAATCCAGGCTCTATCACTTACTAGTTTTCAGTTCTGGCAGGTGAC TTTATCTCTTCGAACTTCAGTTTCTTCATAAGATGGA[A/C]TGCTATACCTTACCTACCTCGTAAAA GTCTGATGAGGAAAAAGATTAACTAATAGATGCATAGCACTTAACAGAGTGCATAGCATACACTGTTT TCAATAAATGCACCTTAGCAGAGGTGATGTGTCTACCAGGCAGACGAAG

DWU-133c	313	A G ---	---	TAATTGGCCACTGCCCTTATTATTACAAAACAGAAATGCTCATGACITTTTTTATGTGTACCATCCT TTAATAGATCTCATACACCAGAAATCAGATCATGAATGACTGACAGAAATATTTTGTGGGCAGTCCT GATTTAAACTAAGACTGGCTTGTGGTTAAATGAATATGTTTCAGTTTTTGAATTTAATAGTAACCTCC AATTCAGTAAATGGTATCACTCGITTTACCCCTTTTAAAGATATGATTAGACT
DWU-133b	236	T C ---	---	TAATTGGCCACTGCCCTTATTATTACAAAACAGAAATGCTCATGACITTTTTTATGTGTACCATCCT TTAATAGATCTCATACACCAGAAATCAGATCATGAATGACTGACAGAAATATTTTGTGGGCAGTCCT GATTTAAACTAAGACTGGCTTGTGGTTAAATGAATATGTTTCAGTTTTTGAATTTAATAGTAACCTCC AATTCAGTAAATGGTATCACTCGITTTACCCCTTTTAAAGATATGATTAGACT
DWU-133a	199	C T ---	---	TAATTGGCCACTGCCCTTATTATTACAAAACAGAAATGCTCATGACITTTTTTATGTGTACCATCCT TTAATAGATCTCATACACCAGAAATCAGATCATGAATGACTGACAGAAATATTTTGTGGGCAGTCCT GATTTAAACTAAGACTGGCTTGTGGTTAAATGAATATGTTTCAGTTTTTGAATTTAATAGTAACCTCC ITCCAATTCAGTAAATGGTATCACTCGITTTACCCCTTTTAAAGATATGATTAGACT
DWU-36	102	C T ---	---	ATGAGATCCTTTAAATCCTTCCATGAAACGTTTTGTGGTGGCACCCTCCTACGTCACAAACATGAAGTG TGTTTCTTCAGTGCACTCTGGGAAGATTTCTACCCCTTGGACCAACAGTTCTTCAGCTTCCATTTGGCC CCTCATTTATCCCTCAACCCCGCCACAGGTTTATACAGCTCAGCTTTTGTCTTTTCTGAGGAG AAACAATAAGACCATAAAGGGAAAGGATTCATGTGGAATATAAAGAT
DWU-387	169	G T ---	---	GTGTATAAATGCAACTGTTGATTTCCTCAACATGGCTCACAAATTTCTATCCCAATCTTTTCTGAA GATGAAGAGTTTAGTTTTAAACTGCACTGCCAACAAAGTTCACTTCATATATATAAGCATTAATTTTAA CTCTTTTGAAGTGAATATAATTTATATACAATGCTTAAAGCTTCTTTAATACTAAGTATTTTCA GGTCTTCACCAAGTATCAAGTAATAACACAAATGAAGTGTCATTATTCAA
DWU-447b	172	--- ---	---	ATTTAGTGCTTTTGGCTTAAATAATCAATTGCAAAAGTATTTCTGAAGTGTCAAGCTGCCAGTCAGAT GGGCTGTTGCCATTTAAATCACTGTAAATTAATTAGTTTGAATAGAGCACAAAGCTTAGCTAATCAA CCATTATTTTCAATTTGTTTGTCTAAGAGGATTGANAATCAGTTTAGTTTAAATGTCTTTCTGTAG GCCTTTCTTCTTACAATGAAGAGATGATTCITCTAGTTTATGGTTA
DWU-447	85	A G ---	---	ATTTAGTGCTTTTGGCTTAAATAATCAATTGCAAAAGTATTTCTGAAGTGTCAAGCTGCCAGTCAGAT GGGCTGTTGCCATTTAAATCACTGTAAATTAATTAGTTTGAATAGAGCACAAAGCTTAGCTAAT CAACCAATATTTTCAATTTGTTTGTCTAAGAGGATTGANAATCAGTTTAGTTTAAATGTCTTTCTG TTAGGCTTTCTTCTTACAATGAAGAGATGATTCITCTAGTTTATGGTTA
DWU-476	63	C G ---	---	GTAATAATTCAGTTTTTTCCAGTTCCTTTTGTGCTGCTTCATAGCGTTTAAAGTGAGTCGAT AAATCAACTGTCCATCAGGTGAGTGTGCTCCATACCCAGCGGTTCTTCATGAGTAGTGGGCTATGCA GGAGCTTCTGGGAGATTTTTT

DWU-505	67	A T	---			TCATACTAGGCGAGTATCTCTCTAGCTAGTGGCCCATACAGAAAAATTTCTATCACCATACAAAAATTA A/TJTGACAGTATTTATGTTTTAAAGCACAGGTGTACCGAAAACTGTGAAAAAGTCTGAATTTATGGGTT CTATGGATGCATTTTGCCTAACCTAGAGAAAGAGTTTGATAAATTTTACCAGCTTTGAAGATGGAT TAACITTTGACITTTGAGCTTTAAACTTTTAA
DWU-512	131	A G	---			AAAATCCAGGCGATTTGGAATCTGTTTTTCATGATTTATAGAGGGTTTACAAAAAGTGCCACTTATTA AGAGCTTCCACAGTGAAGATGGAGAGGTGAACCTTGCTTTGAATATTTCCAGATGTGTTGGTC[A/G] TGCGTATGGCAGTGAGCAGGTATGTGTTTGTCTTTGCTTGCACTGAAAAATTAATTTGCTATCAAGAGC AAACTATGAACGGTTTTTTATCAAGATGTCCTCAGAGTGAAGATGCCGAG
DWU-525	97	A C	---			AACTGCATATAGATAATTATCCAGGATGTGTGGCTCATTCTTTTCAGCTTGTCTTCTATCTACTGTTGTA ATATACAGTTTTTGTAAACATATGATTGA/CJAAGAAGAAAGTCTATGCTTAGGCCAGTCAGTACA CCCAATTTTAAAAAATAACATATCTTGTCTTTCACAAATATAGTTGAACAAGATTTCCCTAAAAAT CCACCAGGATTAATCTCTAAATTTCTAGTCTGATTTGG
DWU-59	94	C T	---			CATTTCTTTGTAAAGGTAATGGACTCACAAAGGGGAAGAAACATGCTGAGAATGGAAGTCTACCCGG CCCTTTCTTTGTGAACGTACATTTGGC[C/T]GAGCCGTGTTTCAGTCCAGGTGGCAGACTCGTTTTTG GTAGTTTGTTTAACTTCCAAGGTGTTTTACTTCTGATAGCCGGTGATTTTCCCTCCTAGCAGACATG CCACACCGGGTAAGAGCTCTGAGTCTTAGTGTTAAGC
EST11	68	C	---			CTTGATCATGGGTGGAATTTTGTATCTGGGCTTCATGGGATGCATAAAAAATTTTCCAGTTGGTAAAG CAGCAGGTGCCGAGGGTCTGGATCAGAAAAAAGGCA
WI-19856b	63	C T	---			CACACTGGCATCTAGGCCTTCGCCTGCAATTCAGAAAGAGAGCCAGGTCCCCCTCCTGGAGAA[C/T]G CTGCGTTCCCGAGCCCGCACACCGGCTTTGCACACAGGCTGTTGAGGCGAGGAGGTGGTAAAGACGT AGCTGTAGACCCAAAGCAACCAAGCCCTGGGACCCCTGCGGGAGAGGAGCACTTTAGAACATGGAA AAGTGTGGTCACTCCCATCATTAGACAAGACACATCCTACATAATAAAAAAGT
WI-18014	40	A G	---			TCCATTTACATTTGGTGGCATTTGTTGAATAGCTACAGAA[A/G]GAATGAAAGTGCAACCATCAGAGT GTAATTAGGTCTGTGTGACCCAGGAAGTGTCTGTAAACAGAGATTTCTCAAGGGCAAGTGGCTTCT A
WI-18036b	97	T A	---			TTCCAATGTAAAGAGTCAAGTACCAAGTTAACTTCTAGAAATACAAAGAGAACATGATAAAATCTG ATCACAGTGGAAAAATTTAATCTTTCATAA[T/A]CTGACAGGTCAAGTAAGCTAAAGGAAACATAT TAGGGATCTGAAGG
WI-18036a	27	T C	---			TTCCAATGTAAAGAGTCAAGTACCAAGTT[C/J]AAACTTCTAGAAATACAAAGAGAACATGATAAAAT CTGATCACAGTGGAAAAATTTAATCTTTCATAATCTGACAGGTCAAGTAAGCTAAAGGAAACATAT TAGGGATCTGAAGG
WI-18046	72	C T	---			TGTAAGGTGACTTCTATAAGCTTCCCTAAAGTGTCAAACTTTCTACTGAGATTATTTTCAGGCCAAT GTGTC/TJTGTTGGGCTGAGATTGATTATCAGCTGGGTAAAGTTAACCTGTCTCTGTTTCA

WI-18063	105	G A	---			AGGCTTTAAACTGATAACAATTGCCTTTAATCACAATACAAAAAAGCTGGACTTTCATTCCTTCCTTC CCATGTTTCTGATTTGATGTAACTTAAATTTGTG[A]TCCTTTAAACAATATACTGAGCTGCA
WI-18078	86	A T	---			AGTTGAAAGATCAGAGAGGTTATGGTTGGTAGTGAAGCTGAGATTCAGATTCAGAACTGGTCCAGTGTG TTGTTTTCAGCATCAG[A]TGTCCACTAGCCAAAGTTGATCTCTGCAGTATCTACATGTGGT
WI-18091	90	T C	---			CCAAAGCTCACTCAGTATTTAATCATCTGCTAATTCATCCTTTGTTAATTCATCAGACACTGTGGT TTTCATCTAGAAAGTTGACTT[C]GGGCTTTTATATACCTCCATATCTCAACTTGTTAAGC
WI-18119	38	T C	---			GCAATCTGTAAAGTTTGGTAGTGGTATTACAGAGGAT[C]TTGTTAAATGGATTGGAGTACTTAC CACTATTTCTGCTCTGAAATAGTTCACTAACCAAACTACTGACAACAGTTTAAATTTGGTTCTT
WI-18142	66	T G	---			TTCAAGATAAATTACAATTGGAAGGGGACCAATAATTCACATTTTAAATCGAAAATAATCTATATAC[ T/G]CCCAATAAACTCACAGTAAATAAGCTTCAAAAAGCCTTAAGACACCAAAAGAGGAAAA
WI-18178	68	T C	---			GCATAGGGTTGAGGGGTGTACAAGAGGAGAACCAAGATTGAGTCCATGCCCTGGAGGTAGTCTGGGG GTT[C]CGGCGGGATGGACACACAGACAGACACATAGATCTGGCATCTGATAGCAGGGCATACAG
WI-18244	35	G T	---			TCAATCTGAAAACTTGCTGTAGCCAGCATGGGGT[G]TGGGGAGGTGATTATGGCTGGGGAAGATG GGCACTCACCGACAGCAGCATCTAGCACCACAGTACAGGGGACGTTGAGGTGGCAGAGGGCTTT
WI-18245	115	G A	---			ACAGATGTCAGTTGTTGAATTTGGCCATTAAAGTATGGGGCTTTCTTGTAAAAGTCATCCAAA AGGCTTGGCAAGATTTGCTATACACGGAGGACAGAGAAACATGA[G]A]CTGGGGAGTAGGCTCT GACAGAAGGTGGGCTGTC
WI-18261	26	G A	---			GATTTGAAGGGATTGCTTTATTAACTG[A]TGAAAAGCGTGATAGAGGAACTGTTTAAGATAAACAA CTTATAAATACCTCCCAATTTGTAGAAGTGAAAGATTG
WI-18268	88	C T	---			TAGGAGGGAAAAGAGGTGGGCTGCCCTGGGCCCTCAAGACATGAGAAACGGGTGGTGGCTTCCAAAGC TTCTTACTTCCCCCATAGAT[C]TCTGACAATGTGCTGCAGAAAGCCTCCAACTGGAAC
WI-18299f	107	C A	---			TCACAAGTCAATCTCCCATCCCAATGACAGTTTGTCTAAGATCATTAACTGGTTTGCCAAATTTTTT ATCTATTTGGGTCTGAGAAATCCACAAATTTGAAGAAATCTTTTGCCAAATTTATGACATATCTG CAG
WI-18299e	101	A G	---			TCACAAGTCAATCTCCCATCCCAATGACAGTTTGTCTAAGATCATTAACTGGTTTGCCAAATTTTTT ATCTATTTG[A]GTCTGAGAAATCCACAAATTTGAAGAAATCTTTTGCCAAATTTATGACATATCTG CAG
WI-18299d	77	G A	---			TCACAAGTCAATCTCCCATCCCAATGACAGTTTGTCTAAGATCATTAACTGGTTTGCCAAATTTTTT T/G]ATCTATTTGGGTCTGAGAAATCCACAAATTTGAAGAAATCTTTTGCCAAATTTATGACATATCTG CAG
WI-18299c	67	T G	---			

WI-18299b	52	G A	---	---	TCACAAAGTCATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTTG[A/J]TTGCCAATTTT TTTATCTATTTGGGTCTGAGAAATCCACAATTTGAAGAATCTTTTGCCAATATTGACATATTCTG CAG
WI-18299a	48	C T	---	---	TCACAAAGTCATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAA[C/I]TTGGTTGCCAATTTT TTTATCTATTTGGGTCTGAGAAATCCACAATTTGAAGAATCTTTTGCCAATATTGACATATTCTG CAG
WI-18307	76	G A	---	---	TCAACTTGTACCAAGTTTAGCAGCAAGAGGATACITTCCTTAGAGACTTTCAGTGGACTTAAACTCAG TTTCCGCTG[G/A]TGCTATGTAAAGCATCCAGGATGGTTTATTGTACTCTGCAATCTGCTTGGTCAC
WI-18324	72	C T	---	---	TTTGGTATGAAATCTTTCTCTGACATTTACCAATCATCACTTAAACTCCGGGGTGGGTACTGATT TATC[C/I]TAGATCCAAATAAAGCATGCAGAAAGTG
WI-18350	48	T C	---	---	ATGAAAGTCACITTCATCATAGGGTCAAGAGAAAGAAATGTTTTCAAGAT[C/I]TAATCTATGAAAA GGTGTATCTGCTTGCATTTAAGAAACAACACAAAGTCA
WI-18395	77	G C	---	---	TCITGACATGATCTGTGAAATAACGTGATTGTGGTTGAAATTCCTGGAAAAATTTGAAGAATAAATTG ATTATTCAAG[G/C]JTGTCATTGGTTTATACATATCTCCTCTCTTAAATGCAAAAGCTATG
WI-18398	62	G T	---	---	TGCAGTGGCAAGACACTCTCTCGAGGAAAAAAGAAAAAGAAAAACAACACTCAAGGGTT[G/T] GATAACATTGCCAGTATAACCATTAATTCAAAACAAGCAGCAGAAATTTGGAGGATAATTTGTT
					CTCGTTGGTATTCTCTCATCC[C/I]TTCCCTTTTCGCTCTTTCTAAATTAAGAAAAAGCAATGGAATT TTAAAGATCATCTAAGAAATAAGAACTTACATATGTAAACATTTAACTTATCAACTTGTACAAAGTC AATGAAAA
WI-18396	21	C A	---	---	AAGATGGGAAAGAGGAAATC[C/I]TTTTTCTTACTAGAGATTTTTCCTTTTAACTCTTTTCAAAAT TCAAAGGATCATCAAAGGAGCAGGTGCAGAAAGCTCTGGGCCAGAGGCCCAAGTGCTA
WI-18409a	20	C A	---	---	AAAAAGGAAAAAGAAAGGATGGAGTAAGAGAGAGAGACAGAGAGGAAACAATAAAGTTTCTGG[C/T] JTTGGCTGATCTGGGTGATCAGGTGGACACTATTATCCAGAAAGGAAACACAAAGAAAAAAGG TTTATAGGTGGGAGAGAGGA
WI-18442	62	C T	---	---	TTGATGTTAATACTGTCAATCTGGAGATCGGCTAAAAATG[A/J]AAAGCATAGTTATTATTAGCTTTGG TATATTCTCGACAGATTAAACAAGTAAGACATATATCAACCTCATATTTTCCAACCA
WI-18452	38	G A	---	---	ATATAAGCTGGAGACTGTGGAGGTGAGAGGAGTGGGACTAGCTGTTGAAAGAGAGAATGTAGC AGTAGTAAAGATGAAAGACTGCAAGGATTCAACA[A/C]GGTTATGGCAATAGAGGTGAAAAAGAAA AGGCCATATAAA
WI-18489	102	A C	---	---	CTGGTGGGAGGAAACAATTTGGGTATATTATACAAATGGAAAAACTCTTCAGAAATAAGAAAGGAA CAAACTGAAATCACACAACATGGACAAATCTCAAATCATATTGCTGATGGAAAGAAACCATTCA TAAGAAATACACAGTACAT
EST5b	93	A	---	---	



EST5	93 A ---	---	CTGGTGGGAGGAAACAAATTTGGGTATATTCATAAATGGAAACTCTCAGAAATGAAGAAGGAA CAAACTGATGATCACACAACATGGACAAATCTCAAATCATTTATGCTGATGGAAGAAACCAATCA TAAGAATACACAGTACAT
EST6	48 C ---	---	TTAGCTACTTTTCAGAAATTGAAGGAGAAATGCATTATGTGGACTGAACCGACTTTTCTAAAGCTCT GAACAAGCTTTCTTCCTTTTGCACAAAGACAAAGCAAGCAACATTTTGCTATGACAGAT
EST8	158 A ---	---	GGACAGGACCTCTATTCCCGCTGTGCAGCAGCGGCTGATGGACTGAGGCCCCAGGGATCTGGGOC CTCTCTCAGGGCGCTCCAGGAACCCAGAGCTGTCTCTGTTTGGTTTCCCTAGAGCTGTGGGCCA GATAGCTGTCTGAGTTGCAAGCAGCATGGAGATTGGACACTGTGTCTTTTGGTGGGT
WI- 18740c	104 GT ---	---	TCCTCATTGTGGGGATGATGAGAAGAAATGATTTGGGAAATTAAGTAACAACGACCTAGAAAAGT GAGAACAAATCTCAATACCATCATGTATCCAGTAGTG[G/T]ATAATTCATTTTGATGGCTTCTATTTT TGGCCA
WI- 18740b	96 C G ---	---	TCCTCATTGTGGGGATGATGAGAAGAAATGATTTGGGAAATTAAGTAACAACGACCTAGAAAAGT GAGAACAAATCTCAATACCATCATGTATCCAGTAGTG[G/T]ATAATTCATTTTGATGGCTTCTATTTT TGGCCA
WI- 18985a	105 C T ---	---	CCAAAGTCTCTGTCGCTATAAAGAAAGTTTGGGATGGGAGAGAATCCAGACCATCTTGGGGCA GCCAGGCCCTTGCCCTTCAATTTACAGAGGTAGCACA[G/T]GATTCCAAACAAACCCCTTCCCC TTTTTAAATGATTTCTGTTCTAATAGCCATAGATCAAGGCCCTCAGAAACCATTTGTGTTTCTCTT TGAAGCAATGACAAGCACTTTACTTTACGGTGGTTTTGTTTTCTTAT
WI-18746	114 G A ---	---	GCCAGCAGCTGAAGTCTCTTTCTCTCTCGGCTGGAAAGCAATCAAGATACCTTTGCGTGGATCA AGCTTGATCTTGACCGTTTTTATATTACTTTTGTAATAATCTT[G/A]TCCACATTCCTACTCAGCT TTGGATGTGGTTACCG
WI-19112j	212 G A ---	---	CCGTGTTACACACACACAATGGCAAGCATAGTCGCTGGTTACGGCCCGGGGGAATATGCCAAGG GACCCCTTAATGGAAACACAGATCAGTAGTGTCTATCTCATGACAACCACAGAAACCGACGACAAA TCTTTTGCAGATTTCTTCTAGTGGCTTAGAAACATGGCTTTAAGAAACACGGTGATATCTTTGAG GGTGACAAGGC[G/A]TCTCTTCAACAGTCCATACCAACTGCTTTGCTCTAG
WI-19092	232 A C ---	---	TGGTGGCTGGCTAGTGTCTACAGAACATAATTTGCCTCTATAGAAGGCTATTCTTAGATCATGT CTCAATGGAACACTCTCTTCTTAGCCCTTACTTGAATCTTGCCCTATAATAAGTAGAGCAACACAC ATTGAAGCTTCTGATCAAGGCTCTGAAATTTTCATCTTGAATGTCCTTTGATTAAACTGAATTTTC TTTTAAGCTAACAAAGATCATAATTTTC[A/C]ATGATTAGCCGTGAAC
WI-19057i	175 G A ---	---	CCCATTTATTATAGGCCAGTGTCTCAAGAGTAGAGGAGCGTCTACTGGTCTTTCAACTCCTTCA GTCTCTGACGGCGGACTTACCCTGACAGCGGAAGTGTATGTACGTCAGGCAACCGCAGCCACTG TCTTCATGCAGGAACCAAGTGCCAGATCCCAAGCTC[G/A]TCTCTTCTATCTTGGTTTGGCCACA

WI-20103	168	C T	---			TGGGACTTCCAACTCAGAGGATGTGGGAATCCCAGCTCAAATGATACAGGATAAACTGGGATGGGCT AGGATGGACAGGCTGTGGATATGGGAGTCATGGGTCAAAGTCTTATCCAGATGGCTCCAGGTACAG TGGGCTTCTGGGCTGGAAGCTGGGTCTCCGCCA/C/TTCATCTGCTCAAAGCTTCTTGAAGGAGC TGGTTGACTTCAACTTGTAGAGCCTAGCCTCATCTTTTCAGTCAACTGGGA
WI-20441	111	G A	---			GCCTTACCCATTTTGCACATATACATATGCACCACCTTTGCAGTGGCAACATATATATCCACACTA TAAACATACCACATTTATAATCTTGTAGGACAAGAAATGGA/GA/TTGAATAAAGTACCCCCCAA CATATACAAGAAAGTTAGCATACTTACCCGTTTTTCACTACATCAGAGGCCAAATAGAAATCTTT TAAGAAATCTCAAGACTGGCTCATGGCAAAATGAATATGCTAAATTTGGGGG
WI-19911b	116	A G	---			TGGTTACAAAACCTAAGCCCATATACAAAATAGGAACACATTTAGATGCCTCTTTTGAAGAAGCGT TTTAGTCTTTTAAACTGAGTTTAAAAAAAATAACAATGCAATTTTAA/GJACACTGTTTTTGAAA ACTTAAAGTCAGCAATA
WI-20613c	165	A G	---			GTCTCAAGGGGGAGAAAACCTGGTCTTTTATGTACAAAGCACAGATGTAGGTACAGTATATAACA GATACGTAGTACATCTGTAGTATTAATGATGGGAGGAGGCGAGTTAGAAAAACATCTAAAC AGTCTCTTAGAAGGCCAATAATAAAGTTGGA/GA/AAAGGAGTTTCCACGAGCCAGTGGTGAGC TGC
WI-20613b	156	A C	---			GTCTCAAGGGGGAGAAAACCTGGTCTTTTATGTACAAAGCACAGATGTAGGTACAGTATATAACA GATACGTAGTACATCTGTAGTATTAATGATGGGAGGAGGCGAGTTAGAAAAACATCTAAAC AGTCTCTTAGAAGGCCAATAATAAAGTTGGA/GA/AAAGGAGTTTCCACGAGCCAGTGGTGAGC TGC
WI-19984	47	A G	---			CAGTAAAGAGTGATTCAAGTTGCAGTAATACACTGACAGGTAAATA/GJTATAACATTAGAAAA GCAAAATCTTTTAACTTAAGGACAGACTGAACCATCAGGTATGGTCTGAGATCAAGTAATACAGG TAGGCAAGAGTTTTTCCACACTGGAAAATGAAGGCAGTTTCCCAAATCTGTGAATTTACAAACAT TGGGGGAAGG
WI-20122	135	T C	---			GCCAGTTGGAATATGGCCTATACGAACCAAGAGTGTATACAAATGGAAGTGGTCATCAGGCAATA ATTGTTTCTTGGAACTCTGCACCGACTGTCCATGCTCTGTGGGAGCTTACACATTCAAGTTTGACAG T/CJTGAAAAACCAACTGGAGCTGCTTTTCCAAGAAATGTTCTGTCTTCAATAGGAATCCATG TTATTCTTTCTGGCTTAAGCTCTTATATCTTTCAAAATGACCTAAGCTGA
WI-18846a	49	G A	---			GAGTGCCATACCTTCTCCAGGCTCTGCCCAAGAGCAGGAGGTGCCT/GA/AAAGCTGGGAGCGT GGGCTCAGCAGGCTGTACCTCCATCCCGTAAGACCTCCTTCCCTCCTCAGCAGGCCCAACATG GCCAGACTCCTT
WI-18959	123	G A	---			AGCAGTGGCCTTATGTCATCCCAACACCGCCTCTTGACCAGGCTGCCCTCCCTTGTGGCAGCAACGGC ACAGCTAATTTCTACTCAGTGTCTTTAAGTGAATAATGGTCGAGAAAGAGGCACC[G/A]GGAAGCCG TCCTGGCCTGGCAGTCCGTGGGACGGGATGGTCTGCTGCTGTTGAGATTCTCAAGGAGCGAGCAT GTCGTGGACACACAGACTATTTTAGATTCTTTGGCTTTTGCACACC

WI-20146	31	T C	---	---	---	TGAGTCTTCTGTAATTCATTGAGCAGTTAGCT/C/CJCAATTTGAGATAAAGTCAAAATGCCAAACACTAG CTCTGTATTAAATCCCATCACTACTGGTAAAGCCTCAATTTGAATGTGTAATTCATATACAGGC
WI-18922	74	G A	---	---	---	TAGGAATTGGTTTACGCCCTGAGGCAATTAGACACTTTTGAAGATGGCATAACCTGTCTCACCTGGAC TTAAGC/GA/CTGGCTCTAATTCACAGTGCCTTTTCTCCTCACTGTATCCAGGTTCCCTCCACAGAG GAGCCACCAGTTCTC
WI-18763b	53	A G	---	---	---	TTTCTGTGTTGGGGTCAACCGTACAATGGTGTGGGAATGACGATGATGTA/GJ/TATTTAGAATG TACCATAATTTTGTAAATTTATGTTTTTCTAAACAAATTTATCGTATAGGTTGATGAAACGTCA TGTTTTTGCCAA
WI-18763a	38	A G	---	---	---	TTTCTGTGTTGGGGTCAACCGTACAATGGTGTGGGA/GJ/TGACGATGATGTAATTTAGAATG TACCATAATTTTGTAAATTTATGTTTTTCTAAACAAATTTATCGTATAGGTTGATGAAACGTCA TGTTTTTGCCAA
WI-18771b	75	G A	---	---	---	CTCATTTCCATGCCATTGTGGAATTGAGCAGAGAACCTGCTCTCGGAGTGCTTAGAAGATGTTGGG AACAGAA/G/A/AAATAAACTGAGTTTAAGGGGGACTTAAACTGCTGAATTCACCTGTGGA
WI-18771a	57	A G	---	---	---	CTCATTTCCATGCCATTGTGGAATTGAGCAGAGAACCTGCTCTCGGAGTGCTTAGA/GJ/AGATGTT GGGAACAGAGAAATAAACTGAGTTTAAGGGGGACTTAAACTGCTGAATTCACCTGTGGA
WI-18820	70	T C	---	---	---	GGGAAAATTTGAGACGGAATACCAATCTAGGATTTTGGTCTTGGTGTGATGAAATCTGAG GCC/T/CJTGATTTAAATCTTTCAITGTTGATTTCCCTTTAGGTATATTGCGCTAAGTGAAACTT GTCA
WI-18742b	51	C T	---	---	---	ACAAAGTCTGTAGCCCTCACCTTTCTGTTTTCACITTTGCCAATGTA/C/JATCGGGTTGGTTT TCTTGATTTAATAACGGTTGTGGTTTCTTTTCCACGGAGGTTCAAGTAAAGCCGCTGCAGGAGA GTTTTACC
WI-18882	94	C T	---	---	---	GTGTGTCCAAAATGGGTCTGCTCCTGCTACCTTGACCGTTCCCTTTCTCTGCTTCTCTCCTCATCA TCATTTCCCAACAACATCCTCTGCCA/C/JACACAACAACAAACGTAAGTTTCAITTTGGGCAAAAATTGA GC
WI-19970b	167	G A	---	---	---	TATAAGCCGAGTCACAGGAGCGCTGTCTGGCCACAGACAGAGGGGCTGCCTGTGGAGCCTGCCACC GGCCCCGGCAGTGCAGTCAGCGGGAGGAGGCTGCCCGTTCTGCCAGTTCTCCTCACTGGGGGACCC AGCAAGGCCCTTCTCACTGGGTGGTCAAAG/GA/JTAGTCACCTTGGCCTGGTGCATCCACACAGGGA TGTTGTTCAAACAGAAATCTTTTAAACGACTGACCTTCTTAAACACAGA
WI-19970a	126	T C	---	---	---	TATAAGCCGAGTCACAGGAGCGCTGTCTGGCCACAGACAGAGGGGCTGCCTGTGGAGCCTGCCACC GGCCCCGGCAGTGCAGTCAGCGGGAGGAGGCTGCCCGTTCTGCCAGTTCTCCTCACTGGGGG ACCAGCAAGGCCCTTCTCACTGGGTGGTCAAAGGTAGTCACCTTGGCCTGGTGCATCCACAGAGGAT GTTGTTCAAACCCAGAAATCTTTTAAACGACTGACCTTCTTAAACACAGA

WI-19067d	202 T G ---				TATTGCTGCTTGTCACTGCCTGACATTCACGGCAGAGGCAAGGCTGCTGAGGCTCCCTGGCTGGCTGTGC ACATTCCTCTCTGCTCCCGAGAGACTGCCTCCGCCATCCACAGATGATGGATCTTCAGTGGGTTCTC TTGGGCTCTAGGCTCTGGAGATGTTGTAGGGGTTATTTTTTTAATAGTGTTCATAAAGAAAT/
WI-19067c	153 G C ---				GJACATAGTATCTCTCTCAAGACGTGGGGGAAATTATCTCATATC TATTGCTGCTTGTCACTGCCTGACATTCACGGCAGAGGCAAGGCTGCTGAGGCTCCCTGGCTGGCTGTGC ACATTCCTCTCTGCTCCCGAGAGACTGCCTCCGCCATCCACAGATGATGGATCTTCAGTGGGTTCTC TTGGGCTCTAGGCTCTG/CJAGAAATGTTGTAGGGGTTATTTTTTAATAGTGTTCATAAAGAA ATACATAGTATCTCTCTCAAGACGTGGGGGAAATTATCTCATATC
WI-19067b	151 T C ---				TATTGCTGCTTGTCACTGCCTGACATTCACGGCAGAGGCAAGGCTGCTGAGGCTCCCTGGCTGGCTGTGC ACATTCCTCTCTGCTCCCGAGAGACTGCCTCCGCCATCCACAGATGATGGATCTTCAGTGGGTTCTC TTGGGCTCTAGGCTCTG/CJGGAGAAATGTTGTAGGGGTTATTTTTTTAATAGTGTTCATAAAGAA ATACATAGTATCTCTCTCAAGACGTGGGGGAAATTATCTCATATC
WI-19067a	57 C G ---				TATTGCTGCTTGTCACTGCCTGACATTCACGGCAGAGGCAAGGCTGCTGAGGCTCCJGJCTGGCTG TGACATTCCTCTGCTCCCGAGAGACTGCCTCCGCCATCCACAGATGATGGATCTTCAGTGGGTT CTCTGGGCTCTAGGCTCTGGAGAAATGTTGTAGGGGTTATTTTTTTAATAGTGTTCATAAAGAA ATACATAGTATCTCTCTCAAGACGTGGGGGAAATTATCTCATATC
WI-19106	247 T C ---				TTAATCCAGCCCTACCTTGTAGTATTTAGGAGACAGTCTCAAGCACTAAAAGTGGCTAATTC AATTTATGGGTATAGTGCCAAATAGCACATCTCCACGTTAAAGACAGTGGATCATGAAAAGT GCTGTTTGTCTTTGAGAAAGAAATAATTTGTAGCGCAGAGTAAATAAGGCTCCTTCATGTGGC GTATTGGGCCATAGCTATAATTGGTTAGAACCTCCTATTTTAA/TCTGG
WI-18944	147 A G ---				CAAGGCAAAATATCAGGAGCTTTTACACACCTACTAAAAAGTTATTATGTAGCTGAAACAAA AATGCCAGAAAGGATAATATTGATTCCTCACATCTTTAACTTAGTATTTACCTAGCATTTCAAACCC AAATGGCTAGAACJAGJTGTTTAAATTCACAATAAAGTCTACAGITTAATTATGTGCATA TTAAACAATGGCCTGGTTCAATTTCTTTCTTAAATAATTTAAGTTT
WI-18952	232 G A ---				CCCATCCCTGTGAAGGAGTAGGCCACTCTTTAAGTGAAGGATTGGATGTTTCATAATACATAAA GTTCTGTAAATTACAACTAAATTTATGCCCTCTTCTCACAGTCAAAAGGAACTGGGTGGTTGGT TTTTGTGCTTTTTAGATTTATTGTCCCATGTGGGATGAGTTTTTAATGCCACAAGACATAATTTA AAATAATAAACTTTGGGAAAGGTGTAA/GA/JACAGTAGCCCCATCACAT
WI-18932d	177 C T ---				CACACCTCATGTAGCCTCACGAACTGGAATAAGCCTTCGAAAAAGAAATTGTCCTGAAGCTTGTA TCTGATATCAGCACTGGATTGAGAACTGTTGCTGATTTGACCTTGTATTCAAGTTAACTGTCCC CTTGGTATTGTTTAAATACCTGTACATATCTTTGAGTTCA/CJCTTTAGTACGTGGCTGGTCA CTTCGTGGCTGAGGTAAGAACGTGCTTGTGGAAGACAAAGTCTGCGCTTG

WI-19042	193 A C ---				TTTGTGAGTTGGCTCTCGCAATGCCATCAGTAGCATCTCAGTGGTGTGAAGTTGGAGATAGATG GATAAGGGAATAATAGGCCACAGAGGTGAACCTTTGTGCTTCAAGGACATTTGGTGAAGTGCACACAG ACACAAATTTACTGCGACAGAACTTACGATTTGTAATTTATGTAATAACTCTAACCA/A/CJGGCTG TGTTAGATTGATTAACTATCTCTTGGACTTCTGAAGAGACCACTCAAT
WI-18984	208 A C ---				ATTGGCCCTGTACAGTTTGCTTATTATAAATTCATTAAAACTACAGGTGTTGAATGGTTAAAA TGAGGCCCTCAGTTCAATTTTCTGAGTGTGACAGACGCTATTTCCGACGTATTAAAT GTAACCTATTATGAATCAGAACGACAGATGTTGGTGAATACAAATATTGTGATGCATT TATCTT/A/CJATAAATGCTAAATGTCAATTTATCAGTGGCATGTTTGAAT
WI-18851	90 T A ---				GCCTCAATTGGCGATTGATTGAGTGGCCACAATGTAAACAGGGTGGTAGTTGTACTCATTTTGAAT ATACCTTTTCCCTTATTGTATTCT/AJGTAAATATAGGATCCTGGAAATGAGACCTGGTGGAA
WI-18821b	76 T C ---				TCAACTGCAGTTGCTTCCCTCCCTATAGGGCTGGAATCTGTAGAGGCCCTCTCTCGGAGGCC ACAGAGGGT/CJGGGGGTAGCCATTGTGCAGTCATGCCCCGGGGAACTTGGCAACCTTCGTGTGAG GTGCTGTGT
WI-18821a	69 C T ---				TCAACTGCAGTTGCTTCCCTCCCTATAGGGCTGGAATCTGTAGAGGCCCTCTCTCGGAGGCC A/CJTAGAGGTGGGGTAGCCATTGTGCAGTCATGCCCCGGGGAACTTGGCAACCTTCGTGTGAG GTGCTGTGT
WI-19021a	20 C G ---				ACTCCTCTGCTGCTGCCAT/CJACTGTCTCTTTGAACCAAGGAAAGTCACAGATTTAAAGAGAA GCAAAATTAACATCCTGAATCGGGAACAAGGTTTATCTAATAAAGTGTCTCTCCATCACGTTG CTACCTTACCCACACTTCCCTCTGATTTCGTGAGGACGTGGCATCTACTACGTACGTGGGATAAC ACATCGTGTAGGCCCATGTATGCTGGGGTAGAGCAAGTAGCCCTCCCTGTC
WI-18908	70 G C ---				TGGAAATTCCTTCATCTGGAACCATCAGAAACACCCCTCACACTGGGACTTGCAAAAAGGGTCAGTA TGG/CJTTAGGGAAACATTCATCCTTGAGTCAAAAAATCTCAATTTCTCCCTATCTTTGCCACCC TCATGCTGTGTGACT
WI-19037b	155 A G ---				CACGGTTCTCTGCATCGTTACAGAGCGCCTTCTGGTCTAGCCAGCCCTGTATGCCGCGCAATA TCCCCAAAGCTTTTGGTCTCAAGTCATGCCGAATTTAGATGCTGGTCAATTTCTGGAGGGGTC CCCTCCCTTTACGAACAC/AJGAAACCCAGCCACATGACTAGCACGCTGAGCTGTGCAGGGACCA GTGOCAGGCACTGGGGGTGGAAGTGTGTGACACAGTGAATGGGAGGTGG
WI-19037a	47 C A ---				CACGGTTCTCTGCATCGTTACAGAGCGCCTTCTGGTCTAGCCAGC/AJCTGTATGACCGCGCAA ATATCCCCAAAGCTTTTGGTCTCAAGTCATGCCGAATTTAGATGCTGGTCAATTTCTGGAGAGGG GTCCCTCCCTTTACGAACACAAAAACCCAGCCACATGACTAGCACGCTGAGCTGTGCAGGGACCA GTGOCAGGCACTGGGGGTGGAAGTGTGTGACACAGTGAATGGGAGGTGG
WI-19054	66 T C ---				TTGAGGAGGTGGGGTGAATGCTCTTGGCAGGATTTGTACACTGCATTGCTGGGCTGTGTTCTT CJGGGCTCTTCTGGACCTTGACCGTGGATACAGGCCATGTGCCATGTGTTGGGCTGTTGTTCTT TGGGTGAATAAAGGC

WI-18972a	112 A G ---	---	AGGCTGTGGCTTATGTCAACCAACAGAGGGTCTCTGAGAAGTCTGGCTGCCGTGGGATGCCCCCTGCC CCCTCTGGAAGGCTCTGCAGAGATGACTGGGCTGGGGAAGCAG/GJTGCTTGTGGCCATGGAGCC TCATTGCAAGTTGTTCTTGAACACCTGAGGCCCTCTGTGGCCACCAGGCACCTACGGCTTCCTCTCC AGATGTGCTTTGGCTGAGCACAGACAGTCAGCATGGAATGCTCTTGGCCA
WI-19016b	184 C A ---	---	GTTTGCAACCAACATGTGCTCTTTTCAGTCATTCACCTGTTTTAATATGACATGGTAGAAGATAAG GTTTATGGCAGGTAATTTTGTAAATGTGTATTAAACGAAGTTCAAAGATTAGAAATACATCTGTGTC CTGAAAACCTTAGATACATAGCCGACTGTATACAGAGGTTTCATCTCAACCTCAACACTATTGAC TTTTGGGCTGGATAGTCTCTGTGTGGGGGTTTGTCTGTGCACTGTAG
WI-19016a	161 C T ---	---	GTTTGCAACCAACATGTGCTCTTTTCAGTCATTCACCTGTTTTAATATGACATGGTAGAAGATAAG GTTTATGGCAGGTAATTTTGTAAATGTGTATTAAACGAAGTTCAAAGATTAGAAATACATCTGTGTC CTGAAAACCTTAGATACATAGCCGAG/CJTGTATACAGAGGTTTCATCTCAACCTCAACACTATTGAC TTTTGGGCTGGATAGTCTCTGTGTGGGGGTTTGTCTGTGCACTGTAG
WI-20096	21 T C ---	---	GGTTTGGGGCATTTATTCTG/CJGATAGAGACTGGCACAAAGCTTTGGGCTAAGGACACCCCGCCCCC ACCCTCATCTAGAAACAATCTCTCGCCAGACTTG
WI-19591b	156 C A ---	---	TGGGGCAATTTTAAACAAACAGGCAAAATATCACATATACCTGAATATAAGGTAACTCCAAGCCATG AGTAAAGATTAAAGCAGTTACTTTTGAACAAAGGAAGTGCAATGAAGCAACTCAGTGTGCCC CTTAGGGTGGGAGCTCTCC/CJACTACACTCCCAAGGCATCAITTTGGGAGAAAAA GTGCTTCTATCTGGCTAGCTGTGTATCTAGGGATTGCACTTCTTACACGG
WI-19591a	45 T A ---	---	TGGGGCAATTTTAAACAAACAGGCAAAATATCACATATACCTGAATATAAGGTAACTCCAAGC CATGATATAAGATTAAAGCAGTTACTTTTGAACAAAGGAAGTGCAATGAAGCAACTCAGTGTGT GCCCCTTAGGGTGGGAGCTCTCCCCCTACCCTCCCAAGGCATCAITTTGGGAGAAAAA GTGCTTCTATCTGGCTAGCTGTGTATCTAGGGATTGCACTTCTTACACGG
WI-20310	125 G A ---	---	TCCTCCAGCTCTGTCATCCTTGTCTTGAGGGTCTGTGTACGGCCCTCCAGGCATGGTTTCTCAT TTAGGTAGGAACAAAGGCCAAAGAACATACAAGCCAGCTCTCTAGAGGCTCCA/GATCAGAA CTGGACCTTTAACTACAAAGGAATCTTGGATGAATTTTGTAGCGGGCTTCAGGAGCAGGTAGC AGAGCCAAAGTGCACACTCAGGCCATCTTCTCCCAATGTCTCCCGGGGG
WI-20860	224 G A ---	---	CTCTCCCTAAGGAGCCTTGGCCTTGAGCCCCATTACAGAGGATGGAAGTCACAAGACAATGAGT GGAGCCTCATGCCCTCCCATGAGGAAGCCCTTAGTATTGCTGACATCTGCCCTTTATCCTGCTCTCCT CCCCAGTCTGTACACTTGGGCAAGCAGAGTGTGGAGACCCAGCCCTTGAGAGCTCTTGTAGACC GGAAGGAAGGGCGGTCA/TTGA/EGGTGATGGCTTCTGGCTCTCTGGCTT
WI-19359a	39 T C ---	---	GACGTGGACAAAGGAGGTTTAAATGAATCTTTGTTTGT/CJCATGTTCAAAAAAAGAGATTAAAT ATTTTGTGACTGCATCTGTGAATGAAGACACTCAAAAGCCATGTTTCCAACCTAGGTTAATAATAA GGCTATTTGTCCACCCACTCTTCGGGCATTGCTGCAATATCTCGGCCCTCAAGTGGGAGGCCACGTG GGAACAAGGCCCTCAGAAACAAGGACATGCAGCCTCCCTGAGCCAGTCTCT

WI-19766b	93 A G ---	---	TGGCCTCAATGACTGTACATTGGAGAAGCTGTGCAGCAGCATCTTTCTGTGGTGGGCAGGGCAGG AGATGAACCATAGGAGCCAAAGTC/GJGACAAACAGAGAAGGCACACCAAGCCTGAAACCCCTC CGGACAAAGAGAGTACCAGCTGAGGGATGTCCCTGGAGTTCTGACCCATGAGAGGCCCCCTC ACCTCTTCACTCTCTCTACCAACCAAGCTCTCCGGCAGTCATGGACTTAT
WI-19766a	31 G A ---	---	TGGCCTCAATGACTGTACATTGGAGAAGCT/GA/JGACAGCATCTTTCTGTGGTGGCAGGGC AGGAGATGAACCATAGGAGCCAAAGTCAGACAAACAGAGAAGGCACACCAAGCCTGAAACCCCTC CGGACAAAGCAGAGTACCAGCTGAGGGATGTCCCTGGAGTTCTGACCCATGAGAGGCCCCCTC ACCTCTTCACTCTCTCTACCAACCAAGCTCTCCGGCAGTCATGGACTTAT
WI-20512d	126 C G ---	---	CTTCTCTGTTGGCTTGCATTTGTGGGATTGGAAAAACCACTTGAAGAAGGGACTTTCTCTGCAA AACCTTAAGACTGGTTAAATTACAGGCCCTAGGAAGTCAGTGGAGCCCTTGAAGTGA/C/GJAAAGC TTAGAAAGGAAGTGAATGCTTCTTTGAATATGATTTAGGGCGGGCGTGGTGGGCTCAGGCCT TATTAATCCAGGACGTTGGGAGGGCCCAACGCGGGTGGGATCACCTGA
WI-20512c	59 T G ---	---	CTTCTCTGTTGGCTTGCATTTGTGGGATTGGAAAAACCACTTGGAGAAGGGACTT/GJTCCTG CAAAACCTTAAGACTGGTTAAATTACAGGCCCTAGGAAGTCAGTGGAGCCCTTGAAGTGAACAAAGC TTAGAAAGGAAGTGAATGCTTCTTTGAATATGATTTAGGGCGGGCGTGGTGGGCTCAGGCCT TATTAATCCAGGACGTTGGGAGGGCCCAACGCGGGTGGGATCACCTGA
WI-19599	230 C G ---	---	GGCTTAAATTCCTCTGTTGGGACTGGTCTCCAGTTACAGCAAGGATCGCACCCCTTTTC ATAACCCCTTCTACATTGGAAAGAGCACACCTTGATACAGAATGGCTCCGTGAAGTCTTTTAAACG GACAAAGGTAATCACAGCTACAAACCGTATGTTGGCTCACACGTAAACCAACACACCTCTTTTCA GAACAGAGAGCGTTAAAGTAAAGGGCA/C/GJTTCCAGAGTAACACTGCTA
WI-20679	82 T C ---	---	TGTTTGAAATAAAAAATTCATGGTCTTAATTGAAGTGTATGTTACTTTCTTTAGAATATCCTTTT TTCATTAAATAAT/TJCTAAACCACTCTATGTGTTCAACCTCTGTTTAAACATAAGATATGGGT TTTTGGAAGGGCCACAAAGTCACAGCTCCATGAAGTGGGGAATTGGTCTTGTTTGGAAAGCTCTC CAGGGTGTCTCCAGAAA
WI-19909a	29 T C ---	---	CCAGAAATAAGCCTGAATATTCCTTTCT/JCTTAAAAATAAATTTTCTCTTTGCTCTTCCAA GTAATCTTAAATGAACCTGTCTAGTCTATTTTAACTAGGCAATTATAACACTACCTAGGCGGG TTTTTCTTTATACCTTGTCTGTACTGTGGAAATCACTAA
WI-20341	221 G C ---	---	TTGAGAGGCTGAGAGAAGGCTGTTGAGACATTGTAATAGTCTTAGGGGATGAGACATTAGGAAG GCCACAAATTATGAGTAATGAAATGTGAGGCTGATGAGAAGCTACTGCTCCCATTTGTTAGCAGGA GGCAGGAAAAGTATCTGGGGTCTCTGGCAGCAAAAGCGTGTGTAATATTTGGGTGACGTCATGC ATCCCCCATGCATTGGTTT/GJATGTCTCCAGTGAGCTGTTGGCAAGTCT

WI-20113	60	T C ---	---	TTC TGG TAC ATG GTA AGT GCT CAG TAT TACT GAG TGA TGA GCA AAG ACCT GAA ATACT GT [C] GGA AAC AGT AAA AGC AAA TTA ACC ACA AAT TAG GAG GAA TAT TTT CAG ACATAG GATATTT AAA ACAT CACT CAAA TACT GAG CAT GATT CAG CAATAA TTTCTAT TCCATAA ACCAGGTAG ATAAATGT CACA GCTTT AAAATATAGTTAAGTACAGTTGATCCTCGTTATTTCATGGATTCCGTATT
WI-20895	107	G C ---	---	TGATGGCAAAGTACAAAGGCTCTGAAAGAACAGAGTAACAAGAGCAGCGCAGTGCAGCGTGTGGC CACTCCCACCGAGGAGAACACTTGACTTCAATTAAGGCAA[G/C]CTTTACTCTGTACTTTTCCTC CCACATAGTTTAACCCAAATAGAAAGGCATTCATTCTCACACTACTGCTCTCTAAGGTCCTAGGAA TATACTGGTACTATAGGCAACAGATGCA
WI-20721	72	T C ---	---	CCTGCAATCACAAAAGTGGAACTAGTTGATATTTTGAATCATACTTGATTAAACCACCTTCAGAAA TTCTATTCIAAAACACTAGCAACTTCCTTTATCAGA
WI-19415c	161	A G ---	---	CTGGATTTAATATTTCTGGCCTAATAACCAATGTAATCAATAAAATTTGGTCAATATCTCCACCTC ATTTCTGCTAACATGTTTTCGAAGATTCCTTAAGTAAGGTATTGACGACTGAGACTAGTCCGGCAAA GTCA TGAGACCTTAGCTGATCTCAT[G]AAGTCCACCTCATGAAGGAGATGATTCAACATCTCAA GCTAAGGTATAAGTGTGGACATACAAAGGCTTACAAGTTTACACTTCCTG
WI-19348c	103	C T ---	---	GCTGCTACTGTAGCCAGCCAGCTGCAGGATGGTGGGTAGCAAGTACGATGGCCATGCACCTTCG GCGGTCGATGAAGAGACTGTTGGTCATGGCGTGA[C/T]GTCCTCTCCAGGCTCATATGGATGTCCT CGAGTTGCACAGGGAACCTGCTGCTGTTGTAGAAGCTTCTCC
WI-19348b	98	G A ---	---	GCTGCTACTGTAGCCAGCCAGCTGCAGGATGGTGGGTAGCAAGTACGATGGCCATGCACCTTCG GCGGTCGATGAAGAGACTGTTGGTCATGGC[G/A]GTGACGTCCTCTCCAGGCTCATATGGATGTCCT CGAGTTGCACAGGGAACCTGCTGCTGTTGTAGAAGCTTCTCC
WI-19635	98	A T ---	---	ATTAGTTCGTGTGGGCCACATTCAAAGCCATCCACACAAGCTTCTGTAGGCCATTGTAACACAATG TTAAAGGTACAGTAAAATACAGTATTATATCTTATTGTAGCACGGCTGTGAGGCTCATT GTTGAATGAAGCATCCTTAGGCAGCACGTGACTGCATGCAGATATGTGTCTGAAAGAAGCTTTGCCTT T
WI-19641a	46	A G ---	---	TCCAATTTTCAGAAACATGTTCCATGTTTATTGTGATAAGCACTAGIAGTATTATAGTCTCATGTTT TTAATTTATGAATAACGCTGATTCACTTTGATTTTGTATTTACAGAAGATGTCAGGGCTATCTCATTC AGTTATTAATAATGGATCAGAGTAGTAAGTCAAGAAATAAGTGCATAATGTGGTTTAAATTTAAAA AATACTCAGAAATGAGGTAGTATTTTAAATTTTAAATTCATCCACCCACCTTG
WI-19642b	52	C A ---	---	ATATAGATACCATCCATGGTTTCAAGCATGGCCTGGACACATTATCCCTTC[A/G]GGTAAACCAG GACTATTGCATGAGCATCTTTAATACGTATTTTGTAGGACACAAGTTTCATGCTATTA
WI-19673b	180	C T ---	---	TCTGCCATGATCACATTGTGATGAAGAACATGATGGTCACTAGTAGGTAACTTCTGTGTCATTGCCT TACTCTCAGTGAGGTGCTAGTGGATTACCTACCCCTGCTTTTGCATCACCACTGTAAATCTAATAGT GAAAAGGCAAATGATGCTCAGTATCACTGTGAAAACATTTTTC[C/T]CTTGGACCAGCTGAAAGAA TCTTGAGGAGCCTGAAGGCTTCAAGGTCCACACGTCAAAAAACACAGCCC







WI-19066	147	GC	---			TGACAGGGAGAGAGGAAATCTACTATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCCATGAACCTTCAGCTGATCGCTTAGCCAGTCCAACTCTCTACGAGGAAC CATATGTTCTGC/GC/JTTGGTCAACCTGTAGCTGAATTAATCTCCATAATCCGGATGCTCAATTAC AGTACCAATTGACGGCAAACTTTTTCTTAAACGCCCTTCACTAGTTCCTTTTA
WI-19066c	100	GA	---			TGACAGGGAGAGAGGAAATCTACTATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCCATGAACCTTCAGCTGATC/GAJTCTTAGCCAGTCCAACTCTCTACGAGGAAC TGGCATAATGTTCTTGGTGGTCAACCTGTAGCTGAATTAATCTCCATAATCCGGATGCTCAATTAC AGTACCAATTGACGGCAAACTTTTTCTTAAACGCCCTTCACTAGTTCCTTTTA
WI-19066b	87	CT	---			TGACAGGGAGAGAGGAAATCTACTATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCCATGA/GC/JTCTTCAAGCTGATCGTCTTAGCCAGTCCAACTCTCTACGAGGAAC TGGCATAATGTTCTTGGTGGTCAACCTGTAGCTGAATTAATCTCCATAATCCGGATGCTCAATTAC AGTACCAATTGACGGCAAACTTTTTCTTAAACGCCCTTCACTAGTTCCTTTTA
WI-19066a	72	CT	---			TGACAGGGAGAGAGGAAATCTACTATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCA/GTJTAAACCCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAACTCTCTACGAGGAAC TGGCATAATGTTCTTGGTGGTCAACCTGTAGCTGAATTAATCTCCATAATCCGGATGCTCAATTAC AGTACCAATTGACGGCAAACTTTTTCTTAAACGCCCTTCACTAGTTCCTTTTA
WI-20660	105	GC	---			TTTACAGCGAGTTTTCCCGTCTCAATAAGTATGAATCTAAATAGATTAGGGTGAAGAAATGTG TGCTAAATAAAATCTCCCTTTTGAATGTATATTTGT/GC/JTTAATAAGGGAAGCATTTAATATTA CAGACATAATTTACAAGGTTCTGAACATGATGATGATCCATTACTGTTTTCTGTACAAGATAGAACAAA AAGCTATCCACCGCCGCCCAAAAATACTGTTTTAACCAACTATGTTTTAAGA
WI-18768	120	CT	---			CTGCTGCCAGCTTCTCTTGGCCCTGCTCCAGATGGCGGTCTCTGCGAGCCTCCCTCAGTCTTCC TCCACCCGCTCTTCTTCCAGCCTGCCTGCATGCATGTGCACCCCTTGGT/GC/JTTCGCTCCATCGCC TTGAAAGCTCTGAA
WI-19087	37	AG	---			TTCCCCAGGGTTCTGTATTGCAGTAAGCTCAATGTATGTTAATCTAGTTGCTCTGCTTTG GTC/TCTTCCCAATGATGCTTACTACAGAAAGCAATCAGACACAATTAGAGAAGCCTTTTCCATAAA GTGTAATTTAATGGCTGCAAAACCGCAACCTGTAACTGCCCTTTAATGGCATGACAAGGTGTGC AGTGGCCCCATCCAGCATGTGTGTGCTCTATCTTGCATCTACCTGCTCC
WI-18790	49	AT	---			GAAAGCCAGAGATTAGCCCCGCTTCCGATCTGTCAACCAAGGACAGAA/GTJGATGGACAAGGGA TGAGCTTTACAAAGATGATGCATTTGGAGATCAGAAAAATTCATATTTAAGCAAAAGTGATACAAACA CAGTGATTTGGGAATGCCT
WI-18987	35	GA	---			AGGAGGCTGTTCAGGAGTCTGCCAGCAGCCTC/GA/GTGGCCAAGCCAGACACTACCCACCTT CCCCAGTGGCCCCGTGGATCCTGGTCTAGGCTGGACACAGGATTCAGAAAGACACAGGCTGCACA GAAAGAGCCAGATGGACCTGAGTGTGGTCAACAGCCCCCTACACTCAAGGCTGAGAGGCCCTCAGGAA AGTCA

WI-18919	26 C T ---			TGGATGAAACACAGGGATTCCGGAC/TGCCAGACCCCATTTTACTTCACITTTCTCTACAGTG TTGTTTGTGTTGTTGTTTATTTTATCTTTGGCCATACCAGAGCTAGATTGCCCAGGTCT GGGCTGAATAAA
WI-18741c	64 G A ---			CTTCTGGTCAAGGCTTTGGACATCTCTCAGTCATCAGACAGAGTATCTCTGCTCTAGACCTC[G/A] CTGGAGTTCAAGCTTGAATTATTATATCAAGTTAAITTTACAAGCCCTGGATGAGGCTACTGA
WI-18741b	38 G C ---			CTTCTGGTCAAGGCTTTGGACATCTCTCAGTCATCA[G/C]ACAGAGTATCTCTGCTCTAGACCTCG CTGGAGTTCAAGCTTGAATTATTATGCAAGTTAAITTTACAAGCCCTGGATGAGGCTACTGA
WI-18741a	23 T G ---			CTTCTGGTCAAGGCTTTGGACAT/GTCTCTCAGTCATCAGACAGAGTATCTCTGCTCTAGACCTCG CTGGAGTTCAAGCTTGAATTATTATGCAAGTTAAITTTACAAGCCCTGGATGAGGCTACTGA
WI-19179a	170 G A ---			TCAGAAGCAGACATGGCATCTGTTCCCTTGGCTTGGTTGGTTGTGTACCTTTACGAGACCTGAATT TTAGAAATGCCAGTGTGCCAGAGTGAGTGAGTGAATCTCTCTTCAGGTAAAGATAGGCTATCTC AACACTGCTGAGTGATTCTATAACATATCAACCA[G/A]TAGCAITTAACCCATTTTATTTCTGTCTCTT AGTGCTGAAGATGCTCACCAGTTTCTGTGTACAGTAAGGCGCATGCT
WI-19212	46 T A ---			CCAAAGTGCATCCATGTTTGAITTTCTGATGAGACTAGAGTGACAGT[A/G]TTTCAGAACCCCAATGT CCTCAGGTAGTTTGGAGCATCTCTATGAGATGGGATTATGCAGATGGCCTATGGAATGAGCTGC ATAATTACACATTATCAAAGTCTCTTACAAITTTATTTCCGCAGCATGTCAAGCTAAGTAGACCCA ATGGGAGAGAAATGCCTGCTTCTTCCCTCTTTTCTGCACTGCCATAT
WI-19183	210 G C ---			CTGTTGAAGGCTTCTCAGGCAAACTCCAGCTTAAAGCCCTAGACAGGTAAAGACACATTGGATG GCAGCATGGGTTCTTCCCATTTATGGCATGAATATGTGTTTAGAATAAGGAACAAGCATTATT CCTTTGCCAACACAGCCTCACTCTAAGAGGCTTTTGTGCTGAGTCAAGCAACACTTGCCTGCTGCCCC CTTGGAG[G/C]TGCAITTTGACCTGCTCTCACTGTTAAGGTGACTTGGTGGC
WI-20014b	214 T C ---			TTGAAATCCCAGTCTCTGCCCCCAGGCGGGTCTGTCAACATAGATGTCTTCTCTACTGGGGTC GTTCTGGCTTTTGTAGAACTTGGTCTGAGATGTTCTTCCCTGTCCATTACCATTCGATGTTCTTT TGTTCAAGAGCAATGTTTCTGTATTCTGAACTGGAACTGAACAGTTTGCCCTTCTCTCTAGTCACC AAGCATACTT[G/C]CTGGCTCCCCAAGTACTTAAITGTTCTCATCTGT
WI-19041	198 T C ---			GTCTCCCCAGAGTGTCTTGCACCCAGCCCTGTCTGCTGTGAAGGGGATACAGAGAAGCTCCCCG TCTCTGCATCCCTTCCAGGGGGTGCCCTTAGTTTGGACATGCTGGTAGCAGGACTCCAGGGCGTG CACGGTGAGCAGATGAGGCCCAAGCTCATCACACAGGGGGCCATCTTCTCAATACAGCC[T/C]G CCCTTGCAATCCCTATTTCAAAATAAAATAGTGTGCTCTTGCCTGTCTGT
WI-19135	20 G A ---			CAGTTACCTGCTTTGCCTC[G/A]AAAGTGTCAATCAITTTGTAATTTAGTATTAACCTGTGAAAAGT GTCTGTAGGTAGTGTATTATATATAAGGACAGCCAAATCAACCTATCAAAGCTTCAAAAACCT TTGGGAAAGGGTGGGATTAGTACAAGCACATTTGGCTACAGTAAATGAAGTATTTTATTAACCT GCTTTTGCCCATATAAAATGCTGATATTACTTGAAACCTAGCCAGCTTCAAC

WI-19236	54	G A ---	---	TACACAGAGGGTGCACCTTGGACTCTGAGGTTGGGTGGAAGGGGAAAGG(G/A)GATGGAGAC CTGCTCCCCAGCTCTCTCTGTACAGCGGTTTACATGGGAACAGGTTAAGATCTGTGTAGGGGAGGT CACCTTACCCTTTTTCATAGGGGAAGAGTGTACACTCTCTGGCTATCTCAGGGGAATGGGAAAG AATCTTTCAAGGGCAAGAACTCGTGGAGGATGTCTGTGTATGTAATACT
WI-19144	222	G C ---	---	GTGCCAGTCTTCAGAAAGCAAGGACTGCCCTTATTCAGCCTTCTGACCTCCAGCCTTCTAAGG CTCAGCCCCACGGGACTCTGGTGGCTGCCAGCTTGTGAGCTATCTATCTATATTCATTTATAGCCAA ACAGGAGACCCCTTTGCAGGACTTGCACAGGAGGCTGTAGCCAGGAACCCCTCTCTTCCCTGGT CTGGCTCTGCTGGAGCGG(G/C)TGGGAACCAACACCTTCAGTCTGGTG
WI-19139b	110	C A ---	---	CCCGTCTAAGGGAGAAAGCTAATGTTTCCACAAGACTGAACAACGTGTATTTACAGAGGGTAGAC GGCAGATGCCCTGACAGAGAGTGGTTGGCAGACAACACACTAG(C/A)ATTTTCACGGGTGTGGGCAC ATGGGTGTGGCACTGGACGTGTGCAGCATGTGGCGTCTCTGTGTGAAGCCACCGTGTCTCTTTGG GGGGCGCGAGATCTAGCATCTCTGAAATCCTGGCTGTGAGGCTTTGAAG
WI-19139a	66	C T ---	---	CCCGTCTAAGGGAGAAAGCTAATGTTTCCACAAGACTGAACAACGTGTATTTACAGAGGGTAGA CTJGGCAGATGCCCTGACAGAGAGTGGTTGGCAGACAACACACTAGCATTTTCACGGGTGTGGGCAC ATGGGTGTGGCACTGGACGTGTGCAGCATGTGGCGTCTCTGTGTGAAGCCACCGTGTCTCTTTGG GGGGCGCGAGATCTAGCATCTCTGAAATCCTGGCTGTGAGGCTTTGAAG
WI-18910	112	T C ---	---	GGCTGGGACCTTTAGGAAAGTGAATGCAGGTGAGAAGAACCTAAACATGAAGGAAAGGGTGCCT CATCCAGCAACCTGTCTTGTGGGTGATGATCACTGTGCTGTGT/CJGGCTCATGGCAGAGCAIT CAGTCCACCGTTTAGG
WI-19235	173	A G ---	---	TTCAGGAGGTGGAGTTCTGTCAGCTCTCTGCTGTGATGTGGAAGCTTCTGATATTTGAAGAAACA CGAATGTCTCTGTAGCTTCTCTTCACTGCCCCAGTATTGCTCTGTATTTATCAGCGATGCCCTCTGT CACTCATGCCCTTGCCTAATTTGTTCAACAATGGTGGAA(A/G)GCTTCATGTAATATGATCAGGACCCACC TCCAGTCTTCTGAAAGTGTGACAGTGTCCAGCCGGTTCTGCAGCACTA
WI-19222	179	C T ---	---	CGTTTCCCTAACTACCCAGTTAGTTTGGGATGATTTGATTTCTGTGTGTGATCCCATTTCTAA CTTGGAAATTGTAGGCTCTATGTTTCTGTAGGTGAGTGTGGGTTTTTCCCCCACCAGGAAGT GGCAGCATCCCTCTCTCCCTAAAGGACTCTGCGGAAC(C/T)TTTCACACCTCTTTCTCAGGGAC GGGGCAGGTGTGTGTGTGACACTGACGTGTCCAGAAGCAGCACTTT
WI-19117	134	A G ---	---	AAATAATGCAACGAGGAGGAGAAAGAAATGCACTAAGACAAGAACATTTCTCTCATAGAACATTG ATCTGTTTTACAGGAACAAACCTTGCCTTGAAATTTACACAGTGAGACTGTACATAATTGCATGAA A(A/G)TAGCTATTTTTCCTAAGACATTTTTCATTCATGAATATTTCAAGTTTTCATACTGTACA CATTCTTAAACACATGATACCAGCAGCACTGAAATGAATGCCGAATTG



WI-18017	87 C A ---			ACAAAGAAAATGGAATAGGTTTGGAAAACTTATCTGCATGTACAAAGTAATCCCGTAGATAA GGAGAGGCAACCCNGGAACA[C/A]ACTGCTGGATAAATCGTTTCAATAAATATATCTCTTGCAT CAGAGCTGGTGGAAATCAT
WI-18148b	101 A G ---			TTATTGCGTTCCTTCGATAAACCTCTCTTTGGGACTATGAGATCATACCAGATGTGAAAAACGAAAGCA GTGATTTTCAGAAACNCGATTCTGAATATCCC[A/G]TGGCGGCATATGCAAGGGAAGATGA
WI-18254	64 T C ---			TATACGGATCATGTATTGTGTGACCACTACCAAGTCAATTTGTAGAGCAGTTAAATCACATTC ]GCCAAATCCCTCTTGCCTCTGTAGTCAGTCTCTCCCAACCCAGGNACTTGGCAACCTGTTT TCCGTTCTAGACATTT
WI-18265b	117 C A ---			CAAATGGGTGGAGTGAATAAAGCATATTGAGAAACAAGACGGCCTTCTGGCCNCTCTGCGTCC AAGGCTGTAAAGGTCAGGATTGCTGCTAAGTGAGCCATGAACGTGGTG[C/A]GTTTTCAACCTTTTC CTGGGTGGTTCTTCAG
WI-18295	40 C T ---			ACCACATTTGTTGAGAGCCTATTGTGGAGAACAAACAG[C/T]TTGGGAAGTAAAGGTTGATTACT TCCTCTCCAAGGATGATATGTTAATGAATCCCTTNCCTTAGCTTCATTCTTCATAATGOCAAA
WI-18459b	64 T C ---			GGGCAAGAGACAGAGATTTAATTGAATAAACTCCAGGCTGTACACGGTGGGAGACACAAAT/ C]GAGTAATTAAACACATAATTTTANATGACAGTGCAATTAATTAAGTCTGGTAAAGCCAGAG GGGAGGAGGGCGTCTTCA
WI-22585	56 A G ---			TTTATTTTAAATTTGCATCCTGAGATAATAAATTTTATCTGACAAGTGAACAATG[A/G]CAGAAGC AGCAGTGAAGTTTCGGAGAGGAGGTATCCTTCAATTTTGGCACAGCTGTATAGATTGA
WI-21155	36 A G ---			GGGCTGTGGAGTAAACAGAACTTGATGGAAAAATTGGC[A/G]TCTGTGAGATGATTTCTAAAGCTTTC AGACAAATGGCAGA
STS-F02766b	88 G A ---			GCCTTGTCTCTTGTCTCCTCAGAGGCTCAGATGGATACGCAGCAACTTCTTTTGAACCTTTTAT TTTCTGGCAGGAAGAAG[A/G]GGATCCAGCAGTGAGATCAGGCAGGTTCTGTGTGCACAGACAG GGAAACAGGC
WI-19888a	98 C T ---			GGCACGATTCAACCCATAACAGAGAAATAACTCCTTATTGGAACAAGGTTTTTATTTGATATGATG AAAAATATTTGGAACTAGAAAGTAGCAGTGA[C/T]TGGACAACGTTGTAAAGATATTAAATGCCACT GAACTGTTTCAATTTAAATGGTAATTTTCATGTATGTATTTCACCTCAATTAAGAATGGAACATGT CTTATAATTGTAATACATGAGANCATATTTATGTTGGAAGTGAACACAAG
WI-21485	82 C T ---			TGAGACCATCCTCCTCAACAAGAATCAGTCAGTTTCAGCACCTAATTTCCACACTGAAGTCTACG CAATTTTCATGCAG[A/C]TGTGCACACAGTACAGTGACAAATCCAGAGGGGCAACACATTGTAATT CATATCATCCGTTTCCAAA
WI-20601a	125 T C ---			TCAGAAATGCTTTCCTGCCCCCAAAACAAAGAAATTAATGAATGCNCTTACAATTGAGATGACTT GAAGTTAAAGAAAGGTACCTTCTTGGAGGTTGCATGACAGGATTAGTCTTCTGTGTTT/C]CTTGGT GCAAGTTTGAACCAAGTATTAAGTACCATTTGCATCAGAGCATCTGTTTCCCTGTGAGATCCCCACTAG

WI- 20561b	94 T C ---			CGTTGCTTATTTAAGATGGCTGTTTATAAGTATAAAGCAGTTTGAGCAACACTGATTGTGCATTATG TACTTCAGATGAAAAATCCTTACATGTC/GJGGAATCAATGCTCTTTTAAATTTTCAGATAAAGAAATTT NCATTTGAGGAGACATACAATTGTAA
WI- 20561a	25 A G ---			CGTTGCTTATTTAAGATGGCTGTTT/GJTAAGTATAAAGCAGTTTGAGCAACACTGATTGTGCATT TTGTACTTCAGATGAAAAATCCTTACATGTGGAATCAATGCTCTTTTAAATTTTCAGATAAAGAAATTT NCATTTGAGGAGACATACAATTGTAA
WI- 20116e	69 T A ---			GCCTTCATTTCTGTCAACCCACCCCTGTCCACAGTTATGTTGGCTTCAATATATGGCGTTAGAACAT A/T/ATAAATCTATATCATATATTTATACACAAACACATTTCTACCAGCACTGTGAAGACACAGA CTAGGCTTACTAGGCTTGGGCTCTCCCATGCCACTTAAATGNGCACAGGTTTGTCTATGCAA GAATTCACACAGAGTTGGTCTGGCCATCAGCTGCAATTTCCCGGAGATAA
WI- 20116c	59 T A ---			GCCTTCATTTCTGTCAACCCACCCCTGTCCACAGTTATGTTGGCTTCAATATATGGCGTT/ATAGAA CATATATAATCTATATCATATATTTATACACAAACACATTTCTACCAGCACTGTGAAGACACAGA CTAGGCTTACTAGGCTTGGGCTCTCCCATGCCACTTAAATGNGCACAGGTTTGTCTATGCAA GAATTCACACAGAGTTGGTCTGGCCATCAGCTGCAATTTCCCGGAGATAA
WI- 20116a	22 C G ---			GCCTTCATTTCTGTCAACCCAC/C/GJCTGTCCACAGTTATGTTGGCTTCAATATATGGCGTTAGAA CATATATAATCTATATCATATATTTATACACAAACACATTTCTACCAGCACTGTGAAGACACAGA CTAGGCTTACTAGGCTTGGGCTCTCCCATGCCACTTAAATGNGCACAGGTTTGTCTATGCAA GAATTCACACAGAGTTGGTCTGGCCATCAGCTGCAATTTCCCGGAGATAA
WI- 20466b	133 G A ---			AAAGATTTCAGTCCCTGGGACACAGTTTGGAAACACTATTTAAGGTTGCACATATTACAACACAG NTCCAAATGGTGAAACTGGTATTCTAAGATGAAAGCTTAATGAACATAATGAAGTGAATAAACGC G/ATGTGAACATAATGTTTAAAGTTAGAGCTTGTCTCAAGTCAGTACAGCTCTTAAGATAATAAT ACAGTAACACTACTTTTATTTCTTTGCTCTTTTATCCCTTTCAGGTTTCGATT
WI-21444	39 A G ---			CTGGGACGCAAGTAACCATTTTAAAGAAATACTCTCAAC/GJAGTTCTTTTTTATGGGGTATTCA GTTGTTAACAAAGTTAAATCTTATTTGGAACATACTTTGTAATTTATTCGAGGAAGAAGAAATCT ATAAGATTGACTTACTCATTTGACTGGTTTGTGAAGCTTACTGGGG
WI- 21034b	148 T C ---			AGAATGGACAATGATGCAGATGATTGTGAGCAATTTGATGAGAAAGTGGTGATTAGAAGGATACAG CATAAATTTAATTGTAAACATGCTTATCTAGCTAACCTAATCTGTTTCTGTAGAAATTAAGTGGTCATGG GAGATTGGATAGAT/C/GCCTAACCTATCTCAATTTTAAGTAATGTGAGCAA
WI- 22091c	205 G A ---			GGCGTGATTTTGATGCAATGTCCAACCACTCAAGCTATCATTTGAATCCAAATATTTCCAGTAGAG ACATGCAGAGCAATGTCAATGTAACTACATACAAGCATATTACCTCCCCCTTAAGTGACTCATAATTC ATTACTTGTCTGTAGCTTTTAAAGGTTTAAAGTTTAAAGTTAGTACATTAAGTGGTATTACTTGAGGGCA ACA/GJAATACGGCTTAACAACACACATAAATCAATGAGGCTCAGGGATTG



WI-21805a	45 A T ---			CAACTGCTGAGGCTCTTCACTAGCTGATTATTAATCCTATATTATJAAAAAAAAATCTATAGTCTG CAGTCTTTGACATACTTCTCAAGGGTGATATGTGGTGAATGCAGACTCCATCAATATGTGTGGTT TTGTTGCTTTTGTAGCTTAAGTCTGTTTGNAAATCCAGAGGAATATGATTGAGGCCAGAGTTA CATTGGTTTCATAAAATCGAACAGTTGAAGGCTGTTTTGTAAATTGCTG
WI-21778b	155 T C ---			AAAAATCCATAATATTGAACCCCAAGTTACAGAGAAAGTTCTGTAACCTTTTTTATTGAATTATTGAC TCTGCCCGGCTGCTGCTGCTGCTTCAACTCCAGTCTGTAATGCCCTGTGTAGTGGGGTCCCCAG GTCTGGGCTTCTGAGGTCCT/CJGGTAGAAGGAGGCGAGTGGT
WI-20907	241 A C ---			TGAGTCAGTGGTCAGATGGGGCAGTTGCGCTCAGCTGCAGTCCCTGACTCCGGAAACACTGTGCCTCT CAAATGATCTAGAGCTCATCTTGGCGGTACATGAGGGGCAGTTGTTGTTCTAGTACCCATTAGCCOC ATGGCTCTTCAAGCCCAATTCACACTGGGAAAAACACACCTCACAAGATGCCTATCCATTGAGTTTC ATACAGGTTTGTAGTAGCTAGAACTAAAAAACATTTTTTA/CJAATTATCTA
WI-21449b	222 C T ---			AACAGCAGCAGTCACTTCCAAAAATGCAAAAAAATTAACAATTTTAGAATAAAATTATAATGTTTA TAATGCGGGTCAGAAGANTTGAAGGTACACAGAAATCAATCACGCAGCACTGGAGCGGCTGGAG AAGCCAAAGCCCACTGGTCAGGGGTCCAAGCTGACAAGAGTCCCACTGAGAGGTCTCCACACCC AAATCATACCCCTCAGCTTCCCA/CJTTCACAGAGCCAGTGTCTCTGGGTTAG
WI-21558a	157 G A ---			GCTTACAAGGAAGCCTGTGGACAGCGAGNTGGGTGGAACCGACTCCAGCTCGAAACCTGCCCTC CCATCCCTTAGCGCTTCTTGGCTTCCGGCTGATTTCTTCGACAGCAGTTCTGGCCAGGGCAAGG AGCTGTGGTGGGGGCGAGTATG/AJAGCCAGGGACTCCCTCCACAGATGAGGCTAGGGCTGCAA AAGGCCCCCGTGAAAGAGAGATGTGGTCAAGGCTTTATGGGTCTCTCCACC
WI-22187b	178 G A ---			TTTGCTGTGGAATCCATGAGAGCCGGAAGCATGCTTGGGGCCGTGGCTAGCAGAGCTCATGNGACCA GTCCTGGGCTGACCAATGGGTGATTACATTTAAAAACCAACCAAAACAAAAATACCAAGA ACAGATCACTTGCCATGGACATCAGTAATCTATTGGTAATGGTG/G/AJAAATTTTCATGAAAAATTTCC CCTAAACCATACAAAAACTGTCTCTCTTACCCCAAAAAGTGTGGAGGAAAG
WI-22187a	110 C A ---			TTTGCTGTGGAATCCATGAGAGCCGGAAGCATGCTTGGGGCCGTGGCTAGCAGAGCTCATGNGACCA GTCCTGGGCTGACCAATGGGTGATTACATTTAAAAACCAAA/CJA)CAAAACAAAAATAACCA AGAACAGATCACTTGCCATGGACATCAGTAATCTATTGGTAATGGTGGAATTTTCATGAAAAATTTCC CCTAAACCATACAAAAACTGTCTCTCTTACCCCAAAAAGTGTGGAGGAAAG
WI-21609b	146 G A ---			TCATGAATATGACGCTCCATAATCTCTCCCTTGTAAACAAACGTGCAGTCCGTTTCAAGCTGTAA AACAGCCCAACCCCAAGACATCACAGAGCGCAAGCAGTGGCAGTGAGAGGGAGCCTGTAAAG GATGTTTCAAAG/G/AJAGGGTCCCGGCTATGTGGCCACTGGATGTAGGCAGTGAGCTGAGTCCAGGC TTTCGGTCTGGGAAGTGGCAGAGGCTGAGACANTGGCCAAAGAGGAGTTGGAG

WI- 21609a	42 C T ---	---	TCATGAATATGCAGCCTCCATAATCTTCTCCCTTGTAACAAAC/CTGTGCAGTCCGTTCCACAAGCTGT AAAAACAAGCCAAACCCCAAGACATCACAAAGAGGCAAGCAGTGGCAGTGAGAAAGGAGCCTGTGA AAGGATGTTTCAAAGGAGGGTCCCGCTATGTGGCCACTGGATGTAGGCAGTGAGCTGAGTCCAGGC TTTCGGTCTGGGAAGTGGCAGAGGCTGAGACANTGGCCAAAGAGAGTTGGAG
WI- 22512a	104 T G ---	---	ACATTCGAGCCAGTTTTTCCATATTGCTCCACTGCCTAAAATCCCTTGGTGCCCTCCCTAGGGCTTCA GGTAAGCCCTGACATCATGCTCTTTGTGATCTGT/CTACCTCACCCATGCTCCCCACCTNAGTTCC CACATTTCCCCACGICTAAGGCGAGGCTACACTTGACTGCA
WI- 21028b	139 A G ---	---	ATCGCAAGCTACAGCCTTAAATCTGAGCTCCTCAAGTGCACAATTTCTGTCCCTTTTAAAGGCTCA CAACACTAAAGATTTCACATGAAGGGTCTGTGATTGATTGAGCAATCTAGGGGATATGTGACAGGG TTTC/AGTGTGCACTGGTACAGAAACACACAGGGAGTTTCACAATTTTTTATACAATGCTTGGGAAT CTACGG
WI- 21028a	121 A C ---	---	ATCGCAAGCTACAGCCTTAAATCTGAGCTCCTCAAGTGCACAATTTCTGTCCCTTTTAAAGGCTCA CAACACTAAAGATTTCACATGAAGGGTCTGTGATTGATTGAGCAATCTAGGGG/AGTATGTGACAG GGTTTCATGCACTGGTACAGAAACACACAGGGAGTTTCACAATTTTTTATACAATGCTTGGGAATC TACGG
WI- 18829d	58 A G ---	---	ACAACATGCCTGTTACAGGGGGGAAATCCTAGGNAATAACTTATGTGACTTCTTG/AGTTCATCA TCATACAAGACAAAGCACAAAGCACCAACCCATGCCTCTGAGGAACATTGGACCATGCACCCCTTGAAA AA
WI- 18829b	35 T A ---	---	ACAACATGCCTGTTACAGGGGGGAAATCCTAGGTT/AAATAACTTATGTGACTTCTTGATTTCA TCATACAAGACAAAGCACAAAGCACCAACCCATGCCTCTGAGGAACATTGGACCATGCACCCCTTGAAA AA
WI-20964	87 G A ---	---	AGCCAACTCAAGGCCAAATAATTTCTTAATATAGTTATTATGCGAGGGGAGGGGAAGCAAGGA GCACAGGTAGTCCACAGAATA/AGACACAAAGAAACCTCAAGCTGTGAGGTCAATTTGTAAATTAA AAGAATACTAAGATTAGATGAACACACACACTCAGAAATACTCTAGGAGAGCTGAAAAAGAAAGGAAC AGATGTTAACAAACAAATTAAGGCTGCTGGGGAACCTGAGTCCATGTTAAGCTTG
WI- 20059a	59 T A ---	---	CTCTGAACCTAAAGGCCCGTGAAGGCGATGATTGGTTTTGGCACACAGAGTGGATAACCAIT/AAACAT TGGCTGGAATGAGGTGGTCAGGAAATAAANTGCACAAATCTAACACCATGTTGAAATCATGTCTGA GTTCTGGAGAAAGTTAAAGTGTAAATAATTACAAAGACTGACATGCAACTCTTTACCTTACATTATT CATCTACAGACTATTTTCTCCCTTAGGAGATGAGGAGTATGGGCTTAGGT
WI- 22130b	165 C T ---	---	TGTTTTTGAAGGCTGTAGCAGACTACATAATGAGCGGTGAAGCGGCTGCCCTTCCCTCTCCTGACAC CAGCAAGGGGGAGGACCATCATACCGGCCCTGCCCATCATGCATCCATGATTACTAGCACTAGGAA GCCAACGGAANAGGACCCCGCGCTTGTCT/CTGTGTTTAAATCCAGTTAAGCTATACACGTTTAA ATACATGTCGGAGGTTACATGGTCTCATGCAGTCCCTCTGTGATGGGAATGAC

WI-21661	117 G C ---	---	GCTAGTCTCCACCCTTTAAATGTACTCTAGGTACAAAATAAACATTATACACATATAAGATCAGTCTTCCAACTTTAGAAATGAATAAGAAATGACATTTAAAAATAAAATAG/CJTTTAGTCACAGTCACAAAACTACCTTCTAAGGAAAACTGTCCAGTGAAGCCGTTAAATTTGTGCTTTCAGCTATGAAGGA
WI-21980a	25 T C ---	---	TCAGTTTAAACACACATTCATCAAGGAT/CJAGATTAAATATGTCAAGGTAGCATAAAAGGGAGATTATAAACAGAAATGTGTTTTCTGGGAACCAAGTTTCAAGTGAAGTTCAGGATAAGTTTATTAATTTTCATGGGTGAAGCCCTGGGATAAAG
WI-21636	71 A G ---	---	TGCTTGATTAATGTGGTGTTCACATTATCCTATTTCACAGATGGAACAGAAAATACACGCTTTTTTAAA[A/G]TAGCAATATCTATTATTAATAAAATTTGAAATAACACCAATAATAATATCATAAGGAAGTAATCTAAATTGTGTTGATTTCAGAGGGGAGAAAACATTACCTCTAGAGCTGAGGCTATTGTGCTCATGCAAACTCCAATCTGAAGGTGGTAGAACTAGGAAGGGACAGGGATTTC
WI-22457a	112 G A ---	---	TTGCTATAATTTCCTTAAAAATGCAAAAGAGTACATCAGCAGAGATATAGCCAAATCACATCATTAGACAAACAGTAAACATACTGGACACGGTTTCAGGCATGAAGGATACA[G/A]CAGTTAAATTAACATAAGGAACAGAGTCCCTGCATTCCTGAAGCATAGGATGGGAAACAGTAATGCAGATTAATACCTGGGGCCAAAACCCACTGAACCTCACCAGCTGAAAACACTGAAGGATACCTGGGTAAAGGA
WI-21524b	97 C T ---	---	GCCGTGAGGGTAGCGTATAATGAAAAGGTGAATAGCCGTGATGACGACCTTCGCGTCATACCTTATAATGGTTAATAACAGCATTCTGTCTACCCG[C/T]GATGATGCTTCTCTGCAATGGACTATTTGCCCAGTTGCAACAGGGCTAAGATTGTGCGACTATGACAATGAGTTGTTGATTGTTGGAGTTGCGGTGTCCTGTCAAGAAAGATTCTTGACTTTCTCCAAGTTACTTCTCCTCCAGGGGATG
WI-21524a	35 A C ---	---	GCCGTGAGGGTAGCGTATAATGAAAAGGTGAATACJGCGCTGATGACGACCTTCGCGTCATACCTTATAATGGTTAATAACAGCATTCTGTCTACCCGATGATGCTTCTCTGCAATGGACTATTTGCCCAGTTGCAACAGGGCTAAGATTGTGCGACTATGACAATGAGTTGTTGATTGTTGGAGTTGCGGTGTCCTGTCAAGAAAGATTCTTGACTTTCTCCAAGTTACTTCTCCTCCAGGGGATG
WI-22652a	32 G T ---	---	TTACCTTCCAAACCAAGGCCACTTTGGAGAAAG[G/T]AAGAGAATGCTATTAAATCAATAAGCCAAGACAAATAGGGACTACCTGGGGTAGACCAAGATGGGCGAGTCACCATACACCATCATCTGCCACAGAACCCTTGACATGCTGCCCTCCCTACTCCGCACTACCTGTCTAATTTGGGACCTGAAGCTTCAGCATCCCTTCTTAGGG
WI-21703d	197 A G ---	---	CAACAGGCTCATGGAACAGAGCCTAGGGATCCAGGAGCATAGGAGGTGGTGGTGGGCGGGGCTCTGCATCCCCCTTCTCAGCAGCAGGACCATCTTACCCCTCTGGGAAAGCAGATTGGAGCCTACACCACTTGCTGCTTTCTCACCCAGGGTAAGAAATGCAGGATTTCAGAGGGGAGTGAGTCTGGGAA[A/G]GTGGGCAGAGCACAGCTAGGGGCAAGGACTTAAGGGAACCTTGTGGGGGAAGAG

WI-21703c	134	A	G	---	---	CAACAGGCTCATGGAACAGAGCCTAGGGATCCAGGAGCATAGGAGGTGGTGGTGGCAGGGGCTC TGATCCCTTTCCTCAGCAGCAGCACCATTCTTACCCTCTCGGGAAGCAGCATTTGGAGCCTACACQ A/GCTTGTGCTTTCTCACCAGGTAAGAAATGCAGGTATTTGCAGAGGGAGTGAGTCTGGGAAAG TGGCAGAGCAGAGCTAGGGCAAGGACTTAAGGGAACCTTGTGGGGGAAGAG
WI-22663c	139	G	A	---	---	CCCTTGTCACTGTGCTCGCTCGCTTCTCACTGCAGTGGCAGGTGAGCCGGCTCGCTAATCTTATTC CCAGTCTCGGTGAACATGGGCTCAGTCTCCCGGCTCAGTGTGGGTTGCACCTGGTGCACCTACAG GC/GA/GAAGAGCTTCTCATTTGCTGAGGGCTTTTCTGAATCCGTGTTGAATGTGGGT
WI-22663b	55	C	T	---	---	CCCTTGTCACTGTGCTCGCTTCTCACTGCAGTGGCAGGTGAGCCGGCTCGCTAATCTTATTC TCCCAGTCTCGGTGAACATGGGCTCAGTCTCCCGGCTCAGTGTGGGTTGCACCTGGTGCACCTAC AGCGGGAAGAGCTTCTCATTTGCTGAGGGCTTTTCTGAATCCGTGTTGAATGTGGGT
WI-22663a	38	C	T	---	---	CCCTTGTCACTGTGCTCGCTTCTCACTGCAGTGGCTGAGGTGAGCCGGCTCGCTAATCTTATTC TCCCAGTCTCGGTGAACATGGGCTCAGTCTCCCGGCTCAGTGTGGGTTGCACCTGGTGCACCTAC AGCGGGAAGAGCTTCTCATTTGCTGAGGGCTTTTCTGAATCCGTGTTGAATGTGGGT
WI-22668	99	A	G	---	---	TCCTTTATCTGCTGCCTGCCTGAGTATCTGGGAATCTCACAAGGATTTGAGGGAGCCCTTGGGATT CCAACCTAACAAATAGTTTTCTGTAAATATTA/GTCTAGTCCATTTAGATTGTGTAAATGATCTAA ATGGNGTAACCAATTAATATCAAAAGTATAACAGCATTTAAGTCAGCTTTTCGAAGAACTTTTATT
WI-22631a	52	T	C	---	---	AAGATATAGTGGCAGGACAAGATTGGTCACGAAATCCTGGCTCAGTCTGATTC/GA/GCAGCACCATT CAAGTTTTAGGCAAGGATTTAACCTCTCAGGCTCATTTCTCTTTGTAAATTTGTATAATGGAACC TATGTACCATCATAGGTAATTTGGACAAATCAACTGAAATTTTT
WI-20258	157	G	T	---	---	AATCCACACTTTCACGAGGGGACAGCCTGCCATGTCTGCCAGGCTACAGCAGCGCGGCTAC TCTGCTGGTGTTTGGTGGCAGGTGGAGATGGTGACGGCGCATTTGGAACCGTAAGGCATGACAACG GGAGCCCGCGGGTGTTCAG/GTCCGCTTGACGCAAGTGCATGGCTGGCAGCGGCCCTCTACAGA AGGAGGAGCGCAATTCACAGCTCTTGACGTAGTTCCGGGGGAAGTAGCC
WI-22714	212	C	A	---	---	ACTACACATATGCTGATTTCAACAGTAAAAATAACATTTACATTTGTAGAGAAAAATCTAGGGTCT ACTAAATAATCTAGTACTGTTTCCACTCTCCTGCTAACTCTGACAGGAGTGTGTGGGAACGAAAGT CTGAAAAGGATTCAAAGGGGCTAGGATTTGCCACAGATCCTGTAAAGGAAAGGATGAGGTGAGCTT ACCAACCCCA/CATGAGTAGGGGCCAAACATCCTTAACAAGCTAGTTGCT
WI-22734a	44	G	A	---	---	TGGGGCTACTTTAGATGGGATGGGCTCAGGGTCTGGGAAGCCCTTG/GATCTTAGAAGACATTACCCA AATGATGAGAGGCAGCCAGTCGTGGAAGCCATAGTTTGGATGGCGAGACTTTCCGGCAGAGGAAAT AGCAAGTGCAAAGGGCCTGAGGAGAAATGAACCTTGGGCTTGTCTACAGGTTGAAGGCGGCCGCT NTGGCTGAGGTTTAGTGGATG

WI-22724	117	A G ---				TGATATGATGTCTGAGATTTGCTTCCAAATATGCCTAGGAAGGGAAGTGTTTAGAGATATAGGA CAAATCAAGATTGTCAAATGTATAGTAACCTGTTAAAGCTTGCTAAGGGT[A/G]GTTATTCTATTTT TGGGATATGTTTGGGAATT
WI-22750	48	G A ---				TGTAACCTGTGTTTCCCTGAAAGTTGAGGAAAGCTGAGGCAGCTAAT[G/A]GGCTCATACAAAGGT TTGGAAGACCCATTCTGACTACCTAAAGGAGAGTCAGCATTTCTGACCATTTCTGACTGTGCT
WI-2275a	60	A G ---				TGCTGTTCTTTAGTTTCATGACGTTTATCACAATGTCGCTACTGTTTCCATTGTTTACATC[A/G]TAGTA GGAAAGGGAATAAATCCCTAAGGCGAGCAATAATTTCTGTCTTTGAATCCTTCATTCAGGCAAA TATTTGTTGAGCACCAAGGGCCAGATGGGAACCTGAGGTATGAGGTGTTGGGAGCCAGGAAAGGAAG GGT
WI-22808	143	C T ---				CTTTAGCTAATGAAACTGGCTATGTGGACTATGATAGACCAAGAAAGCTACCCAAAGTCTGAGGGAG CCTAGTCTCTCTAAATGCAGACAATGTACCCATGACAAGGGCTACAGCTTGGCTTTAGCAACCAGGA GGATGAAGA[C/T]AGCAAACTGATTAAAGAGAGTAGGTATAAGAACCCAGGAGAGTGGGGTCCAAAT ATC
WI-21016	207	G A ---				TCCTCGTGTCTTGAGCCCTATCCCCACCCCTCCAAAGCCCTCATGCCAACACACCCGTGTCCACATT CCCCATCCTCCCTGTCTGCTCCCATCTCAAGTCCAAATCCAAAGGCCAGAGCCCTGGCAGCTTTCTG GGAGACAGCATGAAAGGAGGGAGTGGAGATGGCAGAGATGGGTGGAGCCAGTGGCTGTGGGTC CTG[A/T]TGGCGTGGTATGTGGGGGCCAATCCTGAGGCCAGAGTTCA
WI-21031	31	C T ---				TTGAACACCTGACCTGACCTCTGACATGTGG[C/T]CTGTGTCCCATTTGTCTCCAACGGTGGCACA TCTTCATCTTTGTTATATATCTGCAGGAACACTCAGTCTCTTCAGCAGCCGAGAAACACACACA
WI-21314	122	A T ---				CCATATCCAGTCTCTTTGAAGCTTTCTATTGACTTTTAGGGTTCAGTTATTATATCCTTTATCACTAT GACTTTCAATTTGATTTTTTATTGTTCTCCATTCTCTGCAAACTTTT[C/A/T]TTTGTATTATAA ACTGTTTCTAAACTTCACCTAATCTCTATCTGTATTNCTTGTAGTCCCTGAACCTCTTTTAGAGG
WI-21186	95	G A ---				AGCGACATCAGAATCACCTAGAGGGTTGACTAAACAGACTCTGGACCCAAACCCAGAGCTTCT GATTGAGTAGGCCTGAGTGGGCTTAC[G/A]AATTAGTATTTCGAAGACCTTCCTAAGTGTGCAG ATGCTGCTTGTCOCGGGGAACACACTTTGAGAACTATTGTTCTAAATGTTCTCTCCTTTCTTTAAA GGAGAGACAGGAATCCAGAGAACTGCTAATTTAAGCATAATGTATTGAAT
WI-21187a	94	A G ---				CCACGATAACTATAAAGCAGAAAAATTAGCTTTGAAAAATCAAATAACATATTTAGTAACACACATT CATTTTATAACACACATAAAGACACC[A/G]GENTCTCAGTAATGCTCTAGTCCAGGGGTTCTCAA AGTATGGCTTCAGACAAGCCCCATTTGCATCACCTAGGGGAATTGCTAAATGCAGATTCTCAGGCC CTACCTACTGATCTACTGAATCAGAAACTCTGAGGGTGAGACCAAGCAACCTGT

WI-21190	39	T C	---			TTTTCCACATACCAATGCACCTGTTTGTATAAACTATTCGTTGGGGTAAGCCCTTCCTTTGGAGAC CAGTGACATAGACATGATCCCATATATTAACAAATATTAATAATCTGTACTATTACTGC TTTAGTTATCTAGTGTATTGAGAAAGGAGAGTCAGCATAGTTTATTTCCATGTATAAAAGCTT AACACA
WI-19937d	186	G A	---			ACCATGTGCATTTATTGGCATAGGAAATAGTGACCAAGAAATGCAGCANCTAAACTTGGAAAGGAAA GAACTATTGCACAACCAAAACATTGTACATATCTGATTTAGACAAGCAAAAGCACCTTCATGTTGTCT GTAAAGGTGTTCTATGGCAACAGTGATGACATTGGTGTGTTCTCTCAGCAAGTCGATCCAAACCTTC CAAAAAGAAAGCAGTCATTGAAAAATGCTGACTTATGCATTGCTCAGGAAGAA
WI-19937c	185	C T	---			ACCATGTGCATTTATTGGCATAGGAAATAGTGACCAAGAAATGCAGCANCTAAACTTGGAAAGGAAA GAACTATTGCACAACCAAAACATTGTACATATCTGATTTAGACAAGCAAAAGCACCTTCATGTTGTCT GTAAAGGTGTTCTATGGCAACAGTGATGACATTGGTGTGTTCTCTCAGCAAGTCGATCCAAACCTTC CAAAAAGAAAGCAGTCATTGAAAAATGCTGACTTATGCATTGCTCAGGAAGAA
WI-2117b	227	C T	---			GAAACGGGGTGCTAAACAAGAAAAGTCTCAGATCCCACTGAAAATCTGTTTCAGTTTCACAGGCTC TCTCCAGAAAAATGCATATGTACCAATTTGCATGTACAAATTCAGAGCCTTCAAAATACATCTGGGG TCCAATCACATACCTCAGGTTTCAGACTCTCAGTCCCAATATCTCAGAGTTCTGAAGANTTAGCAGT CCTCTCATTTCTACAGTCTGTATTTCCTACTGAATCTTGGGTGGAG
WI-21122a	42	C T	---			TCACITTTGATCATAATCCCTGTAAAGCTAAAGTTATTCACATCTAACAGGAACTCTGTTTTCCTC TTATTCAATGTGCACAGCCTGACGGTTACTGTACATATCTGACAGGAGACAACTGGAATACT AAACAAATACTGGAATTCACATTACAGACAGCAACCAACATGGGATGCCACACATAACTTCTCT TTGTAGGTTTCACAGAGGCTTATTTGGGTGCT
WI-21254	53	A G	---			CAGTTTGTACAGGAAGGGCCCATGAATGTGGGGGAACTATCCACAGGAGATGCAAGGAGAAG CTGTTCTCTGG
WI-21054	23	G T	---			AAGGAACTGCATGGGTACAAATGTTCCAAATTCATACTTAACAAGGTGGGAAACGGGTCATTCT TGGCTGCTCCAGAAACAGGGGCGAGTCTATGCACCTCG
WI-21059b	181	T C	---			GGGACCAGGGTAACACCATTAGCAATATCCGTTATCAGCCTTATCTTCCACTGAGCCTGGCTGAA CTACAGCTGCCAGCATTCCTGGCTTGCATTTCCAGCTTCGTCACATCTTAATTTCAAGCTGAAA AATCCTGGGGAAGAGACATACTTCACTGAAGTCATTTCTCTATTCGATTTAGCCAGGGCAAAA TGAGATTAGGATTAGCTCAGCCAGAGTTAGGGTGACTATCCTTGCCCTAAT
WI-21059a	63	C T	---			GGGACCAGGGTAACACCATTAGCAATATCCGTTATCAGCCTTATCTTCCACTGAGCCTGGCTGTT GAACTACAGCTGCCAGCATTCCTGGCTTGCATTTCCAGCTTCGTCACATCTTAATTTCAAGCTG AAAAATCCTGGGGAAGAGACATACTTCACTGAAGTCATTTCTCTATTTAGCCAGGGCAAAA TGAGATTAGGATTAGCTCAGCCAGAGTTAGGGTGACTATCCTTGCCCTAAT

WI-20442	37 T C ---				TCACGTTGAAGGAAGAAAAAANGGGGGGGCTT/CJTAAAGTTGGCACAATTTTAAGAAAAT ACCATCCATTTTCTCAGTCTAATCTGAATCCATACATTAAACCAAAAGTGCAGTGATGAGACGAA CA
WI-21235	43 T C ---				GTGACAAGAGTGAAGCAAGGACAAGGGGCAGGCAGTCT/CJCTCGGGCCGATGTTCCAGGG CAAGCTACGTA
WI-22012a	57 T C ---				ATCAGAACTGCAATCTGCACATGAAAAGACCTGGGGGAATGCCTACATCTGGAATT/CJCATTTAC ATCAACGTTAAATTTTGTCCGACCAGTTCTTCATTGCTGATCATTCTTTGATAATGACAGATCCAAACAT GAAACTCCTGAAGCAAAATGAATATTACCTTGTGCTTTTCATGCAAAATTTAGGGACCAAACTCAAAAGG TTTCATCCATGCTGGGACACCAGATCTAAGGAATTGTGACAGGGATCTTCT
WI-21149a	167 G A ---				AGGACCTGCTCTCACACGTTCCCTCACCCACCAGCTTTTGGCAAGATAGTTGACTAAATACCACT AAATAGTGGCTTTTCTTTTAAACAATGACCTTATTTATCTTTTAACTTAACTGAGTCTTATATA CAGACCTGCCAACTGGAAGCTTTTACACGATGCTTCAGAAATCGGGCAGTATTGCACAATGGTT TGGGGCAGGTTCTGTGGTTAAACATGGGATGGAACCCACGGCTCTACCTG
WI-21376b	188 A G ---				GGTGTCAACTTGGAAATAATGGTTTAAAAACAGGATAAGCATTAAAGAAAAACACTTTCAATGTGTC TTCCATTTGATGAATTTGTTTCTCTCTTTATCCCGCAAGTGGAGTTTCATGTCTCGGTGAAACCA GACAGTGTGAATCTGTTCCAGCCCAAATCTGCAGCATTAGGGATGAGTCTC/A/GJGAAAGTGATTCT GAACTGAGCACGCACATGCTGTCATGGGGAACCTCTGGGGAGAAGAGCCT
WI-21382d	125 C G ---				CCATTGCAGTCCAGAGATGAGAAACTGGACCAGAGGCAATCATGAACAGCGGAGTCAAGAGA AGGGGTTCTAAGATGGAGAAGTGGGGCGGTTTGGATCCAGTGGGATNTGGCTTCC/CJGAGGTT GCAACCCCAAGGAAGTCTCTGGAAGCAGCACCACTGCTGATGGGGAGCAGAAGAGCTGCCATCCTC AGTCAGGGTCCGAGTCCAGGGTCCGAGGAGAGCTGCTGCTCATAGTCTCGCAC
WI-21437a	201 G A ---				TCCCTGAGGTTGGAGTCTTAGCATAGTCCCTCCCTCAAGAGGGACAAGGGGTCAGGGGCAGAGC AAAAATCCAGTCTGCTTCAACCACGGAGACTGCTTGGGATGGAAGTTCTGGAGCTCCCTCCATT CTATTCTGTGGGCAGGAACATGCCAGGGCTGCTGGTAAATGGCAGGGTCACTTTACCAGGGC/G /A/CAGGCATAGTGTGGCCCTGCTGCTGCTGGGGCCACCTTGGGAACAGT
WI-21202b	156 A C ---				CAAAATAGAAATCTTTGTGAGTGGATTGACTTAATTTTATTTCTGTATAAGCTAAATATGTC/JTGA GTTTATGAACATGTATTTATAAAATGGTCACAATATATTTTAACTAAGTATTGAGGG AGGAGGAGAGAGTTGACCAA/A/CJGTCTACATGCATAGACAGTCTCTAAAGCGTATCTCAAAACATG A
WI-21202a	61 T C ---				CAAAATAGAAATCTTTGTGAGTGGATTGACTTAATTTTATTTCTGTATAAGCTAAATATGTC/JTGA TCTGTTTATGAACATGTATTTATAAAATGGTCACAATATATTTTAACTAAGTATTGAGG GGGAGGAGGAGAGTTGACCAAAGTCTACATGCATAGACAGTCTCTAAAGCGTATCTCAAAACATG A

WI-21627b	153 A G ---	---	---	GCATGAAAGAACTCCAATCAGACITTTATCAATAAAGCAGCTTTTCATGAATGCTTCAGGTCAGTG TATGATCAGCTCAGCTCCAGTATCAACTTGAGTACCTCATTTATGGATATTTATGCTAGGAATGACAA CAGTAAGGGCATTGCAA[A/G]TCCAAAGTCATCTAATATTAACCATATTTACATAATTTGTAGG GACGTATACTAATACTCTACAATAAAGGGTTTAAAAATGTGTGCTTA
WI-21627a	106 A G ---	---	---	GCATGAAAGAACTCCAATCAGACITTTATCAATAAAGCAGCTTTTCATGAATGCTTCAGGTCAGTG TATGATCAGCTCAGCTCCAGTATCAACTTGAGTACCTC[A/G]TTATGGATATTTATGCTAGGAATGA CAACAGTAAGGGCATTGCAAAATCCAAAGTCATCTAATATTAACCATATTTACATAATTTGTAGG GACGTATACTAATACTCTACAATAAAGGGTTTAAAAATGTGTGCTTA
WI-21399a	75 C T ---	---	---	GGATTTGAGTCCCAACTGATCTCAAAATTCACITTCATGTAAACAAGCTCATTCCTCTAAAGTT TCAGTTT[C/T]TCACCAGTAAAGGAAAGGTTGGACCAGACATGTTGGACCGTAATGCTTGGTAA CTGCCCTCTGCAATTTGCTCTGAGGTTGTGTCTCCTAGGACTAGGATCTCTCTGCTTTCTGCC TTACCTAGGCATAGTGCCTGATAGCAGGCTGAAGCCCAATTCATCTTGT
WI-20329a	68 G A ---	---	---	CGATGCTCTGAAGATAGGAGGTTAATTTTACATGGTGAGTGGTCACAGACAGACATCAAT C[G/A]TCTGTTAGCAGCGAGAGACACTTTAAGTTGCCCAAGAGTACAAATCCCATCTATGAGAC AGCAGTGTGGCTTCTTAAACACAGTAAACCAATCAAAAGAAAGATTAGAGGTTCAGACATT AGGAACAANTGTGGCCAGAGATACCACAGAGCCCTGAAGGGAAAGGCCTCACT
WI-21249	155 T C ---	---	---	TTCTGGCATTCAAATGTACATGTAAATCCAAATTAACAGATCAAAATTTGTACACTAAGTTTCACCT TAGTATCTAAGTATCCAATCACAATTGTATCTAAGTTTCACITTTAAGAAACATTATAAAGGTAATT AAACTCTAGGTGTACTTAT[C/G]ATGGAACAGTATTTATTCNATTTAACTACTGTTTCATTGGGTA AAGTATGTTGTCCCAATTTTCAGCTGTTTAAAGGAATTAATAAACATTGAGA
WI-21504	147 C T ---	---	---	TGACACAGCATCAATTTTCATGAATACITTTGAAGGGCCATTAGAAAAAATAGAGCCCAATTTGGGTC ATTTGAGAAACATTTTCAGCACAATTACAGTGGGGGCACGGGCCGTTCCGCTCCAGCTGGGTTTCCCC AGATGCAACAAT[C/G]GCGGTTCTGGCTTCTCCACTGGTGGGATGGGATCGCGCCTTCGGAGCTCT CAGGG
WI-21242	115 G A ---	---	---	CTGCACCAGGGAGGACAGCTGCTGGCAGGGACTAATAAACCTTCCACCTGGCCATGGTGGTGGTGT CTCTATGGACCGAGGCCCTGAACCGCGGCAGGGAGGGGCAGAGAAC[G/A]CACTAGCTTGGGGGTG GGCACCAGCTTCAGACCCCTT
WI-21475c	181 A G ---	---	---	TAGCCCTTCTGCCAACATCTGGCAATNTGAGCTGGGGTGGACGTTGCCCTGATGTTGCCAGGAGTAG GATGCTGATGCTGCCAGAGAGTAGTGGCTCCAAACCCAGGCTTCTCACTTCTTACTAAGCACAG CAGTCTGAAGCTTTGGGACCTGGGACGTGCGTCTTTTGAGAAAGGCA[A/G]AAAGCCACAGCAGCAAC ACTTAGGAGCAAGACCCCTTCCCGTTCTCCACCCCTATTCTCCCTCCCTGAAG



WI-21475b	117 A T ---	---	TAGCCTTCTGCCAATCTGGCAATNTGAGGCTGGGTGGACGTTGGCCTGATGTTGCCAGGAGTAG GATGCTGATGCTGCCAGAGAGTAGGTGGGCTCCAAACCCAGGCTTCTC/A/TCTTGCTTACTAAGCA CAGCAGTCTGAAGCTTGGACCTGGGAGTGGCTTTGGAGAAGGCAAAAGCCACAGCAGCAAC ACTTAGGAGCAAGACCCCTCCCGTCTCCACCTATTTCCTCCCTGAAG
WI-20893d	207 A G ---	---	TGTTTGTTCCAGCCACATCTTCCAAAGGAACCAACCCAGCCGCTGTGCAGGGTGTGCAGGG CTGTCTCGGCGTTTAAAGTGCTACTGAGGAATACAATCATTTGACGTAACTCATCCGCACTCC AGCGTCAGGCCAAACCTTTCGTTGAGCTGGGNAACCTGCCATTTCTTCTTTTACAATGCAGT TTC/A/G/JACATAACATTGGTAGAGTAACAACAACCAAGCCTAAATG
WI-20893c	179 T C ---	---	TGTTTGTTCCAGCCACATCTTCCAAAGGAACCAACCCAGCCGCTGTGCAGGGTGTGCAGGG CTGTCTCGGCGTTTAAAGTGCTACTGAGGAATACAATCATTTGACGTAACTCATCCGCACTCC AGCGTCAGGCCAAACCTTTCGTTGAGCTGGGNAACCTGCCATTTCTTCTTTTACAATGC AGTTTCAACATAACATTGGTAGAGTAACAACAACCAAGCCTAAATG
WI-19941c	71 C G ---	---	GAGCTCAAGGGAAGACCTTACCCAGATAGGGACTAAGTGGAGGGTGAAGGAACAAGGTGA GGTATC/G/GGTCCTGGTGAGACAAAGCAGGGGGCTGAGAACACAGAGCAAGGTGGTTGGAG GGAGCACAGCAGGGTGCAGGAAGGAGATGGGGACATTTCTATTCAGTGCATGTCCCTTAAAT AACTGGGTACAGGAGCATTTGGAAGGAGAACCAAGGACAGAACAAAGCG
WI-21552b	166 C A ---	---	TGGGTACATGGACAGATGATATGTTTATGGTTATATGAGATATTTGATACAGATACACAATGTG TAATAATTACTTCAGAGTAATCGGATCTCTCACCTCAAGCATTTATCCATAGTTTACAAGAA TCCAAGTACTCTTGATTATTTAAAATGTACAAATTAATTTGAATTTAGTTACCCCA ATTGGCTATCAAAATTCATCTTATTCATCTTTGTAACCTATTTATTGTA
WI-21552a	66 G A ---	---	TGGGTACATGGACAGATGATATGTTTATGGTTATATGAGATATTTGATACAGATACACAATGTG /AJTAATAATTACTTCAGAGTAATCGGATCTCTCACCTCAAGCATTTATCCATAGTTTACAAG AATCCAAGTACTCTTGATTATTTAAAATGTACAAATTAATTTGAATTTAGTTACCCCA TTGTGCTATCAAAATTCATCTTATTCATCTTTGTAACCTATTTATTGTA
WI-21512	54 C G ---	---	TCCTCGTACTTCATGCTCCCTCCCTGCCCCAGAACCTTACAAAAATATTTCTGTG/GTAGAGAGGA AAGAGCTGGTGGCTGCTGGAGGCAACGTCAGGTCGGGAAAGGCACTGGTGTCTGTGATCTGTC TCAGTGATGGAGGTCTCCACTCGCCCCACAGGAGCCTCGGGCCAGAGATGAGAATATGCTGTAA TCCAGTACAGGGGCTGGTGGGTCCCAACAGCTCTCTTTGGGGG
WI-21513b	192 G A ---	---	CACATAGTTTCTCAAGAAAGAGGATGAACCTGAAAACCTCTTAAGGCAGGCAAGCAACTTTCCATT ATTCTTAGTTAGACCAGAACTTTAAATTTATATTCTCTTTAATAACTGTCAAAATACACCAATA CTTAGAGGAAAAATATTCACAGTATACCAAAACATTTTAAGATAAAGGAGGTGTAA/G/AJAGTAG TATTCTCTACATACCACAGTATACAATGATGCCCTTCTGTCAGGTTTAGGAAC

WI- 21514b	133 C T ---			TTGAACCTCTGAAGGTGGCTTATGTCTCGACTCCTCTTCTAGGACTGGTCATGAGCTGACAAGCATAG AGGCAAAAGTATCTCAACATTACAAAACCCCAATCTTCAAGAAAGGAGCACATTACCATGGAGC[C /T]ACAGGACTCCAAAGGACCTCAGAAAGCATTTAGCCAAATCTCCTTATGCAGGAAATAAATGAGG ANITTAAGGCTCAGATGGGTTAAGGGTATTGTCAAGGGTCATAAGGAACT
WI- 21514a	100 A G ---			TTGAACCTCTGAAGGTGGCTTATGTCTCGACTCCTCTTCTAGGACTGGTCATGAGCTGACAAGCATAG AGGCAAAAGTATCTCAACATTACAAAACCCCA[AG]TCTTCAAGGAAAGGAGCACATTACCATGGA GCCACAGGACTCCAAAGGACCTCAGAAAGCATTTAGCCAAATCTCCTTATGCAGGAAATAAATGAGG ANITTAAGGCTCAGATGGGTTAAGGGTATTGTCAAGGGTCATAAGGAACT
WI-22020	27 C G ---			ATGAACATGTTGCAGTGGGATGAAT[C/G]TTATCATGATGCTAAGTGAATAAGCCAGACACAAAA AATCCAAATGTATCATTTCTACCTGTATGAGGGTACTT
WI- 19576a	113 A G ---			TTATCGGTTCTTAATACAGTACAATCCTTTTGTGAAACAAAAGTCACACTGGCAATGATTATTACA GATCCAAATAGACTCAGGCTTCAGACATAAAAAATTTAACATT[C/G]TCTAGTTCAAGTATTAGT CACAGAAATTAACATCTGCCAGATGTACACAATTTGGTAAAAACTACAGCTTCTCTCCACGGGGA G
WI- 21695a	141 A C ---			ATACAGGCCACAAATTGCAGGATGGAAGGAGGAGTGGGCACTTGGAAAGTGAATGACTACACATGGCAATA AGCAGCCTATCTCTTTACCAACAGAAAGTTCTTGGGGCATGTGATGGTAGGCCAGACCCCTTTCCAA GGGAAT[A/C]TACTACACTAAGCCTACACTGTACTGTGAGAGTCATGTGGTGAACAAGGCCACAGGC AGTGGGAGGAAATGTGATGACTTCACTGTGTTTCAGANTTCTAAGGCCAGCAT
WI- 21574a	235 C T ---			AAACCCAGAAATTTAGGTACTTTTGTATTATGAGGAAGTCACTATACTAGGAAGCAACTTATGAGTG TGTAATATTATGATCTAGCAGCAACTTTCACCTGATCTGGAGGTGACAGCTCTCAGTGAACAGCGC TCATCACTAAAGTGAGAGGCTGTCTATTCTCATTTGTGAATGTCCCTCAGAGTCACTAGGGAGCCATT GGGCAGGCCAGGGAACCTTACTGCCTACTTCTCTTCTGCTGTGAGGTGGGA
WI- 21644c	151 T A ---			TGACTGCCAAGATTTAGGCCCAACTTAGGAGCAAGGGTCACCTTAACCTTTTCAGGAAGTCTTGGGT GTGACCCACTGCATAAATGGATTTTACCANTANTTTAACAGACTCAAAGTGTACATACAAGCTTG TTTCATAAATAAGGGA[T/A]TTCATCAAGATCCATGGAATGATGCAGTTTAACATGTGTCTCAGC TTGCCTACTGACCAGCTTCCCTTTTCTAAATATGGCAACAGCACAGCAAGTC
WI- 21614b	55 G A ---			TGCTTTAACCTCAAAAGTCCAAATAAACATATAGACATTTTANTATAGCTATC[G/A]TTTTAACA AACCTCATTTATGATCACTGTGCAATTTTCAGTCACCTAAATACGGAACCATGACTATTAAATAACA TTTACTGTGTGGGTTTGTGGGACTGAACATAAACCATACGTGTATTCTTAAGGTACTAGGGAGTT GGAAACAGCTACTACGGGTCAATGGTATTTTGGGCAGTTGGCTGTGTGGG
WI- 21615b	151 C T ---			GACCGAAAAAACTGCAAGGCATATGATGTTTGTGCAAGTATCACATGACTATTTCAAGCTTATAGA GAAACTTGCAAAAAAGTACAAAGATGGCTATTTTAAATTTTACATATTAAGATAAGGATGGACT CTTTCACCTGAGTATTATTC/TAGGACACAATCGACGGATGTAATCTATTTGANTTATACCATAGGCC TATTCTATTTGGCCAAAGGGAAGTAGGATGGGTACTGTGGAAACCGA

WI-21981	61 T A ---	---	TGTCATCTCATTCTGGAGAATCATAGATGTGGCAGAAATACATATTCTTGAAGAAAAAAAT/AJGT CTCCCTTATGGGTACTGTGATTTCAATAGGGTGTGGGATAGTACATGACAAATGATGGATGGATAGA CACTCTGTTCTACAGATCCGTGCTTTGGGAATTACAGGAACATAAAGGATATAATGGATGGGTT ATTACTTTTACATGTGGACAATCTAGTTGAGGCGTTTAAAGTTAAATTTGG
WI-21660	120 C T ---	---	TCCCAACTAGCCTCTCAGTATTTAGATGAGGATAGAACAGATACGGTGTAAACACGCCCTCTCCACTGCT TACTGTGTACCAAGAGGCAGAAAGCAGCTACCCAAAGCCTAACCTGGCC/CJTJGTCTTTTCAG GCTTCTCAGGATGCCACACAGCACATACTAGGGAACTGGGATGCAGGGGAGAACCCAGGGTCTGTCTTC AGGAGGGTCACAGC
WI-19105c	211 C T ---	---	TGGAAGTAGCCCTTCTGGACAGAAAGAATATTTGTGGTCCATGTGGTTGAGTCTGTTAAGAAGGA CACTAAGGCACATGGCTGGTGATCTTTGCGTCATAGACACGGGTGAGCTCATGTGGAACTCCTCTT GTCTGATGTTTCCAGGGCTGGCCACAGAGGTGAGGGCAGAAATNTGGGGTCCCAGTGATCTOCCC ACAACTTC/CJTJCCAGGGGAGGATTTCCACCCAGGGGCCAGGGTGCCCG
WI-19105a	33 T C ---	---	TGGAAGTAGCCCTTCTGGACAGAAAGAATATTT/CJGTGGTCCATGTGGTTGAGTCTGTTAAGAA GGACACTAAGGCACATGGCTGGTGATCTTTGCGTCATAGACACGGGTGAGCTCATGTGGAACTCCTC CTTGCTGTAGGTTTCCAGGGCTGGGCACAGAGGTGAGGGCAGAAATNTGGGGTCCCAGTGATCTC CCACAACTTCTCTCAGGGGAGGATTTCCACCCAGGGGCCAGGGTGCCCG
WI-21760c	81 C A ---	---	CAAACTTAGTCACTCTACTGATGCAAAATGATTGGAGGTGTTCTCTAGCTTTACAATAAGNGGAGG GACCTCTGACTGCA/C/AJCCCTCTGTCTCAGTTTCAGGGCA
WI-21760a	35 A G ---	---	CAAACTTAGTCACTCTACTGATGCAAAATGATTGGAGGTGTTCTCTAGCTTTACAATAAGNGG AGGGACCTCTGACTGCACCCCTCTGTCTCAGTTTCAGGGCA
WI-21569b	198 T C ---	---	TCTGCCATATTGTTCCAGCACCACTATTACTGTTATTATTCTCTTTGAGGAAACCAGGNATTAAG AAATCTGGTTTGAATTTCCATGATGCCCTAACTCTATGGTTAAAAATCCTTTTCCTTACCAAAAAAGGA ACTTCTTAATCACCAGAGAAACAGAGGGAAGACTGAGATATGTTGCAGAAATTTATCTCTAC/T/CJ AGAGACAATTCATAGTTTCATAATCTTTCAGGGTTGTGCTTTACTTGGGGGGC
WI-20934a	72 T G ---	---	CCAACATGCAACATAGTCTTCATTTCTTAAAGTACATAGTAAAGGTATGAAAAACATTTGTATTCA GAGAA/TJGTCTAAGACAAATGGTCAAAATATTCAATGGCTGGCACTAGTGGTAATTCAGCAGAC AAACAGCATGAGAAAGGCCGGGAGACAGTAATAATACGTGCCCATTTGCAATGAGTTACCCCAATC AAGCCCTTTTACCTCCTTAAGATGGCAGATTAGAAGACCCCTNTTCCCGAGGAGA
WI-21561	55 T G ---	---	TTTCCATTTTATCAGCCGGGCCATCAGAAACAATAGCATCTATACCTTCGAAACQ/TJGJCTCTTAAC CTCTCCAGGCAAGGAAAAAGTGATCATATTGAATTCCTCAGAATGGTGGGATCTCAAGACTT TTTAGAAAGTGCTTATTAAGTATAAGAGGCTTGAATATAATGATGATAAATGGTAGCCCTTTCTGGA AATAATTTTGTGTAATCTGTTTAAAAAGATTTTGGATGCATTGTCCCCA

WI-21961c	200 T G ---	---	AGCTTGGCTGAAATTTGGTACTACTACCTTTGCAATTCCTTTATTTATTATTACTTTTATTTTCCGTAAGTTATGGGTACAGGAGTATTTGGTTATATAAGTCTTTAGTGGGATTTGTGATTTGGTGACCCATTACCAAGGAGTATACACTGCACCATACTCGGTCTTTATCCCTCGCCCTG/GJC
WI-21961b	73 G A ---	---	TCCCACTTTCCCTCAAGTCCCAAAAGTCCATTGTATCATCTTATGCG AGCTTGGCTGAAATTTGGTACTACTACCTTTGCAATTCCTTTATTTATTATTACTTTTATTTTCCG/AJTAAGTTATTTGGGTACAGGAGTATTTGGTTATATAAGTCTTTAGTGGGATTTGTGTGATTTGGTGACCCATTACCAAGGAGTATACACTGCACCATACTCGGTCTTTATCCCTCGCCCTC
WI-21956	26 T G ---	---	TCCCACTTTCCCTCAAGTCCCAAAAGTCCATTGTATCATCTTATGCG CCCACTTGGGTCTCTTCAAGTGAATTT/GJTTCCCTTCGTCTCTTAAAGCCCTTTTAAATGAACCTCCATTCCTGTAACCTTGCTAGTCTGTTTCTGCTTCATGCCCTCAGTCGAATTCCTTTCTGAGGGCAAGGACTGAAGTCTGTGGACTGTAGGGTTCGACCGGTAACCTCAGGGTAACCTCCTATCTCTCCACCGGTAAACAGAGGGGTACATTATGGGGTCCAGGTT
WI-21966	148 G A ---	---	CAAAACATACATTATGGCTGCCTTTATTTAAGAAATGTTTACTGAGATCTGTACTGTAAACAACATATTTTGTAGAACGATGAGTGAGAGTGTGTGTGTGTGCGCGCGGCGACGGCATGGCACTGAGGGATTGCAATGGG/GAJAACAGAGTAAAAAGGTATAAAACTTGGTCCGAAATCTTTGCTTTATTAACCTTGGCCCTGCTCCTCACAATGTTTCTACACTTAATTCATAAGAGAGGTAGA
WI-21930c	146 G C ---	---	TATACTGGTTTTGGTTACATGGATGAATGTCATAATGGTGAAGTCTGAGATTTAGTGTACCCATCACTGAGTAGTGACATTGTACCCAACTTGTAGGCTTTTATCCCTTACCTTACCTTCCACCCCTCCCATTTTGAGTCTG/CJATAGTCCATTATATCACTCTGTATGCCCTTTGCATACCCATAGCTTAACCTCC
WI-21139a	165 T C ---	---	GCTCTAGTGAAGAAATTCAGGACGCGGTCTTCAGAGCAGAGGGCTTGTTCAAGTCCCTGTTCTGCCACTTACTAAGTGCATGACCTTGAGCAAGCCACTTAATTTCTGTCTCTCTCTGTGAAATGGGTACAA
WI-20317b	217 G T ---	---	TGTGGGTACAGCAGTAAAGGAACATAACA/TTCGTACAGCACTTCAGGACAAAGCCTGGGCACACAGCACTGCATGGAATACACAGGTAAACATTTTAAACAGTGGGACAAAATTTAAGTACGTGGCCAGCTGTGGTGTCTGTGGTCATTAAAGACAATGTTAAGANTCAGGAGTACTTAAGTGTAGTGGTTACA
WI-22082e	179 G A ---	---	AATTTGTCTCTTCAGTTTTTCATTAAGTAAATCTAATAGATGATATACATATTACTGCAGATAAAACCATCATCAGAAA/GJTTAATAATTAATTCATATTTTGAGGCTACTCT CAGGACTTGGTTTGGTGTCCCAACTGCACATAAATGTCCCTTTTGTGTTGAGTTATGGTTGTGTGCGTTTTCTCTTTTGCATAAGAAATATGTCCATTTAGTCCAGAGGCTCTTGTCTTATCCGGATGACGGAGGTACACGGGGGCTCCGCTCAGTTCGCCGCGAAGGACGTATTG/AJCTGAACCTGGGACGAGTCTACTCTCCCCCACAGGAGCCACGATTTCAAATCCTCTTTGTCTGCAACCTCT

WI-22082b	67 C T ---	---	---	CAGGACTTGGTTGCTGCCAACTGCACATAAATGTCCCTTTTGGTTGAGTTATGGTTGTGTC /TGTTCCTTTTGCATAAGAAATATGTCCATTAGTCCAGAGGCTCTGCTTTATCCGGATGACGG AGGTACACGGGGCGCTCGCTCAGTTCCGCGCGAAGGACGTATCGCTGAAGTGGGACGAGTCTACTC CTCCCCACAGGAGCCACGATTTCAAATCCTCTTTGCTGCAACCTCT
WI-20993	139 A G ---	---	---	AACACAACTCCATGCTTTCAAGATTCCACACCCAGATACTAAGACATATTAAATTTACAGCAAT TAAACAGTGTAGTTTGGTACAATAACACATATAGCAATGATACAAATAGGGGAAAAAACCTGG GCTTCT/GJTAACAAAGTGAATACATTAAAGACAGTATTGAGAAATGGCTTCAGGATTAAATTTGA TTAATTTAGAGAGAGCCTATTTCAGGCTCTCTAGCTCATCCACACATCACC
WI-21723b	125 A G ---	---	---	AAGCGATTTTATTAAATTGATTGGACATACTGTAGGTCAAATAATATTTCTGAAGATAACAATTA TGGACTTTAAAGCTC/GAJACATAAAATTAGTAGCTTCAAAGGGTTAGTCATATTCCCCAACACA GCATGATAAAATAATTCAACTATGTAGAAATATAGAACTCTAGGACTAGCTGGAAACTCGGAAATC ATT
WI-21723a	82 G A ---	---	---	AAGCGATTTTATTAAATTGATTGGACATACTGTAGGTCAAATAATATTTCTGAAGATAACAATTA TGGACTTTAAAGCTC/GAJACATAAAATTAGTAGCTTCAAAGGGTTAGTCATATTCCCCAACACA GCATGATAAAATAATTCAACTATGTAGAAATATAGAACTCTAGGACTAGCTGGAAACTCGGAAATC ATT
WI-22132	99 T G ---	---	---	CAACAGATGCTTGAGCCAAAAGCAACATAGGCAGAAATACAATTGAGAAATATCTTCATGTTTC AACCCTTTAATCTGACTTGCCCTTTTACTATCCTT/GJCCCCATTTCTCTAATCTCTTTGGCTTACAA TATATTACCCTCTAGGTATCACCTCATCCTATAGGAATGCCCTCTAGTTTAAATGTCCTGCCCCAAACA ATACTAACCCATTGAAGGATAACTATGGAAACCTTTAAATGGGACAGTGGG
WI-21006a	106 A G ---	---	---	TGACAGATCACACCACATTTGTTTGTAACTTTTCTCCTTCAAGAGTCACCTTAGCTTAAGCCAGAA GATTCTTTAAAGAACACATACACACATGTGCACACAC/GJAGAGGGCAAGTACAAAAATGTAACC CCACCAAGTGCATGTGAATGAAGTGCAAAAAAGGCTTCATTTGCAAACTCTGAGGATCATTTCTCT CTGCTTCAGGAAATAACAGAAAGGTCCTAACTGCCCTAGGCCT
WI-21761b	138 C G ---	---	---	CTGAGGCCCTGCTCTAACTTCAATNTGACGGAGCGAGTTCTCGCTTGGAAATAACTGAAAAGATTCT TTTCTCTTTGTGTACAAAGGATTCAAATATTTTACATCTCTCTGCGAGTTAAACGTGCCGTGG CTC/GJCAATACACACCAAGCAAGCGTAACCTTGGCTGCCTCAGGAAGGCTGGGAGGAAGTGCCAG ATGGTA
WI-21079c	166 G A ---	---	---	AATGAAAATGCCACCCAGAGTTAACAGCTTGCCATGCATGCAACTGTGTGCGCAAAATCAAGTTGT TTTAATACAGTGTGCAGCTTTGATTCTCCATGAAATTAAGCTGTGTGCTCACTTGTTTACATAA CTCAGGCCACCCCTGAAATATCTGCTAGTGGG/GJAAATTTACACCCACTGACCATCTCAGCTCAAA GCCAGATGACTATCACTACACATCTGCCAGGGTAATAGGCATGGGCAAT

WI-21079a	50 G A ---	---	AATGAAAATGCCACCCAGAGGTTAACAGCTTGCCATGCATGCAACTGTGTG/AJCGCAAAATCAAGT TGTTTTAATACCAAGTGCAGCTTTGATTCTCTCCATGAATTAAGCTGTGTGTCTCACTTGTTTACA TAACCTAGGCCACCCCTGAAATATCTGCTAGTGGGAATTTACAACCCACTGACCATCTCAGCTCAAA GCCAGATGACTATCACCTACACATCTGCCAGGGTAATAGGCATGGGCAAT
WI-22129a	45 T G ---	---	TCTGTAGATTTAGCCATGCCATATATTTAACTTTAAGGAAAAGT/GJTTATATAACAGTCATTGCT TGGTAGAATCCAGTCTGTAATAAGTTAGCTTAACAGTTAACAATTGAAGTCTTATACCTTATATTTA AATGTTTAGCAATCTCTACTACATTTCAAATATAAATAATTTGGTTGCAAAATCCAGNAAAGGGCA TTAACCAACATGGGACTGATCTGGGGGCTTCCAACTGACTAAGGTTTTA
WI-21941	79 A G ---	---	TGGAGTTAAGTGGGGCTCTGCTATTTCCCCCAAGAGGACTCGGAAGATGTTGATTCAGGGCAGAGT GAGGGCAGAC/A/GGGATGAGGCTCTTCTGTAAAGTCCAACAGACGCTCACAGATGCTGGGAGGCT GGGACTGCCAGTTGGGAGCTCACCCAGAGAGGCTCACTGCATTGACCCACACCCACCACTCACCC CAGCACACAGGCACACGAGGGCACACGCACACACGNTGCACTCACCAACGC
WI-18916b	42 C T ---	---	AATGGCATCCCTGTGATACCAACATCTTCAGCAGCTCAGC/C/TJGGCTTCCCACCTCTTGGTACCC GGTTAACTGCCAGNGGGTGACAGTGATGCCAGGGCTGCCCACTACTGCACTGGACACAGCCTCACCC AATGCCACCTTCATA
WI-18916a	35 G C ---	---	AATGGCATCCCTGTGATACCAACATCTTCAGC/A/G/CJTCAGCCGGCTTCCCACCTCTTGGTACCC GGTTAACTGCCAGNGGGTGACAGTGATGCCAGGGCTGCCCACTACTGCACTGGACACAGCCTCACCC AATGCCACCTTCATA
WI-19828c	200 A G ---	---	TTCCCTTCTCCCCAAGAGTGGGCAGAAAAGCTTTGTTAACCTCCTTTTACAGATGAAGAAAAACAA GATCAGAGGTGCTAAGTGTGTAGCCTAGTGCAGGNCCTTGGCCCCCAATTCCTGGGTCTCCCCAAG CCCATGCTTCTCCACTTCTCACAATCTTTACTTCTCTGACCCCTCACCCACCAACCAAAAT/A/G JCITTTAATCTGGAAAAGAACCCAGCTGCACACTGGGCACACTTGACCT
WI-21863b	47 C T ---	---	CACAAGAGTCTGTACAACCTTAGGGACACAGCCCTGGCCCTGCCCT/C/TJAGCTGCATGCCACCCCTC ATATCCACCCCATCCAGCCTCTGCCCCGACACCCCCAGGCTCCCTGCTCTGGTTGAAGTATTTT CTCCAAGGCAGGAATGAGTCTTGATCCAAACACAGCATCT
WI-19860	51 C G ---	---	TTGACCTAAAGCCTAGCATAAAATAGCTAAGTAGAATGTTTCCAAAGATG/C/GJCTGCATCAGTAT CTCCCATCCACATAATTTCTGTTTGAATTTGGCAATTCACCCATAAAATGGTGGGATCTACCTCCCT CCTTGCAAATTTGAGCTGGNCCTCTGATCCTGTCTAAGGATCTGAAGCC
WI-19889b	80 C T ---	---	ACCCAGCTCCTCTTACCCCTGTGGCTTTCAGTAGGCTTTGGTAATGGCCANTGAACACTGCAGGGCAAG AGGAGTAGGGG/C/TJACAGCATTTATTTCCCTCTTCACTCCCTGTTAGCTTTGGTAGTGGCTGTAT TTCTCTACTGATAGTCTCTTGCCACAGTCGTAACCTATTCG

WI-19891c	172	C G	---				TGTTGGTCTGAGATTACAGCTTACTACAAGGAAGCTGAGAAATGCTTGGTGCCCCCTCCCCCGG ACTCCTCTGTCTGGGAAACGTGGCTTGNCTCCAGACACGTGTAGATGCGAGCTCTCTCAGCGG AGTCCCGATCCCTCAATTTGCCATCTGTCTGACTC/GCGTCTCCCGGGCGTGGGGCGTGTGT CAGGAGCGGGGGGAGGAAGGAAGGAGATCCAGGGTCTGTCTG
WI-20155a	81	C T	---				GCACCTGTAGGGGTAGCTTCCATGTTCTCCAAAGCACGGGTGTACATTACCTTAGGCTGAACAT TCCCTTGGGGGGG/C/TGCAAAACTGCTTTGAGGAAATNCCCCAGGAGGAATAAACTAGAACGCG ACCTGCTATTTCAACCATACTATGGAGATACAGCTAATGAAGTGGTGGCAGAAGCTTGGCCGTGTGA GTGCCCCAGGGTAAAGTCTCTCTGTCCAGTCCAGAGCAGAGACTTCTC
WI-20270b	91	T G	---				AGCCATACAATGCATTGCAAAAGAACAAAGCAGCTGTACAGGAGTGGGACGCGTCAGTGTACAAT ACATTCATGTCAGGATAAGGAGCA/T/GJACACCAGGATTTATACACGGTGGCAGCGGCTATAGGCA CGATGATACAAAATATAAAGTATATTTCCATCTATATAAATACACAGCTGGGTGGGAAAGGATGCT GGGTGATCTGTTTCCCGCAGAGGGCTGGGAGGCGAGGNGGGTGGTGGAA
WI-20270a	53	G A	---				AGCCATACAATGCATTGCAAAAGAACAAAGCAGCTGTACAGGAGTGGGACGCG/G/ATCAGTGTAC AATACATTATGTCAGGATAAGGAGCATACACAGGATTTATACACGGTGGCAGCGGCTATAGGCA CGATGATACAAAATATAAAGTATATTTCCATCTATATAAATACACAGCTGGGTGGGAAAGGATGCT GGGTGATCTGTTTCCCGCAGAGGGCTGGGAGGCGAGGNGGGTGGTGGAA
WI-20622	130	T C	---				CCACITTCATATTTTACAAAATGCTCAGCGCAGCAATATGAAAAGCTTCAACACTTTCCTTTGTA ACTTGCTGCAATAAATGCAACTTTAACAAACATACAAATTTCTCTGTATCTTAAAGTTGAAT/C/ TACTAATTTTATGATGTTACTCATATTTTATTCATATACATTTTAAATGACATCATTTGCCAATACATA CATTATTTCTNTAACTTTATTTTACAATAAGCCAAACATCTGTCTCATGCAG
WI-20768b	190	C T	---				TTCCACTCAAAACTCCACCCCAACCTTCTGGAAGGCGAGGCTAACAGGACCTCCTGCCTGCCTGC TCACGACTGATTACTTTCAATCCAGCTGCAATGCAAACTGAAACTCATTTCTGTATATCACCACCTA CAGGAGAGGTCTATTTCTGGGCAACCCAGAGNITCAGCACACATCTGCTGGGA/C/T/CAGGGACTC GTAATTCGCTTGGTCCAACTCTTCTATGGGGTTTAGCTGCCCTCATTC
WI-20768a	71	C T	---				TTCCACTCAAAACTCCACCCCAACCTTCTGGAAGGCGAGGCTAACAGGACCTCCTGCCTGCCTGC TCA/C/TGACTGATTACTTTCAATCCAGCTGCAATGCAAACTGAAACTCATTTCTGTATATCACCACCT CTACAGGAGAGGTCTATTTCTGGGCAACCCAGAGNITCAGCACACATCTGCTGGGACACAGGACTC GTAATTCGCTTGGTCCAACTCTTCTATGGGGTTTAGCTGCCCTCATTC
WI-21909	153	A T	---				TGTTTGTCTTGTGCCAGGTACTCTACTGCTTTACATAAAATATCTCATCTGTACATCTAACGGCAA CTAAGTATACGCTTACATCTGCTAGTGGCACCTAAAATAAGGATATTGTTGGTCACTCTTTAAAGAAA TGCTCTAACATACCAAAG/AT/JAGTGGAAATCAATAGAAATAAAATATTAAAGTCTTACAAAGCGTAC GACACTAAAGTAATATAGGATACCACATAAATTTATATTTCTATGTATGGAAAG

WI-22202	128 A G ---	---	---	TGTTGCTTTGGTTGTTTCTTCTGGAACATATTGGAACACTTGTTTTCATAAGCTGTCTGACAGT GGCACAATCCCATCCATCTTCAGGCCCTTTAATAAGGTCATTATGAATCTGAATTTCT[AG]TTAAT ACTCTGGTGCAATTCATCTGCAAAAGCAACTGGCACAACCACTCTTCCGGTGCAGCTCTCGG AGAACATCTAATATTGAGTCTAGTCTGTGCGGAACCTTCTCCAGCTCAC
WI-22189	70 C T ---	---	---	CCAAAGGATGAAATTTCCACATTTATTTTNCCTTTATGTGAATAGAAAATGGCAGTGAAGTGTCTATG AA[CT]GAGGCGAGGAATGGCATGGCGCTGCGGTACCAAGCCTGGACGTTGTGCTTCCAAAAGTACAC TATGTGGTGGAGACAAAGGGT
WI-22283	109 T C ---	---	---	GGGAGGCATCATAGAAAAAAACCCCTCAGCCAGAAAGTTAGGACATTTGTGATTCTCAGCCACTAACGA GCTGTATGACCTTGGTCACTAGGCCCTCGCAGGCTCTGGTTG[CT]TCATTTGCAAAATAAAACCCA GACCGGTGTCATCTTTCAGTTCCTCCAGCTCTATTATTTATGATTTGCTCTTAGTCTTTATGAGCCA TGTATGATTTATCAGTCTCCTGATGCACCTCAACTCCAATGATGCAAAAG
WI-22290a	136 C T ---	---	---	GACGTGTCATCTGAGGGCTCTGCCAGGTGGATTAGGTGAAGAGAGGTTTATGGGCTCTAAGCACCG GCCAGTAGTGGGAATGCCACATGCAATGGTGAAGTGGGATCTGGGGGGTCAAGGAGCTGACGCTTGTCTTT [C]/TTCCAATCTCTCCTTCTTAGCCAGAACTTTGCGAGAGCCCTTTNATTTCTCTTCCCTCTATTCC CCTCCTTCCCAAAATGCTAAGGTCCCAATTCAGACCCCTCCAG
WI-22292	53 A G ---	---	---	CCAGTGGAAAGGGTTACAGCCATAGTGAGGTTCCCCCATTTGCTCAGTACCAGA[AG]GTTTGAGTAC GGTCGTTTAAAAAATACTTATCTGACCACAGTGGAAA
WI-22387	186 C T ---	---	---	ACCTTGACACCTGCCATCCGGTGCCATCTCTCGGTGGCACAATCTATCCCACCTCTGGCTCTGAAAG GCTTGTCAACCAAAATGGCAGCTGGGGTAAGGCATATTTAAACAAAGGCTCCAAAGGACCCCTT TCACCTGGGTCTAGCATCCAGCTCTCTCAGCAAAAGGAGGATTGTGGT[CT]CCTTGTGTTTCTG AACAGGGCCAGGGCAGCAAGGCATGCCATCAGTGCAGCACTCAACCT
WI-22395b	127 A G ---	---	---	GCCGTTCCAGTATTGATAATAATTTGTGTTTAAATTTCTATACAGAAATGGTTCTTCTTGAATATTTT GTAGGATGGATGAATTGAAAGTGAATTAAGTCAAGATAAAGGGGCAACTCTTTAAT[AG]AAG GAAATGTTACCAATCCATAGTGAAGAGTAGAATATGTTCTTTAGAGTAGNTAGAAAGTCCCCAGG CTCCT
WI-22405	90 A C ---	---	---	TTTATGGCTCTGAGTGCCCTCACCCAGCTACACTTTACCTTGTATCTATAAAGTGAATTTAGAGT AAATACATTGGCTGTAAAGTCG[AG]GATCAGGTGCTCTCCACCAAAAGCAAAACAAACTGCTGA AATGTGCAAGGTTCTCAGTG
WI-22419b	67 T C ---	---	---	CCCTCTGGACAGTTTGTCTTATGTGTTTCAGACAATCAAGNTGCGCTTCCAGGCACAGCCAGTGCT [C]CTGGATGGCATCAGCAGGCTCCCTGCCCCGGCTTGAAGCATGGCTGTGTGCAAGAT
WI-21342d	59 T C ---	---	---	ATTTTCCCTTCTGTGTTTGTGTTATTTCCCTTTTGTGAGTAAATNAGCAATACACTGA[CT]TGGAA ATCTGCATGATTAATAACATTAAACAGTTTCAACACACCCCCATATCAGAGTATAAAGCAAGAG GTTGAAAAATATCCCCCTAACCGAATGCAAAATTAGGTATCCCTCAAAATGGCACATTTCTCCTCTAGTT T



WI-21763b	154 A G ---				CATACCCCTTTAGGTGCCACACATTGATCTTAGTTAACAGTCTTGTAGTCCCTCTTAGGCTTCAAGA TAATTGTGATTTTCATCGCACCCAGATACTTCCAAGTGGAGCCAGGCTCAGACTGTTCTCAGTCACT GCTCTCCACAGCTGATTAGJGICAGACATTGCCTGTGCTTCTTACCCAGCAGCTGCTAGTGCACCTT GA
WI-21763a	135 T C ---				CATACCCCTTTAGGTGCCACACATTGATCTTAGTTAACAGTCTTGTAGTCCCTCTTAGGCTTCAAGA TAATTGTGATTTTCATCGCACCCAGATACTTCCAAGTGGAGCCAGGCTCAGACTGTTCTCAGTCACT T/CJGCTCTCCACACAGCTGATTACAGACATTGCCCTGTGCTTCTTACCCAGCAGCTGCTAGTGCACCTT GA
WI-22440	64 A C ---				CAGTCCATTTGAGTCCCAGTCGAGGGTGCAATCTTCCCTTATCTTGTGTTAAGCCACTTGGGTAA/C/] TCCATTCCAGCTCTGCACCTTCTCCAGTTTCTCATGTCAAGTCCCTGGAGGGAGGCTTCTGCG AAAT
WI-22449	74 T C ---				CAATGAATGTTGTGGCATATGATTNCCATTGTGTGACAAATTTATTAGCTGGCATCCGAATACAGTAC TTCCTTTT/CJGAAAAAATACACAATGGGAACGTGACA
WI-21965a	112 A G ---				CAGGTCCACGAGAGGCTTTTATTCAGCCACTCAGAACCTGGCTTCTGCTCCAGGCACTGAACA CAGTCAGGCTCTTAAACACTGGCAGGACCTCCCCACAGCAGJGJCCCCACAGGGTCTCTGTT TCCCAGTCTGATGGATTACAGCAAGACCTTACACATTCACCCACTACTCTGCTGGAGAGGGGTC ATAGGCAGCCTGTGGTGCCAGCTCAGTGTGACACACTGCCAATGTCG
WI-21687c	115 C G ---				CACCTGGCAGTTGAGTCAGATTGTAGGAAAATTAACCCAGATGGGTCTACATTTTNTTCAAGTTCA AACCACATGGTTTCTTAGTCAGAAAGTCTCATGGACTTCTTCTTAAGJGJGTTCTATGATCAGAC CACCTCCTAAATGTGGCTTTTACCCATTACAGGCTACAGTTGAATCAGGCAGGAGCAGCTGCTGGAG AG
WI-22374a	149 T C ---				AGCTTTTACAACAAAGCGAGGGTTTAAGGAGCCTGAGAAGAAATTCACAACCTATTGACTATACAGAG TCTTCAATTCCAAACACAGTTAATAGTAACCTGGTGGCACATACACATGCATTGAATACTCTGTAT TATTCAGTAACTAAAT/CJAGGNTCCTGCATCATCTCTTACACA
WI-22250b	132 C T ---				ACTTGCTTTCAGGCAGGCAATTTCTGGGATCTAACTAGAAATCCTTGAAACAAATAGTACCAGCCA CTTTGAGGAATGTGCATTCAGTGTAGTGGGTATTATGGGTCTCTGCCTCCTGGCTGTGTATG[C/T] GGANCCAGGAGTGGAGGAGGCCGTGGAAATAGACAGGGGAG
WI-22250a	89 G A ---				ACTTGCTTTCAGGCAGGCAATTTCTGGGATCTAACTAGAAATCCTTGAAACAAATAGTACCAGCCA CTTTGAGGAATGTGCATTCAGTGTAGTGGGTATTATGGGTCTCTGCCTCCTGGCTGTGTATGCG GGANCCAGGAGTGGAGGAGGCCGTGGAAATAGACAGGGGAG
UTR-04932-2b	192 G C ---				GCAGCCATCTCCTCTCCAACACTCCAGGCCACCCCTGGGGCCAGAGCAOCTCATGCCAGCAGCAC CTACGTGGCCCGAGTACGGACCCGCTGGCCACAGGTTCTCGGCTCTCAGGACGTCOCAGCAAGTGA GCCAGAGGTTTCTGGGACTCCAGCCAGGGGATGAGGCCAGCCCCAGAACCTG[C/C]AGTGGCTTC TTTGACGGGGCCCGCTGCTCAGTCTGCTGCTGGAGGTGAGGAAGGAGGT

UTR-04932-2a	149	C T	---			GCAGCCATCCTCTCCAACACCTCCAGGCCACCCCTGGGGCCAGAGCACTCATGCCAGCAGCAC CTACGTGGCCCGAGTAGGACCCCGCTGGCCCGAGTTCTGGCTCTAGGACGTCCAGACGTCCAGCAAGTGA GCCAGAGGTTTGCTGGGACTCCAGCCAGGGATGAGGCCAGGCCAGAACCTGGAGTGCTTC TTGACGGGGCCCGCTGCTAGCTCTCTCTGGAGGTAGGAAGGAGGT
stFIBBb	412	G C	---			GTGAGGAAGATGGACCTGGACAGACAGTCCACACCTTGGCTGAGCAGCTGTGATTGTGCCA CGGAGCATGAGCCCTTTCCACCGCCCTTGCCACTGTCTCTGCTGCTCTCTGATCATGCCAGG TTTGACACAGCCTCGAGTCTCCATGTTGTAGTACATTTCTCAAGATGCAGCCAGGAGCCTCTCTGA AGGACCAGTCTGGTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGTT
stFIBBa	341	T C	---			GTGAGGAAGATGGACCTGGACAGACAGTCCACACCTTGGCTGAGCAGCTGTGATTGTGCCA CGGAGCATGAGCCCTTTCCACCGCCCTTGCCACTGTCTCTGCTGCTCTCTGATCATGCCAGG TTTGACACAGCCTCGAGTCTCCATGTTGTAGTACATTTCTCAAGATGCAGCCAGGAGCCTCTCTGA AGGACCAGTCTGGTACGATGGTCTGAGCTTCTTAGAACCTTCCATGGTT
stGLV2	61	T C	---			GTCACAAGAGGACGCTCTCGGGAGCTCTCCACCATGGCTGGGCTCTGCTCTCTCACTT/CCTC CTCACTCAGGACACAGGTGACGCCCTCCAGGGAAGGGTCTTGGGACCTCTGGGCTGATCCTTTGGTC TCCTGCTCTCAGGCTCACGGGGCCAGCACTGACTCACTGGCATGT
stSG1001 7c	70	T C	---			GTTCAGGCTCATTTGAACCTCTGGTGTCAAGCGATCTCCACCTCGACCTCCAGGGTGTGGGAT TAT/CJAGGCATGAGCCCCACACCTGGACACAAAATACATTATATCTCTAAAGTATAGGATTACT TTAAGAGAAGAACTAAAGTATGATGGCTTACTTTCTAATCC
stSG1001 7a	33	G A	---			GTTCAAGGCTCATTTGAACCTCTGGTGTCAAGC/GJATCTCCACCTCCAGCTCCAGGGTGTGG GATTATAGGCATGAGCCCCACACCTGGACACAAAATACATTATATCTCTAAAGTATAGGATTACT TTAAGAGAAGAACTAAAGTATGATGGCTTACTTTCTAATCC
stSG1002 3	63	A T	---			TAATGATAATTAGGGCATTTCTCCACACGAAAGATGACACAATTGACCCAATATCATTTGAGGC/A/T AACAGTTTGGGCTGTTTTCCAGTAGTATGACAGTGA
stSG1009 6	36	G C	---			GTGGAGAAAGATCGTCTTCTCTCCCTCCCATGACC/GCJGGCTTCCCGGGGCACCTGTGGCTTTCC ACCCGAGACGGCTTTGTAGGGACCCACTGCCACTCCGCTGCTGTGGCTGGGTTCCGGCTCTCTAG GGCTCGAGTGTTAAG
stSG1011 8	107	C A	---			TAGGCTTAAACCTGGAATCTACAAGCCAAAAGTCCCTCCCTGCTGAGGGCAGTACCCCTCCATTGGGC ACAGTCCAGACCCAAAGTCAAGATGCCCATTTCTTGGC/AJCTCAGCCCTCAGTTCTCTTCAATTTCC ACCAGGCCGTGCTGTTGTAGTTTCTCTCCAGTGAAG
stSG1012 0	89	T C	---			TAGTAGGTAAGAAAAGCAAGGAGGATTGCTTATCGGATGACTGTTTACAGTGGTGTGACACTATGC CGTGTTCACGAACACITTAATAT/CJGTTGTTGTAATCTGATTTTATCTCTGCTCTTACAAATG
stSG1017 8	42	C T	---			TTGAAGCAATATTGCTAGCACTCTGCTGGACATTAGTCCG/CJGGGAGGAGAAAGTGAACAGGAA TCGATCTTTGCTTTTAACTGCCCTTAGTTAGGAGATGTTAAATACTTGGC

stSG1019 3	136 GA ---	---	---	GGAAACAATACTACCTAAGGACAAAATACTATTATTAACAAAAAAGCTCTTAGTGATATTTGTGTAACACATTTCTGGAGCTGGTAGGAATAACCATTTTATTTTCTGTAGTGCCATATACAAACCTTTTAC
stSG1020 2c	143 GT ---	---	---	TG/A]TTTGAAAACCTGAGATTAAAGTTGCAAACT AAGCTAAGTGGTGAATGGTGCCACTCAAAGGCTCTCCGAGGGAAGCTCAGTCTGGCTTGGGAGAGTCAGCCTTGGTCACCTCATACGGGGCTCCAAAGCTAAGGGGTCAAGGAAGCAGTCCCACTGCTTCTCGCTGTCA/GT]CAAGACCAACAAGGCAGATGCCACTGCTGCTCTTTCCTTGTCTACTTTCT
stSG1020 9b	75 AG ---	---	---	TCCTTTCTCTTTTCACTCTCAGTCACCATGATTCATAATAAACTAATTCCTTAAGATCCACATTTATTTTTA/G]CTCCAATAAATGTAATTATCAGCTGCTGAATT
stSG1020 9a	34 CT ---	---	---	TCCTTTCTCTTTTCACTCTCAGTCACCATGATTC/TAATAAACTAATTCCTCTTAAGATCCCACTTTATTTTAACTCCAATAAATGTAATTATCAGCTGCTGAATT
stSG1021 8	29 TC ---	---	---	TACTAGACATGCAAAATGAGAAGATTACA/T]C]GTGAATATTTAAAGAAGTTATATTGTTTGACATAAATGCAATGTACCCGGGCATAATAAAGTTAAAGCCAGTTATTTCTGA
stSG1025 2	108 AC ---	---	---	ATAGGTTTCAGGAACAAAATCATTAATGGAATAATGAGAAGAAATCTTTATTTTGGACCAATTTTAGGCACTTAAGAGTTTCTTTTCTCTCTTCCCTTGATCA/A]C]AGTGAAGATATGATAGGGAATTCAGAAATTTCTCTCTTG
EST10915 0	123 AC ---	---	---	CTGTATTAAATTAAGAAGGCACATAATTAAGGGACGGGAAAATCTACCTGTACACAAAATCTGTACTTTAAACAGCATCTTCAATAAACCTTTAAAGGATAATGGTTACGATCATTTTAAAG/A]C]ATTTTAAAGAACTGAGTTATTTGGAC
EST11023 1	166 TA ---	---	---	TTTTTTGTTAAACCAACCCTGAAAGTTTCCACATGTGAATATAGATACACAGTGAACAAAAATATGTGGCCTCCCATGTACATTTGGTTACCTATGTACAAGTATCTATACACCAGTAAACAGCAGGGCAATTAGTCAATTAACAAAAATAGTACATGTTA/T]A]GTGTAATAAAATTAATTTACAAAGGCTTTTCCACTCGTGGATTGATTCCTTTTGGAGGGAGGAGTAATCTCTGG
EST14096 8	71 GC ---	---	---	GGGATGTATATTACAGATAACACAACTCACAATATACCATCAGACATTGAAAACTAAGGCCATTCTGTGA/G]C]T]TATTTTAAACCTGGTGTTCACATATGATCTTAAAAAAAATGAATTACCAAAACCAAGATTCTCTCTTAAATGAAAAATTAATGCAGGTACAGGATAACTTTAGGGCTATATCTAATCTGAAG
EST22113 6c	125 CA ---	---	---	TGCAATTTGTAGAAGGCAGCAGGGGCCAACCCCTGGACCTCATCTCTGTAGATGTGAGGTGTCAGGGATGCTTAAGTCTTCTCTGGCAGAGACCCGAGGTGCAGAGATGATTTCTTCTCA/C]A]CCCTTCTCAGGGTCTGGAG
EST22555 7	60 GA ---	---	---	TCAAGCATGTGTAAAGGCACCTGCCCCGCCAGACCCCTTCTAATCTTGCACACTGGAAGGTG/A]AAACCTGGGAGAGAGACACTCCCTCCCTAGCTTCTACCTGGGCAACCCTCCAAAGATGAGCATTCATCTTGGAGACCAAAATAAAAAAGGACAAAAGACCAGGGCTCAGAG

EST22917 6	74 C T ---	---	---	GTAAACCTTGCAAACGCCATGCTAAATGAAGCCTGACTGACCAGGGGCTCTGGGCTCTCAATGCA ATAGAAAC/TTGACATGGGGCCAAAGACTTCCAGACAAAGCAGCGAAGGTAGAGGATATAG GTTAGCATCATCTGGTTGTGA
EST36458 6	65 A G ---	---	---	CAAGTTAGAACCATGCATCAGCTTTTCATCCATGGTGAACCTTAACCCCTCAGGCTGTCTACTCA/AV GTTGGTTTGTAGCTCAGCTCAGTGCACACAGGAAGCTTGGAGTTTGGAGGCTCCAAGTCACTCTCCA
EST36745 3	56 A G ---	---	---	GAGGGGAACCTTCAAAGAGGATCCCAACAGTGAAGCAGAAATCATGGGCAAAAGTCA/G/CTATGG GGCCAGACTGAGGTGGACCCACACAGCACTCCAAAGCTGGGCAATCCCAACCGCTGGTGAAGCGCG ACAGCAGGAGTAGOCAT
STS- R37410c	201 A T ---	---	---	TGTGACCATAACCAACCTATGCAATAAAGAAAAAGAAAAATCCTCACTTAAAAAACAACAAAA AACCTTTGCAATGCTATCATTTTTCAGGTCTTTTGAAGTGTGAATAAAGTTTCATAGCATTTTGGGA ATTTATGGTTTGAATAAATAACAAATGTGTGATCTCCTGAGACACATTTATAACACATTTCTGGTATG T/ATTTATGTGAGTGGTGTCTAGTGGCCAAT
STS- R37410b	139 G T ---	---	---	TGTGACCATAACCAACCTATGCAATAAAGAAAAAGAAAAATCCTCACTTAAAAAACAACAAAA AACCTTTGCAATGCTATCATTTTTCAGGTCTTTTGAAGTGTGAATAAAGTTTCATAGCATTTTGGGA ATTTATG/TTGTTTGAATAAATAACAAATGTGTGATCTCCTGAGACACATTTATAACACATTTCTGGT ATGTATATTGTGAGTGGTGTCTAGTGGCCAAT
STS- R37410a	48 C T ---	---	---	TGTGACCATAACCAACCTATGCAATAAAGAAAAAGAAAAATCCTCA/CTTTAAAAAACAACAA AAAAACCTTTGCAATGCTATCATTTTTCAGGTCTTTTGAAGTGTGAATAAAGTTTCATAGCATTTT GGAAATTTATGTTTGAATAAATAACAAATGTGTGATCTCCTGAGACACATTTATAACACATTTCTGGT ATGTATATTGTGAGTGGTGTCTAGTGGCCAAT
STS- R42778	74 C T ---	---	---	TATCGTGGGAAGTTCCAACCTCATCTATGCTGCTTTCTACTTGTCTAATATTGGATGCTCTTGCCA GGCTC/CTTTAAATTGTGCTGTAACTGGGAAGAAACCTTCTACTCTCCACAACCCCTGAA
UTR- 04350	125 C G ---	---	---	CAATCTGAAGAGATGCATAGCGGATTGGTGGCTTTCAGCAGCTGTGGGAGGTGGGACTGAGGAGCG ACTGCTAATCAGTATGGGTTTCTCCCGGGATGGTGAAATGTTCCGGACCTAGATA/C/GT/GACGA AGGTAGCAGCACACTGTGAGTGCACATAA
stSG1026 6	55 T C ---	---	---	GAAATAAACTAAACTGCAAGCAATCACTGTTAATAAGAAATGTTCTCTGTTT/C/GACAGTTG AAGTGGGTGTGAGATGGGCATAGCAATGAACAGTGGGAGCCAATGAGGTCTCAGAAATGCGGGCAAA CTCCTCTGTGAAATGTAT
stSG1028 2	70 T G ---	---	---	GTATAATTCAGCATAAGCCAAAGCCTTTTAAATAACCAATACTATCATTTTATGAAATCTTTACA AGAT/G/AGCAGACAGTAGTACAATATTTAAGCATCTCAAGTCTCCATTTAAGAGTTGACTATC
stSG1031 0	128 C A ---	---	---	CACCTTAGATATGAGAAATGGTTTAAATGGACACAAAGGAGTCAGCCACGTTGGAAACCAACATAG TTTCATACCACGTTGAAACCATGTGTTTATGATGCAATACAGCAATAATTTTTTCACTC/A/TTG TCAATGCCAATGCATTGAAAGGCCAGAAAATGAGAAAAGGATAACAACTTTTGATAAAAAAGGTA AGAATTTCTGTGTG

stSG1033 1b	116 T C ---	---	TTTAAAGCTACATGCTGAAAGATGATGCTGCTGATTGAATAAAGGAAGAAAGGATGCATTCGG GCTCAACCTGTCCTAGGAAGCCTAGACCTAAACACCAACACCTCCA/CJGCAATTCCTCTTTGG CTACTATGCTCTTTCCCTGACTTCTGCTCTCCAGCTCTCTGGGCTGCTGCTCCACCTGTTTCATCTGA CTTAGGACCCCTCC
stSG1033 1a	107 A T ---	---	TTTAAAGCTACATGCTGAAAGATGATGCTGCTGATTGAATAAAGGAAGAAAGGATGCATTCGG GCTCAACCTGTCCTAGGAAGCCTAGACCTAAACACCA/CJGCAATTCCTCTTTGG CTACTATGCTCTTTCCCTGACTTCTGCTCTCCAGCTCTCTGGGCTGCTGCTCCACCTGTTTCATCTGA CTTAGGACCCCTCC
stSG1243 b	225 G A ---	---	ATTGGCAATGGGAAATGACACCAATCATTTGATTACAGAAAATGGTTTTATAAATCCTCCTCTTG AAATTATGTTTCCAGCCCGCATGTAGCTTATGCTGCAATCCCAGCACTTCGGGAGGCGCAAGGAGA AGGATGCTTGAGCCCGAGGAGTTCACACCCAGCTGGGCAACATAGTAAGACCCCATCTCTGTTTTT TTTAAAAAAGAAATCTGTTG/CJG/AJAAAGTATTCAGACCAAAAGGAGGT
stSG1345 b	60 G A ---	---	AACAGCTATCACAGGGGCAAGTATCTGTCTATAAATTTGAACATGTTTGCCTTCTTAC/CJGCT TCACATTTTAGCATGGCCAAATTCAGGAGATGCCATGCAATGTCCATAAATGGGCAA
stSG1345 a	54 T G ---	---	AACAGCTATCACAGGGGCAAGTATCTGTCTATAAATTTGAACATGTTTGCCTTCTTAC/CJGCT TCACATTTTAGCATGGCCAAATTCAGGAGATGCCATGCAATGTCCATAAATGGGCAA
stSG1385 b	117 T G ---	---	TAAATGTCATCCAGGGAGGGCCAGGATGGAGGGAGGGTTGAGGAGCGAGAGGAGTTATTT TGGGTGGGATTCACCACTTTTCCCATGAAGAGGGAGACTTGGTATTTG/CJGCAATCATTAAGAA GACAAAGGTTTGTGAACCTGACCTCGGGGGGATAGACATGGGTATGGCCTCTAAAAACATGGCC CCAGCAGCTTCAGTCCCTTCTCTGTCG
stSG139	69 T C ---	---	TCGTCTCCTTTCCAGTGTCTCTGCCAGAAATCCCATGATGTTGACCCGACAGCACTTTGTGTCT T/CJGCTTTGAGCACTTGCCACTCTGGCTGCTGCTGCCACTGATGTGACTGTCTTGTCTGCTGCC GATCTGTTCCAGACAAGGCTGATTCAGAGACTCCACGTGGTCAAGGCTCTGTTGTTGTCATCCCT TGGCTCCTCCACTTCCAGTTTGGCTTCTGCTC/CJGACTCTCTCCATGTGGCAACAAGATGGC TACTGTTGGTCCAGGTTACGTCCTCTCAGCTTGGAATCCAGCAGCAAGAGATGTCTCACTCCCA AAGTCCATAACTCAATCCTTGGGAAG
stSG1427	103 T C ---	---	CCCTGGAGTTTCTGAACATAGGAAGAGAATGCAAGTCATGTGTTAGGTC/CJGCTCCTTGCATGA AATGTGGGAGAGGGAAATAAAGTTAGGCAACATTTAGCAATCAACAGAACCCCTTCCCTATCCTACC GCA
stSG1471	50 A G ---	---	CAAAACCAAAATCCTTCCACGATATATTACTATTTAGTCTAAG/CJGTTTAAATCAAGGTTGAGA ATGACGAATTCAGAAATTTCTTTCATACATAAATGCTTCTTCCCTTGTCTGCAGATGGGTA
stSG1483	44 T C ---	---	CACACCCACAAGTTTTCATGCTAATGCCAAGTATCAACTCTTGAGGACAAAGGCAAAACCAAGTGTGCA [CJG/AATGTGGAGGATGTCTGTTGAGCTGTAGTACTAATGCAGGAAACCCCAATGCAAAAGAGGAA AATGCCTGA
stSG1696	67 C G ---	---	

stSG1847 b	95 G A ---	---	TTGCAGACAACAATGGAAGCTTTAAACCTCTTCAACACAAATGCTACCCCTAAATGAAAGAATTT AGAGGTTAAATAAAACAGTGAGAGACC[G/A]TTTACTTACATCAGTTGCGTTTATAGACATTTGAA TCATATCTGAATGACTGACTGTTTCCAAATGTGAAACCAAAATTAATAAATACTTGATCACTGTGCT TCAACACAACTG
stSG1847 a	49 C A ---	---	TTGCAGACAACAATGGAAGCTTTAAACCTCTTCAACACAAATGCTACC[C/A]CTAAATGAAAGA ATTTAGAGGTTAAATAAAACAGTGAGAGACCGTTTACTTACATCAGTTGCGTTTATAGACATTTGA ATCATATCTGAATGACTGACTGTTTCCAAATGTGAAACCAAAATTAATAAATACTTGATCACTGTGC TTCAACACAACTG
stSG1897 a	83 A G ---	---	CTTAATGCCCTTCTCTCTCTGCACAGGAGACAGATGGGTAACATAGAGGCATGGGAAGTGG AGGAGACACAGGACT[A/G]GCCACCACTTCTCTCCCGGTCTCCCAAGATGACT
stSG2022 a	86 T C ---	---	TGCTTGAGGTTTCAAATCTGAGATATCTATGGCAAGTTTATAAAAAGTACATTTGATCAAGGTACAA TTTTAACATTAAATATACAT[C/A]TTCCATAATCTCATCTATTTAACATTAAACACAGGCCCTTTGTTGT TGTTATTTTTTCTCCCTACAATATTTCTGACTCTGTAGGACAGTGGGCCCTCAGTTGGGGGTTGAC T
stSG2076	104 C G ---	---	AAACGTTGTCCCAAAATTTGTTCAGTTTCACAAGTATAAAATAAGACTTCTGAAAAAAGTTTACA ATTAGTTATAAACACACTTAAGAAATATATTTGACATT[C/G]ACATCACAGTGGGCAATTTT
stSG2108 c	71 A G ---	---	TTGAGCAACAATGATTTCGGAATTTGGCAGCTCCAAACCAAAATGATT[C/G]AGGGGCTCCACAG AGAGAGCATAAGGGGAAGACTTTTATAGGACAACCTGTAGAAGTAAGCAAGCAGACGTTTGATTG GTTACAGTTACACAGTTGCTCTTATTTGGTCTATCTTATTTGGGAAAGTCTGTAGTTATGTAATTGAAG TTTGTGGGCTGTGCTGA
stSG2108 a	49 T C ---	---	TTATCCAGGGGACAAGCTGCACAAAGGAATGTTCTTCTATTTATTTAAACAAATGACTGCGTGTAC TGAATCTGACTGTGTGAATAATCTCAGAATGGCAGCACCACTGGCATGGCGATGGTGCAGGTGGT GCAGTTCCCTGTGGTCTCTATTGCTTGAAGAGAGAAAG[A/G]AAGTTCCCTATTATTATTTAAGGC AGTTTCAGAGCACTGGCATTCTTGTTGCTCG
stSG2141 b	173 A G ---	---	TTATCCAGGGGACAAGCTGCACAAAGGAATGTTCTTCTATTTATTTAAACAAATGACTGCGTGTAC TGAATCTGACTGTGTGAATAATCTCAGAATGGCAGCACCACTGG[C/T]ATGGCGATGGTGCAGGTG GGTGCAGTTCCCTGTGGTCTCTATTGCTTGAAGAGAGAGAAAGTCCCTATTATTATTTAAGGC AGTTTCAGAGCACTGGCATTCTTGTTGCTCG
stSG2141 a	113 C/T ---	---	

stSG2148	50 A G ---	---	---	TGGAAACAACCGGCTATAGTCTAGTGCATATTTTAGACCGTGATTTTC[A/G]AAAGAAACAATAA ATGTGGATTAGAAAGGAACATCCATTACTGTATTTTCGATACTTGTGATGTTCCACAGACGAGCTC ATCAC
stSG2175	68 C T ---	---	---	CTCAATGAGGACTCCATCAGCCCAAGCGTTTATATGGCAGATGAGCTGTACAAATCTGTTGTGTGCT [C/T]GCCGCGTGACTAGCTAATGCTACCGGGTTGGAGCGCACACGAGCCAGCCACCTTTTCCAT ACCTGGCAGAGGGAAGGGAGTGAAGGACCA
stSG2189	41 C T ---	---	---	CAAGTGGTGAAGCTGGGATTTGAGCCTGATATTCACACTA[C/T]CTACATTCCTCCAGTATAATA GGAATCATCGCTAACTTTGAGCACTTAGTGTCTGAGTACTTCGTATAGGTTATCTCAATCCTACTC CAGCTTTGCGAAC
stSG2200	49 T C ---	---	---	TGTTGATGACCATAGAGGATGCAAGCTCCGGGCTGGTCTGTATGATG[C/T]TTATATTTATGTAT AATGCTTTACTGATGATACCCAAATATTTACTAGCCTTATAGATGAGGATGGATGGCAGCTTGGCTG GTCAAT
stSG2243	85 G T ---	---	---	CATTTCTGCCTCTGCTTCCCAGTACTACCCCGTCCAGCACTGCTCTCGTATAAATAAGTATCAA GATGGTCAGTAGAAAAG[G/T]AGAGCATCTCTCAGCCCTGGAAGACAGTGTGGGAGCTTCAGCT
stSG2257	65 A C ---	---	---	TCAGTGATTGTAGGAGCTGGCTAAGTCATGCTAAACTCTGTGAGGCAGGCTATCAGAAGGGCAG[A/ C]CTGTGAGGAACTCTCGCCAAAGCACTGGGCTGCTCTCAGGCAGAAATTTCTTCCT
stSG2306	67 A G ---	---	---	GTCACTCAGCGTAGAGGTCACTGGTATAACAACAGTAGCTATATGATATTTGGGAACTATTTTACA [A/G]TATGCTCCCATTTGGGTTTTCCAAACTGATACAACCATGAGGTGAACACTTTCACCTGTTTCACAG TTCTCCAGAGA
stSG2334	70 T G ---	---	---	GAAAACTACCCACAGCATCATGTTAAAGAGAGAGATGAAGAAAAAATCCCCGCAAAAAACA AAAAAT[G/T]GCAGTGGAGGGGCTGTGGGAGGGTGAATG
stSG2339	63 T C ---	---	---	AGAGCAGAATGGTGAATCAACAAGACCTCAAATTTGCTTGACTGCAGAAGTAAGTGTGCTAC[T/C] GTTCTCAGAGTCACCATACGGTGACTGTGCTATCTGGCTGTGCTTCTATTCATCA
stSG2465	76 C T ---	---	---	CAAGACTAAGAAGCCGCAACCCGAGTGGTCCCACTCAAAAAGAGATTTCTGATTCTACCTCAAATG CAGAAACCA[C/T]TACAGATTAAAGAGAAACACACACACACTTTGAGAAACTCGCCCTTCCTC ATCTTCAAAGTGTGGGTATGCA
stSG2549	140 T C ---	---	---	TTGCAGGCTTGATTCCACAATAACAAGTCATGTATAGAGAATGTGAATGATACTTGAAAAACCAA GATATATAAAATATTGAAGTCATTTATGCCCTTTTGATGACTGGTTAAATATGCAAGCAGCTAAAG GAATAT[T/C]TACACCACCCACCCCTTTTAACT
stSG2577	123 T G ---	---	---	AATTGCCAATGGAAAATTCAGAGGATTTTAGACCAACTTTGCCCTGTTGCAATCCCAGTTTGGT CCCAATATAGGCCCTCTGCAAGAAGAGATCAATGCCGAACCCGAACTGTGAAGCA[T/G]GAACAATC CCGGCCCAGATTAAATTAT
b				

stSG2577 a	121 C T ---	---	---	AATTGCCAAATGAAAAATCCAGAGGATTTTAGACCAACTTTTGCCTGTGCAATCCCGTTTGGT CCCAATATAGGCTTCTGCAAGAAGAGATCAATGCCGAACCGAACTGTGAAAGC/TATGAACAATC CCGGCCAGATTAATTAAT
stSG2700	58 G A ---	---	---	ATCTCTGACTGCTTTAGTGGGAAAGGAATCAATTTATGAACGTGTCGGGCCCG/GA/AGTCAC TCAGCGTTTGGGAAATAAACCACTGGTCCAGAGAGAGAGGCTACTTTGAGCCGGACACCA
stSG2724 b	101 T G ---	---	---	AAACAAGCTTTGTCATTTCCACTACATTTTGTGTGCTTTTATTAATAATTTGCAAAATGCTATAAT TTAATACTTAATCCAAATGCTTGCTGCATAATCAT/GTTTTTTTAAATCCTGGGGTGTGAAAGAAC
stSG2776 a	65 G A ---	---	---	GTGGCCGATCTTTACTTTTCCAGAAAGGCGGTAAATAAAACCTGTAGAAAGTCTCGAATATGC/G/ AJATTGGCCCTTTTGAGTTAGGCCAGGAACCTCAACAAGGGACACTGCTGGCCCAACCAAAAA ATATCCACTAATCCCGAATATAGTAACCCGTGCTTGTCCGAATG
stSG2791 b	109 G T ---	---	---	AAGGAAAGGTGGAGGGAAGGGAAGAAATTACAATGGTTAGAAAAGAGCAACTAAAGATTATTTT TATTACTTCTGAACGGTAAACTAGCAATTTTAAATAATTTG/TGGGTCCACTTAAATCTATTA AAGCAGAAAGTAAAGCTATCTCCATTAGTGAAGAGATGAAGTGACAAAAACCAATCAG
stSG2791 a	100 A G ---	---	---	AAGGAAAGGTGGAGGGAAGGGAAGAAATTACAATGGTTAGAAAAGAGCAACTAAAGATTATTTT TATTACTTCTGAACGGTAAACTAGCAATTTTAA/GTAAATTTG/GGGTCCACTTAAATCTATTA AAGCAGAAAGTAAAGCTATCTCCATTAGTGAAGAGATGAAGTGACAAAAACCAATCAG
stSG2826	85 C T ---	---	---	CCGCAATTTCAACACACATCTATGAAAACCTAAGGGTGGATCATGTACAAACACAAAAACAAGC TCCCTCCCTCCAAAAACAA/C/TJGAACAAAAATAAAGAAAGAAAAACCCATGAAATGCCCCAGGTTTA ATTTTTTTCC
stSG2850	88 G A ---	---	---	ATGGGTGCATTGTAAAAGGCAAAATTAATACTTTTTCAGGCAGGGCTGGCAATTTAATGAGCTGA TGTGTCCCAAGGGAGACGGCC/GA/GGCTCACACATCCCATCAAAATACCTOCCAT
stSG3031	71 T C ---	---	---	ATACTACGGGGGCTGAAGGCAATGTGAAGAGTGAAGTCAAGTCCCTGGCATTTTCTGTGGTGTGACG AAAT/C/GCCCCCTTTATTTAAATGATTCAGACATCTGGGCAGCATAGCT
stSG3058	81 G A ---	---	---	GTCCCAACTCCTCTCCTCTTAGAGAAAAAACTGTGATTACCTCAACTTGAATATGAAACTGTGATTG AAAAAAGTCAAAAC/GA/TGAAGAGCATCAAAAGCCAAAAAGGCAAAACTGGCTGAGGC
stSG3092	94 T G ---	---	---	CAGCATCTCCAGAACATTCCTAGAACTGAACCATTTCTGTCACTATTGAAAAACAAGCCAAAGTTC CAAATCCAAATAATAATGAACGTGC/T/GJGATAAACATTCCTTATGTTCCAGCCCCCTACTTT AGTT
stSG3230	95 A G ---	---	---	AAGAAGTACTTTGGTAGCTATTTAATAAGAGGGGGTGGGAATGAATGTGAGATACGAGCACCTG CATCTTTTAGTCAATTGTCAGTGGAGTC/GJGTGGGGTGTAAAGTGTCTGAACCTGAAGTAG
stSG3245	160 G C ---	---	---	ACATCTCATACCCAGTAAGATGCAAGAAAGGAATATCTGAGAGCAAGAGCCCTGCTCCAGGGGCC CAGGTATGTGAGAGGCCAGTGGGGTGGCCACTTGGTGTCTTACCAACCCCTGCCATCCAGCTG GCCCCAGTACCTACCTGGGAGGTG/CJ/TGACTTGGCTAAGTACTTATGCTTTAT



siSG3265	42	T C ---	---	AGGTGAATGAGTTACTAAATGTAGCATTTATTTATAAGGAATGCGCAATGTGTAATGTTCTCAG TTTTATTATGAAAGATGATGATTTAGCCACATTCAGTGATGTTCTTAAATAACACATCGAC AGGACTGCTGTTGAGTACATGAGGACAGCTTTTTCAGGGCAATGGGATTTCTTGATAATGCTAA ATCTGCTTGTGAGCTGAATTTCTGGGCTTTAIGGGCAGTGTGGTAAAA
siSG3269 b	141	C T ---	---	TGTAATTACTGTGTCATCTCTATCCATCCCTCCCTGAGCCTGGACTGCTCTCCAAAGGGAGACTAGG AGTGAAGGGAGGAGTCTCCCAAGTTACCCCTTAAGCTTGATAATTAGCTCCATAGCCATGCTAAA GCATGA[C/T]TGTAAGATCCCAAGTCCCTGACACATTTCTTCTAAGAAACT
siSG3269 a	24	A G ---	---	TGTAATTACTGTGTCATCTCTATCCATCCCTCCCTGAGCCTGGACTGCTCTCCAAAGGGAGACT AGGAGTGAAGGGAGGAGTCTCCCAAGTTACCCCTTAAGCTTGATAATTAGCTCCATAGCCATGCT AAAGCATGACTGTAGATCCCAAGTCCCTGACACATTTCTTCTAAGAAACT
siSG3284	130	C T ---	---	TTAACTCAAGAACTTTCAGTTACAGGAAGATTATCTAATATTAATGACTAAATTACAAAAAGC ATAAATGTTTGAAGCCATTTTAAAGTTGTTTTGAAATCCATATTAGCACTCAGACTTCCCCA[C/T] TCCCTAACTTTTGTAAATGCTGTATGGGACATTTGTTTGTATCTACCC
siSG3292	99	A T ---	---	GTCTCAAGTGAATCTGTAATACATTTTAAAGTCTGACTTCAAAATCGGTACATGAGGCTTAGACATA CACATCAATTGGACAAGTGACTTAAATATCTAA[AT]TACAAATCAAAATAGCATTTTCCTAACCTCAA TAAATGTCATATCTTTAGCTCTCACT[C/A]CCAGTGTATCCATTTTCCCAAGCCGTAGAGCTTTTCTG TTTCTGTAGATTTGCCCTGCTGGACATTTGATATAAATGGAGTTGCTGTATCATGTTGAGACTTCTCTC ACCTAGCATGATGTTTTCAAGACACATCCATGCTGTAGCATGCTGAGTCTTCTTCTTCTTAA GATCCCCAGTATTATTTCTAATTTGAACCTTTGTTGGAATAAAAATCTGAGGACCCTCAGAG GG[C/T]ATAAGGGAACCCCTTTTGTCTTAGTTTCAATAGGACTTTCT
siSG3369	69	C T ---	---	CAAGACTGTAAAGAACGTAGGCCCTTTGTGAGAGTGAAGGAAGGATGCTCGAACTTGCCCAGGACTCAGG CTTCAGCTTCACAATCCCGAGGAAAGGAATGACATTTCCAAACTGTCACCTTTGTAGC[G/T]CTGGGT CAAAGTCTAAAGAGGACAAATAAATAGAGACT
siSG3398	125	G T ---	---	TCCTACTCTGTTAACTCAGTCTGGAGTAAAGGATGCAATCAGG[AG]CTCACTGTAGCCTGGACCTCC TGGGTTCAAGTATCCTTCCACCTCAGCCAACTGAGTAGTGGCCTGCAGGACAAGTCACCATGCCTA CCTAAGTTTTGTAGAGACAG
siSG3416 a	43	A G ---	---	GTAAGACAAGGTTTTGCTATGTTGACCAGGCTGCTTGAACCTCTTGGCTTCAAGCGACCGTAGCA CCTTGGCCCTCCCAAGTTGCTGATATTACAGGTGTGAGCCACTGCCCCCGGAGCTTTTAAACTGAAT GTTGAAATCACTCTGCTCTTTGCTGGGTAACACTGAT[TA]CAAGTTGCTTAACTTTGTGAAACACAG TTTCTTATCTGTAAACAAATGGACAACAGAACTTTTCTTCTCTC
siSG3424	173	T A ---	---	GTTTCATGTTAAAGATTAGGAAGCTGTGGATGTGAGGGGTGAGGTGATGGAGGGCCTCAGACA ATGAGTGGCAGAGAGGGGCCCT[TA]GAAATAGCTTACTCTGTTTCTCTAIC
siSG3436	88	T A ---	---	

stSG3463	103 C T ---	---	---	GATACAGAAGATAGTGTGGTATGGATGGATAGTATGAAGGACAAATAATACAAATATATTTATTG AAATAAACAAAAATGCATACACAGCTCAATGGGTCACTC/TJGGAAACAAACTTGTCTTGAATATATTA CTGA
stSG3491 b	71 G A ---	---	---	CAAGATACCTTCATTGTCTCTAAGTAGTGCAGTGTGGCAATATTTCTACGAAACGAGGCGATTG AAGA/GA/GTGGAAATTACTGTGCAAGGAGTACTTTACCTCCAAATAGCTGCAATTTAGCAGTCTGA ACAACTCTCTAATCTTTTACTGGCACCTGTGGATTCTATTAACTCATTTATATACTATTTCTGTGATG ACAGAAAAATAAGTTAAC
stSG3523	33 C T ---	---	---	TAGCCATCTTACTCTAGTCTTTTTGGGTTTTA/C/TJGCATATATGTGTACAAACACACACACACACC CCTAATTCCTCAAAATGCTCTTGGCATAAGTTTTATCTTACTGGTCTC
stSG3536	213 A G ---	---	---	AGTACAAACACAGATTTAAAGAGCTCAGCAGTATTGACAGCTGGAAATTAATGGAGACATCCACTT ACTGGAAGTAAGGAGCTGGTAGCCTACCTACACAGCTGCTACAAAACCAAAATACAGAAATGGCTTC TGTGATACTGGCTTGTGAAACGCATCTCAGTGTCTATTGTTTATATTGTTAAATGAGCTTG TGCACCATTAAG/GTCTGCTGGGTCTTCTCAGTCTTGCATGAAGTATG
stSG3583	112 G A ---	---	---	GAAAAAGCTTAACATACGATCCATGTGCAAAACCCAAACACAGGATCTACGAACCTCTGGCATGATCCA CATCGCTACACATACCATGCTGGAAGTGCACATCCACACAGGCAC/GA/JTAACATACACAGTACTGT CTAGTTATCAACACCTAC
stSG3586 a	60 G C ---	---	---	CCTAGTAACATAGTGAGACCTCGTCTCTACTAAAAATTTAAAAAATCAGGTGTGGTGG/GC/JACG CCTGTAGTCCCTACTTGGGAGGCTGAAGTAGGAGGACTGCTTGAACCCAGGAGATGGAGGCTACAGT GAGTTATGATGGCGCCATTGCACCTCCAGCTTGAGACTGTTCAAAAA
stSG3589	101 T C ---	---	---	ATATAGTGTGGTAGCATTATAAATCCTTTAAAAAGCAATCTGGCCATATCAAAAGGCCAAAAAAGT GTATATACCAACCCCTGGCACAAAAAACCCCAATGA/T/CJCTATTTCCCAAGAATGTATCCAGATGAAA GTATCCAAACAAAAAGCTATATACAC
stSG3590 a	70 A T ---	---	---	GAGAGATGAGCTATTATTTCTTTTACTTAATGAAGATGAAGAAATGATCTTCTGTCTTCTAAAAA AAA/A/TJTTTCTCTGATGTCTCTTGACCCTGTAGGAAACACATTCAGTTTCTACACT
stSG3619	78 A C ---	---	---	CAGTGAGACTTCTCATTTTATAGCAAAATACATTTTTCAGCTTAAATTTCTTGAATTCATATACGCT TCTGTCAATTA/CJAACAAACTTCCAGAGAAAACTGGGCTCTATATATTTAAG
stSG3644	40 T C ---	---	---	ACATATGTAAGTCCATTAGTAGCCATATTTAGGATGAGAT/CJGGATTGAGAGGCATGAACCAAGG ATGCGTAATAATCATTTATGAATAATAAGTTATCTGGGAAACGGCCATTTGTCCCAACATTTACTAA GTGCGCTACTA
stSG3646 c	70 G A ---	---	---	CTCATAATTAGATTGAGATTGTGCAATTTTGGCAAGAATATATGATGATAACAATAATATGCTTACT GGT/GA/JATAATTAACCTTGATACTTGGTTAAGATGGTGTCTGCTAAATTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA

stSG3646 b	55 A G ---	---	CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGAATATATGATGATAACAATA[A/G]TATGTCCTT ACTGGTGATATTAACTTTGATACCTTGGTTAAGATGGTCTGCTAAATTTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA
stSG3646 a	43 A T ---	---	CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGAATATATG[A/T]TGATAACAATAATATGTCCTT ACTGGTGATATTAACTTTGATACCTTGGTTAAGATGGTCTGCTAAATTTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA
stSG3693 b	85 A C ---	---	ATTGTTTCCCTGAACATTCCCGTGGTCTCCCTCTGAAAGCGGATGACCATCCAAOCTGGACTCACCT GAAATATCTACGAGGC[A/C]TCGCCCTCCGAGACTGACGATTATTAAOCCACCCACACGGAAAAAGG
stSG3693 a	30 C T ---	---	ATTGTTTCCCTGAACATTCCCGTGGTCTCC[C/T]TCTGAAAGCCGATGACCATCCAAOCCCTGGACTCA CCTGAAATATCTACGAGGCATCGCCCTCCGAGACTGACGATTATTAAOCCACCCACACGGAAAAAGG
stSG3698 b	145 G A ---	---	TCTTGCCCTTTGTGTACCCCTAGAGAGATGGCACCCCAATCCOCCAGGGTTGCTCTCTGACTTCCACCAT TCACTGACTTTTATTGCCAGAGGAGCTOCCAGGAATCCACAGTTCTGGAAGAGAGGGGCTCTAAGTCT TTATTGGG[G/A]AGAATACCCACCCACCTTCCCTCACTGCAGA
stSG3698 a	51 C G ---	---	TCTTGCCCTTTGTGTACCCCTAGAGAGATGGCACCCCAATCCOCCAGGGTTG[C/G]TCTCTGACTTCCA CCATTCACTGACTTTTATTGCCAGAGGAGCTCCAGGAATCCACAGTTCTGGAAGAGAGGGGCTCTA AGTCTTTATTGGGGAGATACCCACCCACCTTCCCTCACTGCAGA
stSG3724	107 C T ---	---	ACCAGCTCATGTGCAGAGGGTCTCCTGCTGGATCCCCAACTGGAGGCATCCCTGGGCCTAGACTTCT GTCTCCCTCACTTCTAAATGAGTGTCTCAGTGATGTGAAG[C/T]ACACAGGAGTCCCTCAGGGCAAAA GTGGCTATGCTGGTGCT
stSG3725	104 G A ---	---	GCCAAACAAAAAGATCTTTGGAGTTTACTGACGGCAGCAGTTAATAGCACAGTCAACAGCATTAA ATCAATATATTATTACAGCCAACAGCAACAGACGCC[C/G]A/JAGCAGGAATCGGCACATAGTCATAA ATAACATCAGGGGTAATAACGGCACATTTA
stSG3751	128 G A ---	---	CGGAAGAAAGAAACACAAATCCACAGGAACAATCTATGGTTTCATACCTTTTAGAAAGATGATTTTG AGGGCTTCAGTATTTAAAGGGGAAAGCAGGCTGGAGGGGAAAGAGAGAGGATATGGTCCC[G/A]TT GCTGACTCCATGTGTGCAAGAG
stSG3787	49 T A ---	---	TTCTGTGCAAAAGAATCCACATCATTTGTTGGTAGCAGAGGATCTCTTA[T/A]AAAGTCCCTAAGA CACTGAGGGCATAAAACCAACAAATAAAATAAGGAGTGATAGGCTAAAGCAGTATCTTCCCT GACAAGAGGGAAGAGATCGGCCAGAGACAGGGCTGGGGCAGCTGGGGTCCCTGAGTGCACAGGCGC CACCACAGTCTGTGGTCAAGGCCCTCTCTGGGGAGCAGGTCTA[G/C]GGCACGGAGGATGCAG GGCTGGGAGGGGACCCACCTCGGGGACCCAAAGGAGTCCATTCTGCCCT
stSG3880 b	115 G C ---	---	

stSG3880 a	36	G C	---	---	GACAAAGGGGAAGAGATCGCCAGAGACAGGGCTG[G]CGGCAGCTGGGGTCCCTGAGTGCCAGG CGCCACACACAGTCTCTGGGTCAAGGCCCTCTCTGGGAGCAGGTCTAGGCACGGAGGATGCAG GGCTGGAGGGGACCCACCTCGGGACCCAAAGGAGTCCATTCTGCOCT
stSG3895	44	A G	---	---	AATCAGCCATTGTACACATTGCAGCTATGTATTGTAGTGT[G]GJTTTTTTTTTCCATTAACTAA TACATGCCCTCATAGATATATTCATTAGTGTATCACCATTGGGAACAAGATGCTGATTCGTCAACTG AAAAT
stSG3902	104	T C	---	---	TCGTGTGAGACTGGAGAGACCAAGGTACCAAGCACCAGCTCTGGTGGGAACCTGGCTTCCTGATAACA TCATCTATTTACCTAAATGTGAACCTGCTTCTTTTC[C]TCAGCTCAATAGCTTAACATCTAAATTC ATGTTGCTCCCTTTGCTGGACAAT
stSG3935	50	G A	---	---	GGGTGCTGACGGACAGGCACACCCAGAGTTTCAACAAGCAATTTGTCC[G]A]CTAGTGTGCAGGC TCCTCCCCCAGTTTCCACAGGCTGAGTACTATGGGGTCACAACCTTCCJGGACGT
stSG40	25	A G	---	---	GAGGAAGAGGTTGAAGAAGTGTGA[G]GJAAATATATTAAGATTTCTTGGGGAGAAATCTCGTGC CCAAACCTGGTGATGGATCCCTTACTATTAGAATAAGGAACAATAAACCCCTTGTGTATGTATCA CCCA
stSG4009	32	A G	---	---	GTGTGGGCTGTCTGATGATGAATGGCGGCTC[G]GJ]TACTCTTTACGGTCTTACACTTTTATGCTCCT ATGAATCTCTGATGGGCTTTAAGGGCTGAACCATATCTGAAGTTTCCCACACTGCTTACA
stSG4033	123	T C	---	---	AGAAGCCTTGGGGACAATGGCAGTGCCTTTCTGAGTAAGACATGAATGCCATCTCGAGGATCCATT TGAAACTACAGTGCAGTAACCAAGAACCCTAATGTTTCAAGCATAAAGGTACTTT[C]JGTGAAC AGGTGGGCAACAC
stSG4038 a	29	G A	---	---	GCTGAGAGCAOGTGTACAGCCACGCCTG[G]A]CGCAGGCCACTCTGTGCAATAAACATGTTCTGCC CATGTTCTCAGTCAGGAGGTTCAGGCTCCCGGAGAGCAOCTGAGGGTTCATCACT
stSG406	53	T C	---	---	ACTGTGGTTCAACAGTATTGCGTTGTCAGACTAGGAAGCTAAACGAACAAA]T[C]JGGTTTTAGTT TTGCTGAAGACTGGCTTATTAATGGACAGCTTTCCTAACAGAGATTATTAACTTTATCAGGTGTT AACATCTGTTTCAGGAACATGGCA
stSG4095 b	55	G T	---	---	ATCTGGGCTGAATTAGTCAAGCAGGTCAGATACTATTGTCTGCTAGATGTTAG[G]TATAAAAA GTTTGCTTCTGTAATACITTTAAAGCTTGCTTATCTCATCTGTAAACCTATGTGCTTGAGAATCAAG CCITTGACTAACCCAGGGCATTGCCCTTCATCCTGG
stSG4095 a	27	A C	---	---	ATCTGGGCTGAATTAGTCAAGCAGGTC]A]C]GATACTATTGTCTGCTAGATGTTAGGATAAAAA GTTTGCTTCTGTAATACITTTAAAGCTTGCTTATCTCATCTGTAAACCTATGTGCTTGAGAATCAAG CCITTGACTAACCCAGGGCATTGCCCTTCATCCTGG
stSG4120	65	G A	---	---	TGCATGTTCCACATCTTTCATAACAGCAAAATGTATAATAAACTTACGTACTTATGGATAATCAC[G] A]CTTTTCCCTCAGAGAGCCCCACAGTTAAACAGGTTCCAGCACACCATTAATCCACCGAGCT

stSG4128	54 A G ---	---	---	CTTGGCAGATAAGGGACTCGTTTGACAGATATGACTTTCCTTTGTGTACATTCTT/GTATATTATTT TACTTCTCTGAAATGCCACATAATTTGCAATAAATGATTCACCTCTAGCTCCAAAAGCAAGTCC TTTATCAAAATGCAAATGTTCCAGAGGG
stSG4209 b	128 G A ---	---	---	CACGAAACAGATGCAGCCTACACAGTGTGTAGGACCGAGGCTCACAACATCCACATGGCACAAGC AGGCCGGCCACTCCAGGCAACGAAGCCACCCGAACTTGCAGAGGCCGCACTCCCTC[G/A]GC AGGGGAACACCGAGGCGACAGGTGCTTTGATGCTCCGAAGAGCTGAGCTCCATTCCA
stSG4209 a	65 G A ---	---	---	CACGAAACAGATGCAGCCTACACAGTGTGTAGGACCGAGGCTCACAACATCCACATGGCACAAG /A]CAGGGCCGGCCACTCCAGGCAACGAAGCCACCCGAACTTGCAGAGGCCGCACTCCCTCGGC AGGGGAACACCGAGGCGACAGGTGCTTTGATGCTCCGAAGAGCTGAGCTCCATTCCA
stSG4254 b	31 G A ---	---	---	CATTACCCAGAACGCCATGGAGGACCAGAGC[G/A]CCACGGCCGGGACTCCCGCGATGGCTGGGGGG GCTATGGCTCTGACAAGAGGATGAGCGAGGGCGGGGGCTGCTCTCCCGAGGGGCGAGACGTGAC TGGGGGAACCATGGCCGAAGAGAGGATGACCGGTCAIG
stSG4301	81 T G ---	---	---	TGCAACAGCTCTGAGAGGAAATCCTTGGCAGATCAAAAGAGAGGAGTGGTCCACACTTTCCAT TTAAGCAATAAATTT/G]AGCTTCTGAGTAGTTGTTCCAGTTTACCCCAACATTTTG
stSG4331 b	71 T G ---	---	---	CTCACAAGGGCCCAACACAGAAAAAGATACAAATACATTCCAGCTAAATTTAGTTTATGACAC AGAGT/G]TTTCAACAAGTTTAAGTGTACCTGAAGAGCATGTTAAAAAGTTTAAGTTATCACTT GGAGAGCAGATTCTTGGCCTCGCCCTTGATGCTGTTTGAGGGGTGTGC
stSG4340	76 G A ---	---	---	TTTTGCAACAACATGGATGGACCTGGAGGCCATTAAAGTGAAGTAATGATACAGAAAGTCAAAAACC ACATGTTCTC[G/A]TAAGTGGAGATAACAATGTGTACACCTGGACGTGGAGAGCAGAA
stSG4361 b	109 A C ---	---	---	TTCCCAACCATTTGAGTGACAGAGCTCAGTCATGCAGAACTCAGGTTTGCATGACTCAAAATAGGCAC AAGTCTTGGAATTTCCATAAGGGATAAAGTGCATCTTTTGCACCTTCACAACACTAGAAACGACTC AGCGACTTTTCTGTGAGCAATGTCGAGG
stSG4361 a	24 T C ---	---	---	TTCCCAACCATTTGAGTGACAGAGCT/G]CAGTCATGCAGAACTCAGGTTTGCATGACTCAAAATAGG CACAAGTCTTGGAATTTCCATAAGGGATAAAGTGCATCTTTTGCACCTTCACAACACTAGAAACGACTC AGCGACTTTTCTGTGAGCAATGTCGAGG
stSG4376	73 A G ---	---	---	TTTCACTGCTACTGGTTTCGGTGTCTGAGTCTCAAACTCTGCTTTGCAAGTGTCTTCCAAAGGGGAG AACAG/G]CTGGAAGTGGGCTCTGCAAGAGGCCATTCTTCCAAAGCCATTCTTCTCAGCTGC
stSG4381	50 T C ---	---	---	GAAGGCCACAACACTCCATAGCCAGAGATGACAACTACGATTTTCTT/G]C]CAGTCTTTAGT ATCCACAGTAGTGTCTGTCCATGTACAAAGTGTCTCCAGAACACCCATTAAATTCATGCC
stSG4410	79 A G ---	---	---	ACCAATGGTCTGCTATGTGCATCCGATATTTTGGCCGATCTGAAATAGTCAAGGGCTTAACCAT TCAACACCCG[G]TGACAACGAACCCAGTGGACTGTGAAACTCAGGCTGCAGGAGGGTGGCTTGT CAGCTGGGT

stSG443	65	C T	---			AGCAGATCAGTCCACCTTGCTCTCTCTCTTTAGGAGAGGCTAGGCAGTGAACACATCA/C/
stSG4430						TJGTATGCAATGAGAAAAATAACCAACTGGTAGGGGGAGGGGAGGCAATAGGCAC
a	54	A G	---		---	AAATGGAATTCATCTCTGGCTGTCTCTCAGGTC
stSG4448	99	G A	---		---	ATGCACATTAATGAATGGCCTAACTACTGGGAACCTTTAGTAGTTCTATAAGGT/AGJATTAAACATA
						GGTAGGATCCAGTTCCTATGACAGGCTGCTGAAGGAACAGATATAGGCATCAAGAGGGCATT
						OCTCCCTCCCTTCCCTTCCCTTCCAGTCTTTCCATACTGTTCCTCCCTCCCGCCCAACCCAGGCTCT
						CGCCTAGCCCTGCCCTCTGGGTCACTGC/AGJGGGTTAGGCCCCCAAAAAA
stSG4449	92	T C	---		---	ATTAGCCATTCACTTGCACAAATGCTTTACTGTAACTAAGAGTACTGTACTGATGATGTTTACAAT
						TAACTTTGGACAACCTTAAACCTTA/CTAGTGACATTGCTGTCTAATAATCAAACTACTTCATCATA
						GGCTGAACATAATTATTAAGAGCAAAAGTTACCCCTCCC
stSG4467	42	C A	---		---	CAGACATGAGGGATGGCCCTGTCTCTCTGGGACAGAGCCCTCA/C/AGATGATGTCCATGTTTGTGT
						GAATGAACTCAACACTCTTCAGTTTTTAGAGTCACTTTCTGGTATCGAGCGACACACCGAGGAG
						CACACCTGCTTCCAGGCTGCTGCCCTCTGCACACAGT
stSG4475	21	A C	---		---	ACATGTCACTTCTGACCAGG/ACJATTAAATAGTTTATTTAGAAGAAATGAGTTGAAGTGAGCGA
						TTAAGAGACACAACTGGACTTTTGTCTTTCTTTACTGTAGCACCCAGGTTTCATG
						GTAACATCTCTGGGGTGGGGTGAGACAAACA/AGJATGAACCAATAATTAACTACAATTATACATT
						TCAAGGAGACTTTTAATCTAGTTAATGTGAACCGCAGCCATCAATGGTTGTTCAGGAAAAGGGAGA
stSG4477	32	A G	---		---	TGAAGTCTTGTCTCTGGGCAACGTTTGGCTCATTGCAGTCAGACTTGGC
						TGAACCTCAGAGCTGGTGGGAGCTGCAGGCGAGGGAGGCTGGGGGCGCAGATGAGCGCGGGGA
						CAGCAGGCGTCG/C/CGCCACGCTCTGGCGTTGGTAGAAGAGGACATAGGCTGCCCTTGGACTCGATCT
stSG4531	79	C T	---		---	GATCTCATTGACAGGGGAGACGCTGTTGTCAATCA
stSG4550	86	G A	---		---	TGCATTAAGGAATGATACGGCATATTTGGGGGACAGAGAACAAGGCTTGATGAGGACAGAGTCTATTT
b						AAAGAGACAGTGGGCACC/AG/CAATTGGAGGGGAAGCGGGCAGGGTTTAGAGAAC
stSG4550	85	C G	---		---	TGCATTAAGGAATGATACGGCATATTTGGGGGACAGAGAACAAGGCTTGATGAGGACAGAGTCTATTT
a						AAAGAGACAGTGGGCAC/C/GJCAATTGGAGGGGAAGCGGGGAGGGTTTAGAGAAC
						AATCAGGCACAAGCTCGGAGAGAGCAACAAAGCTCTTCTGCAC/AGJATGGGAGGGAGACAC
stSG4590	47	A G	---		---	CATTGAAAAGGCATCGTTCCTTCTTCATGCAAGCAGGCGCTGCCACAGGCATGGTCTCCTTG
						AATCTGTATCACCCAGCGCTGGT/C/CAATGTACTAGTAGCTTCCACAGGGATTTTTTATACATTC
						CTATAAGGTTTTATCATGAATAAAAAAGCTCACAACCTCTTTTCAGCCATTGCAGATTCACATTTATCT
stSG4623	22	T C	---		---	TAATATTCCTGTTCAAGATGCTCTGGAG
						TAAAAAAAACAACCCCCCAAAAAACACCCAGAAGTTTTTGTAGTTTTTATGTTTTTTCAGATTTAAAG
						GTATTTCTTTCTAGCTTCTAAATTTTGAGTCA/AGJATCAGAAAAGTCTCCCTACTCCCAAGGTGA
stSG4843	102	A C	---		---	GAAAGGA

stSG4850 a	38 C T ...	...	GGAACTAAACTGGGAATGGCCGAGGAGGAGGGGCTC[CTGTGCACCTTGCAGGCCACGTCAGGAG AGCCAGCGTGCTGTGGGAGGTTTCCAAAGTGCTCGGTGAAGAGCATGGGCAAGTTGTCTGACAC TTGGTGGATTCTTGGGTCCC
stSG4879	86 A G ...	...	AACCTCTCC AACTCTGAAGGGGGTGACCTCAACCCAGCCCTTGTCTGTAGGTCCTGCTTTTGCAGAATGGCCTG CCCCTGGGACTGGAGCAG[AGCTTGGGTGAGCTCTAGGTGGAGGGTGGTGGGAGGGGCATAGAAAT AAACCTTCC
stSG4885	104 G A ...	...	ACTGACTGGCTGCTTGTGAGCCGGCTGAGCGGCTGAGCGGCTGGGACTCGGGCTGACCACTCGCTCTCAG AGACTGCGCCGCGGTGACCACGACTACGCTCTGCC[GA]GTGGGAAAGCAGAGGAGGACC
stSG4896	112 C T ...	...	AAACAAATCAAAACCCAAATCCACAGCAGTCTATGTACAGGGCCACTCCCTGCTCTGCCATAGAGA GGTTGGGGGCGAGCTGAGGAGTGGTGGGGCTGGGCACCTTTCT[CT]CAGCCACAGGCGCCCTGAGG AATTAATTGACTG
stSG4932	22 G A ...	...	ACAGTGCCGATGGTTACACAA[GA]TTGTAATGTATTAATCCACCTTACGAATGATTAAATGA TAAATCTTATGTTTATTTATCATCACTACCAAAAGGCTGGGTGCAGGGGTGCTGTTTCTGGTCT
stSG4950	24 A G ...	...	TCATGACTCCAGGAAAGGTCCT[AG]TCTTAGCTTCTCTCCCTACTTTCTCTACATGGTCAGC ACTGTAATGTAGCTAAGATATAGTAAGGCATTGCTCCCTACCCCTACACTTCAAGG
stSG4957	136 G A ...	...	AGATACGGGCAAAACACTGGGATGGCTTCTGACAACTTAAGAGGTCTCCGAGTTATTTCTGGTT GGGAACACTGACCCAGCCCTTATTCCTCAAGGACTTAGTCATTGGCAAGGAGGATTCTAGGCC CC[GA]GTGACACAGATGGGGCCCTGCTCTATATTCAC
stSG4961	91 C T ...	...	GAAGGTGCTCTGAGGAGGTGTGACTCTCCCTGGCTGACAGGGGAAGGCTTAGCAGAGCTTTGTCTTAG AGGAGTAGATGAAAGGAAAGTA[CT]AGAGAGGGCAATTCAGGCCAAGTCAGCAACACAGACAA
stSG4967	72 A G ...	...	ACTGGTGCCTCTCAGCAGATTCAGGGGTGTCAGGGCTGGTTACCAACAACTCAGTAGGAGTGCAA GGGCT[AG]TACCCCGGAGCTAGACAGCCTGGGTTTGAATCTCAACTTCTCCCTTTTCTTGTGTGC AACCTTG
stSG4997	22 T C ...	...	CAAAGGAGAGTAGGAGCCCA[AT]CTTTTAAATGGTTTCTCTCCCTCATGCTATTTGATCCAAAA CTATATACAAATTTGTAGCAGTCTCTGTATAGTTATTACACATGTTTAGAAGGAGGGAGGCAAGAA GGGATAGGGAGAATGGTGATCCAAAAT
stSG6312	37 C T ...	...	ACAGGTTCTCACACTTTGAGCCCTTAGTGCAAAAACA[CT]TATGCCATGCGGGAAATAAAATGCTT ATCCAGTGGAGCGCTCCCTGATGCATTGAAATATTAGGATACTCAAGCAGAAGAC
stSG6345 a	107 G A ...	...	GCTCTGGTCAAGCAAATTCAGGACAGAAAGCAAGGACAGTAACACACATGTATGACCCCTTA CAAGTGCCTTAAGATTTTAAAAATGTGATGTTTGTCCAC[GA]TAGTTCAGGCAATTAAGAATAT GCAACCCAGAGAATTTCTGTGAAAACATTTGCTCTTTGGCCTGGTGTGGACAGAAAGGGTGGCCAA ATGGATTGAGTGATGAGCAGCATG





stSG8145	97	C T	---	TTGTGGACTTCAAATCTTTCTTCCAGATTTTAAATGACATTATGCATGTACATATTTTAAATTT AGACACATTTTAGAGAACAAATTTGTGAA[C/T]ACAAATCTAAGAAATGAATGAGATGTTCTGAAA TCTGATCAAACACTTATCTTAACTGACTTCGTCAATCTCTGTCCTGTGAAG
stSG8150	36	A G	---	ATTGTTCTTGCAATTGCTTGGATTTTCAGAATAGT[A/G]ATAAATAATAACGGGAATCCTAGGCAT TCGTGTTTTTCTATGTTTTTAACAGGATTTCTCTAATGTTTCGCTATTAAATACCATGCAGGAAATT GGGAAAT
stSG8340	30	C T	---	AGAGGATTATGGAGAGAGCTGGGCAGGATC[T/C]AACATTATGACCCCTGAACCTCCAGAAC TGGAT TCACTAGAAGGAGAGAGAGAAAAACGCTCATCAAAA
stSG8466	111	G A	---	TGTGTATTGGTGACTGTAGCCTAAGGATAAATGAAATAAATGACAGCAATGTTATAAGCAGTGGGA GGAGTGAAC TGGGA TACTTGGTTACAAGGTATTTGCAC TACCT[G/A]TGAAGCAGCAGCAGCATTAT TTGAAAG
ESTD-ACE	--	--	---	GATCAAGCAGTGCACACGGTCAAGATGGACCAGCTCCACAGTGCACCATGAGATGGGCCATATA CAGTACTACCTGCAGTACAAGGATTCGCCGTCTCCTCGTCGGGGGCCAACCCCGCTTCCATGA GGCCATTGGGGACGTCTGGCGCTCTCGGTCTCCACTCTGAACATCTGCACAAAATCGGCCTGC
ESTD-ADA	--	--	---	ACCATCTTACTATGGCAGGTAAGTCCATACAGAAGAGCCCTCTCTCCCTGGGATTTGAGTGGGGTC CCCAGCTCCACCCAGAGCCCTGGGGAATCCAGGGTCACTGTTCTCTCTGCTCCCTGTGGGAAT CAAGCCAGCTCCAGGCCAGAA GTGGGACTGTGAGGACATGGAGGCCCTCGGCACTGAGCTCAGACCC GCAGACCAACTCCTGAGCTTTCTGGGCCTCTGAGTCTTGTGCTC
ESTD-AK-168	--	--	---	GGGAGTGACAGCTAGAGCACCAAGGGGGCTCTACAGCTGTGTTCTCATGGAGGACAGGCTTCTGCTC ATTCTGG
ESTD-ALB	--	--	---	AATCCCAGCAC TTTAGGAGGCTGAGCGGCATATCACAGAGGTGAGGAGTTTGAGACCAGTCTGA CCAAATGGTGAAACCCCATCTCTACTAA AATACAAAATTAGCCAGGCATGGTGTGCATGCCTGT AATCCCAGGAGGCTGAGCAGGAGAAATCGCTTGAACCTGGGAGGCGAAGTTGTGGTGAGCCGAGAT GGCAOCATTGCACCTCAGCCTGGGCAACAAGAGTAAACTCTGCTCTC
ESTD-ANT1	--	--	---	TCTCCTGTGTCATTCCTACTCCATTAGTTCAAAGGTGAGTGAAGAACTGGGGCAATTAAACCAAGTAATTCA TGGACTGCCCAACTGCGAAACAAGAGGGCGCAGTGGAGCAGGAGTATTATGCTACGCGGTTACCTT TTTTATGGAGGACCGAACTGAGGCTGAGCTCAGATGATCCTGT
ESTD-APOA2	--	--	---	CCAGGTGTTGTGGCAGTGCCTGTAATCCCAGCTACTCGGGAGACTGAGGCATGAGAATCTTTTGAAC CGGGGAGGCGGAGGTTGCAGTGAGCTGACATCGCGCCACTGCACCTCAGCCTAGGTGACAGAGCAAG ACTCC
ESTD-ARSB	--	--	---	GGAAGAAATGGAGCCTGTGGAAAGGAGCGCTCCAGGGGTGGCTTTGTGGCAAGCCCTTGCTGA AGCAGAAAGGCGTGAAGAACCGGGAGCTCATCCACATCTCTGACTGGCTGCCAACACTCATGAAGCT GGCCAGGGGACACACCAATGGCACAAAGCCTCTGGATGGCTTCGAGTGTGGAAACCACATCAGTGAA GGAAGCCCATCCCCAGAAATTGAGCTGCTGCATAATATTGACCCCAAC

[illegible]



ESTD- CTLA-4	--	--	--	---	---	---	ATGGCTTGCTTGGATTTCAGGGGACAAAGGCTCAGCTGAACCTGGCTACCAAGGACCTGGCCCTGCAC TCTCCTGTTTTTCTTCTTTCATCCCTGCTTCTGCAAGCAATGCACGTGGCCAGCCTGCTGTGGT ACTGGCCAGCAGCCGAGGATCGCCAGCTTGTGTGTGAGTATGCATCTCCAGGCAAAAGCCAC
ESTD- CYP2D6	--	--	--	---	---	---	CAGGCCAGCGTGGTCGAGGTGTCACCATCCGGCAGAGAACAGGTCAGCCACCACTATGCACAGGT TCTCATATTGAAGCTGCTCAGGGTTCCTGCTGGCCTGAGCAGGGCCGAGCAGCATACTCGG
ESTD- D11S1873	--	--	--	---	---	---	AAAAAACATTTTAACACCTTTTCAATCATATACACCAATAAATTTCCATTTTTCACATAAGTCAGTT TGAGCTGAGTTTTTCCAAATTAATGCAATCTAAATGTATACTGATTAAATGCAAGTTCAACAGACA ACTTCCCAAGCATCTACGATCAGAAAGGTCAAAATATTACATATCTGGATTAAATATATGCCCATAT CTGCATGTC
ESTD- D17S33	--	--	--	---	---	---	CATCCCAAGCCCATCTCTTAGCCACTGGCATTTTTCGCCCTCTGACAGATACACTCAGGGCCGT CATGCTGCACACATCCAGGGGCGCCCTACCTTTGTAGTCCATGGGAAGGCTCCTCTGGGGGGTG GGGTGTGTGGCTATGTGTGGTCTTGTGTAGACGGGGCTTTGGTTTCAGTTGCACATTTGGGTTATT GCAGATTGCTTTGTCTTCCACCTGAGCGAGCCTC
ESTD- D18S8	--	--	--	---	---	---	TTTGAGACCACCTGGCCACATGGCGAAATCACATCTCTACCAAAATACAAAATTAAGCTGGGTGT GGTGGTACATGCCTATCGTAATCCAGCTACATCGGGAGGCTGAGCGAGGAAATGCTTGAACCCA GGAGGCAGAGCTTCAGTGAGCCAAAGATCACACCACTGCACCTACAGCCTGGGTGACACAGTGGAGA CTCTGCTCAA
ESTD- D3S11	--	--	--	---	---	---	AACTGATTAGAACCTGAAATACATATTTATCTGAAAAAGTCGAGTTATTGGCTCATCACATTGG AATTTTGCATCATTAATAAATCCAAATAAGTACACTGTAATAAAGAAATTAACAGAAATATCATTTGT TTATTCAAACTATTTATCATTATTTATTTGGTAAGCCACTACTAAATTTCTAAAGCATGTTTCTGAAAG TTTA
ESTD- D3S12	--	--	--	---	---	---	AGGTTCCACATTATTGCTGATGTTTGTGATGTTTCCAGGAGCCTTGATGTCATTTCTGTATCTCCTCAG GTATCCACCTTGAGACGTACTTTTCAAAAACCTCTCTACAGCCGTTGTTGTTATTAATTCAGGTTGA ACATAAAGTA
ESTD- D3S2	--	--	--	---	---	---	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTTCTCTGC TGAGTCTTATTCAAACTGACAGCCATTTATGCCACCTGAATATGGTCAGTTACAGCTGATATCCC AGAAGTGAACATACTGCTCCTAGAACCCAGAGTCATCTGGATGTTCTGTTCCGGTCTTCACGATGG CAGGTATGAAATATAATAATCTGTCTTTATTTGGGAAGGATGCCGGTATGT
ESTD- D4S338	--	--	--	---	---	---	TTTTCTGTTTACCTTGTTTCAGATCCTTCAGAGGAATCCCTATATATGGCAGGTATGAAATGTATTT CTTAAACAATAAAGTTGAAAGTCCAAAATTAATCCTTGATCCATGGACTGCAGAAATAAATGTTATTT TAGCTGTCAGAAAAACAATACTAATCTTGCATATGTTTCATCAGAGCCCTTGGGTGACCAGGTGTATT GCCAATAAGCAGTAATTTTGAGAGGAATCTGTTTTCATGCACTAG
ESTD- D4S95	--	--	--	---	---	---	CTTTCATGCACGATAGGCTTCTCTACTAATCACAGAAATTTTGAGAAAGAGCAAAACAACTTTCAAGG ATAATGGGGCAATCACCTTCTTTCTTTTAGAGTCTACCGG

ESTD-D7S399	..	--	---	---	---	TGAATCTTAATTGCTATCTCTACAAAATGTATAAATCCTGAATCTGACATCTAGCCACCTCCATAGAT AACTGCTAGAGACCCAGTCTCCTACATCATCCTTTTACAAACATTTTCCATCCATGGACTCCATAG AATATTTGAAGAAACAAACATGACAAACATTTTC
ESTD-DM	--	--	---	---	---	GTGGGACACCGAGGGCTCCAGGCTGGGGCTTGACAGTGTGGCTCAAGCAGCTGCTCGGCCTCCACT TCCATGGGTGTGGGGCTGGACCTCACTGTCCTGGGAGAGAGAGGGAGTGGGGAGGGAGACA GAATGCTGATTATCTGGTGAGAACCAAGAACTTCTGGCCTGTGGTAGGGGAGCTGCTTCCAAGAC TCCTGATTTGAGGAAGGGAGCAGCAGAGCGAAGAGAACAGAGT
ESTD-DRD1	--	--	---	---	---	TCCCAGCCTATCGGTCTATTTGGACTATGACACTGACGTCTCTCTGGAGAAGATOCACACCCATCAG ACAAACGGTCAGCACCCCAACCTGAATCGCAGATGAATCCTGCCACACATGCTCATCCCCAAAAGCT AGAGGAGATTGCTCTGGGGCTCGCTATTAGAAACTAAGGTAC
ESTD-DRD2	--	--	---	---	---	TCTGCCTTTGGTGAGGAGGCTGCCGGCGAGCCAGGAGCTGGAGATGGAGATGCTCTCCAGCACCA GCCACCCGAGAGACCGGTACAGCCCCATCCACCCAGCCACCAAGCTGACTCTCCCCGACCCG TCCCACACGGTCTCCACAGCACTCCCGACAGCCCCGCCAACACAGAGAAGATGGGCATGCGAAAG ACCAACCCAAAGATTGCCAAGATCTTTGAGATCCAGACCATGCCCAATG
ESTD-DRD3	--	--	---	---	---	AAGAGATGCCAGGATGAGCGGAGTAGGAGAGGGCATAGTAGGCTGTGGGGGGGGCTGGCTGG CACCTGTGAGTTCTCTGCCCCACAGGTAGTTTCAAGTGGCCACTCAGCTGGCTCAGAGATGCCATA GCCAGAGGGAGTGGGTGATGCCAAGGGGCTTCTGTGAGGAGA
ESTD-ERB2	--	--	---	---	---	TCTTCAGGATCCGCATCTGCGCTGTGGTGGGCATCGCTCGCTAGGTGTGAGCGGCTCCACAGCTGG GGTGAGGGGTGGTGGGTGAGTGCGGGGGGGGGTGCAGACCCACGCGGGCTGGGAGGACTTCAOC CGCCTCACCTCCGTTTCTGTCAGCAGTCTCCGATCGTGTACT
ESTD-ETS2	--	--	---	---	---	ACTCACAGTGTCTTTAAGTGAAATGGTCGAGAAAGAGGCCACCAAGAGCCGCTCCTGGCGCCTGGCA GTCCGTGGGACGGGATGGTTCTGGCTGTTTGAGATTCTCAAAGGAGCGAGCATGTGCTGGACACAC AGACTATTTTAGATTTCTTTTGGCTTTTGAACCAAGGACAGCAAAATGCAAAAACCTCTTTGAGAGG GTAGGAGGTGGGAAGGAACAACCATGTCTATTTCAGAAGTTAGTTTG
ESTD-F2	--	--	---	---	---	GATAAGTACACTGAGGCCCCAGGAGGTTATTGCCTAGTAGCCCAACTGTGCATGCACGCTTAACCTCT GCACCAATGGCTCCAAAGCCCGTAGGGGAAGTGGGGGATCTAGGGGATGGGTAGGAAATGGCCC AGCCAGTCCCGGCGGTGCTGGTGGTCCAAACAGAGAGGCGGTGGAGGAGAGACAGGAGATGGGC TGGATGAG
ESTD-F9	--	--	---	---	---	AGATCCTGATGATTTTTTCTCTATTTTTTCTAAATGTTTTACAGTTTGAAGTTTTAGATTTATGCCCA TGCTCCATTTTGAAGTAAATTTGTAAAGTATGATGTTTAACTCAAACTTCATTTTTTTTTTCCATA GGTATGTCCAAATTTATCCAGCACAAATTTGTTAAACAAAAAC



ESTD- IGHV4-6	--	--	--	--	---	---	---	TTTACTATTTCAATGGATACAGAAATTGTGGGAGTCACTATATTCCTATGAACAAAAAATTCAGATTT CAGTTTAAGTAATGTTGCCTACATTTGTGTAGTGAAGGGGAGTGGTGGATCCGAGAGTGGTGGG TGCACGGACATAATGATTCAGAAAGCAATATGGAAGATGAGTATCTATGGATACGAAGTAAAGT ATGTAATACTTCACAAAATACTAATAACGGAGTTGAATATAAAACCCA
ESTD-IL1A	--	--	--	--	---	---	---	CAAAGTAAGCACCCCAATAAATGTTAGCTATTACTATCATATTATTATTATTATTTATTTT AGATGGAGTCTGGCTGTCTCACCCAGGCTGGAGTGCAGTGGCACAATCTCGGCTCACTGCAAGCTCTG CCTCTGGGTTTCATGCAATCTCTGCTCAGCCTCCGAGTAGCTCCGAGTACAGGCAACCCGCCACT GTTCCCGGCTAATTTTGTATTTTAGTAGAGACGGAGTTCAACCGT
ESTD-IL1B	--	--	--	--	---	---	---	CCACTACAGATGGATAAATGGGTACAATGAAGGGCCCAATAGCCCTCCCTGTCTGTATTGAGGGTGT GGGTCTACCTTGGGTGCTGTTCTCTGCTCAGGAGCTCTCTGCAATTCAGG
ESTD- KRT10	--	--	--	--	---	---	---	CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTCCATGTCAGTGTACCTTTTGGCAATAT AAAGGAAGAAATGCATTTTAAAGTAACTGCTAAGGTTTTTCCATTAAACCATACTTACTTCTAAG AGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGAGTCTCTTTTAAATAGTCTC TGCCAGATACATCTCCCTATATAAGTTATAACCATTTGATA
ESTD- KRT8	--	--	--	--	---	---	---	ACCTCACCCCTCCCTTAGCCGTGGGAGCAGGAAATCTCTCCAAATCCATGAATACACATCGG ATTGGACACCTTGAGAGTCTTAAAGCAGGGCCTGACATGAGACCTCAGACAGAACTTCTAGAGTT TGCTAGAGGTCAAGGTCAAGACTAAAGAGGGGCCAGAAATGTTAAGTACAAAAGTGAAGGCCCATAG GCTGCCTATCTCTCCGCTCAGGTTTACCACGTCAACATTGACACA
ESTD- LF79	--	--	--	--	---	---	---	GGGTGATTTGAGGCTCAGTTAATTTCAAAATTTAACCCTAGCAAACTGCATTGGTATTTAGA AAAATAAAAAATTTCCAATATGATGCTGTGTTATACCTGCCCTCTGCCATGCAGCATATAGCCTGT GGGAACAGAGGGCTTCCCTTACCACCCAGA
ESTD- LMP2	--	--	--	--	---	---	---	TACACACTTTCCTTACCATTCACTGAAACGACTCGCAAACCTGGAGCCTTGTAGGAATGGAGTTGA CCTTCCCAAAAAGCCACTATGATAAGCTATTTGGTG
ESTD-LPL	--	--	--	--	---	---	---	TGTCAGTGTCCCTAGGGGCACTCACCACCTCCAGCTTCTTCAGCTCTGGCCTGTCTGCTGCCTGCA AGGTTTTGCTTAATCTCAATTCATGCTCTTCATCTTTTAGCAGCTGTGGGTTTTGTTGTTTC TTCTGTTTTGCTTAGTATCTGACTACTTTTTTAATTATAAAAAGAGATGTATCTAAACAAAAATAGAG ATTGTTATCAGAAGTTCACAACATTTATTAAAAATTTTTCACCTG
ESTD-MOC	--	--	--	--	---	---	---	TTGTCAGGAGTGTGCTGATGCTGCCCTCCCAAGCTCTGCCCTAGCCGAACCTCAGGACAACGTGCAG CATCCATGTAGGAGAGCCTTAGTCAAGTGAATGCTGAGGAAGCAGTAAACAGCATGCATCCCGAA TCTCAGGAAGTCTCTGCTTTCCAAGGGTTTGGTCTAAGTTGCTGATTACCCGGATTTTCTGACGATC TTTCAACTGCTAGAGCATCTGGTCTCTGTTTAGCATGG
ESTD-NF1	--	--	--	--	---	---	---	ATTATCCAGATGAATTTACAAAACATAACCAGATCCCACAGACTGATATGGCTGGT

ESTD- NFKB1	..	--	---	---			AACATGGACTGTATATTGTACAAAAAGTTTATTTCTAAAAAGAAAAAGAAAA AAATTTAAAGGGTGTACTTATCCACACTGCACACTGCTAGCCAAACGCTTATTGTGGTAGG ATCAGCCCTCATTTTGTGCTTTTGTGAACCTTTTGTAGGGACGAGAAAGATCATTTGAAATCTGAG AAAATCTCTTTTAAACCTCACCTTTGTGGGTTTTTGGAGAGGTTATCA TGTCCTTAGGCCAGCCCTGCTTGCTCCTCCCTGGCTGTATCTTCAGTACTGCAAGAGAACACAGAC AT
ESTD- NPPA	..	--	---	---			GGAGGAGGAGGTGGGAGGGGCTGTCTGCTCCAGGTCCACAGACCAGAGAGCGGCTCAGTG TATCCCCACCCCAATGTGGCGCTGGGAGATGAAGAGGAGTTGATGCAGGT
ESTD- NRAMP	..	--	---	---			GTGTTTCTTAATCTTTCCAGGAACAGAGTGACCATATTTCTTTCTGCAGGCATATAGAAATTTGGT GGGTTTCTTTTATGTAGGGTGATATTGGATCTTTTGTGTTGTTGTTATATTAGCAATTTGAGGG ACAAACAGATAGGCAGAAATGGGCTTGAATAGTAGATGCTTATTTAACCTTGGCAATAGCATTCG ATTCCCTGTGGTTTTTAATAAAAT
ESTD- NRAS	..	--	---	---			GTGACCTTCTCACCTTTAAAAAACTTTACCGGAGAAGAAATTAATATATATGCTATGCTATCAGCAGA TCTGAAATTTAGGATAAAACAGAAAGGAGAGGTATGTAACA
ESTD-OTC	--	--	---	---			GCCACCAACCCACCCAGCACACCTCCACCTCAGCAGCAAGGTTGTTGACACAGAGAGCCC TCAGGGGCACAGAGAGAGTCTGGACACGTGGGAGTGACGCTGATCATCGGAGCGCGCGGCAC ATGGCAGGATGAGGGAAGACCAAGAGTCTCTGTGGGCCCAAGTCTAGACAGACAAAAACCTAG ACAATCACGTGGCTGGCT
ESTD-PAI1	--	--	---	---			CTCTTCAGGAACCAACAGTCTCTTACCAACACGACTTATTGCTGCCGAGAGGTACAAACCGTAGA ACTTCTCTTAAGTAAATTTAGTTAAAGGAATCGAACTGGCTCTGAAGACATGGAGATACTGCCT AATCGACTGGCTTTCATTAGCTCTGTGAGTGTTTCTTTCACCTTTCTGTGTTCTAGAACGTTTCTAG GACTGGCAGTTTAAAGCTTTCAGTTAGGCTTTCTGTATACCAATGCC
ESTD-PAR	--	--	---	---			CCTTCTCATGCCCAGATGGAATTCAGTCCCTTCAGGATCTGCCTAACCTGTGACAGTCTAAAGAGT CTGAGCCGTGGCTGGGAGGGCAGGACTAATCCAAATCTACCCGAGCTTGCTCGCATACAGACG GACAGTGTGGGCAACATTGAAGCCCTCGTACC
ESTD- PBDA	--	--	---	---			GGGAGTAAACCTTGGATTGGGAGATTTCATTCTACAGTGTCTGGTTGGTAAGCCCTCAGCAACA GCCAGTGGAGACTGGAACACAAACCATAGCCTATTTCGTAGCCATAATTAATGGTTTGTGCCCTACATT ATTACTCCTTGCCATTTCAAGAAAGCATTGCCAGCTCTTCCAATCTCCATCACCTTTGGGCTTGTTTT CTACTTGGCCACAGATTATCTTGTA
ESTD-PS-1	--	--	---	---			ATGAACATGGTTCTTTAATTTATGATATGTTTATAGTATCTTAAAGGGCTCTTTTTTTTAA ATGCAGAAAGAGGGGAAAGAGCGAGCTGGTGGACAAGGTGTTTTTCTCAAGGCTCATACAGA TTCTGAAATCATGGTCCCTAGAACATTTGTAAAGAGGTAAGICTTATGAAATTAATCTT
ESTD- PXMP1	--	--	---	---			ACCTACAGACGTGCTGGATGTGTGTGTCACCCAGGAATCTGAGAGCGAGAGCGGCTGGCTG CTGGAGAGAGAGCGTGGCGGAGACCTTGAAGGCT
ESTD- Per/RDS	--	--	---	---			



ESTD-RDS	--	--	--	---	---	---	CCCGAGGAATCTGAGAGCGAGAGCGGCTGGCTGCTGGAGAGAGCGGTGCCGGAGACCTGGAAGG CCTTTCTGGAGAGTGTGAAGAGCTGGCAAGGCAACAGGTTGAAGCCGAGGCGCGCAGACGAGG CCAGGCCCAAGAGGCTGGCTGAGGCGCTGGGCGCCCTCCCTCCGAACTGAGAAATAGTGCACCT CCAGAAACGTGGATCTCCCTCATCCAACTCCGAAAGTCTGAA
ESTD- RYR1	--	--	--	---	---	---	CTTCGTACGGGAGGTACGCTCTCCGCTCTTTCATGGACATATGGATGAGTGTCTGACCAITTTCCC CTGCTGACAGTATGACCGGAGACTTGTCTACTATGAGAGGGAGCTGTGTGCACTCATGCCCGC TCCCTGAGGCTGGAGCCACTGAGAAATCAGCTGGAGTGGAGCCACCTGCGCTGGGGCCAGCCACT CCGAGTCGGCATGTCACTACCGGGAGTACCTAGCGCTCACCGAGG
ESTD- SPTB	--	--	--	---	---	---	TGAACACCCCTGTGGTCCGGAGCCAGGTTGTGTTCTCTGGAGCCCTGAGGAGTTGTGTCTGTGTG CAGTCCCCCGGCGCACCTGCTGGTTGAGCCTGGACATACACCTTCACCTCTTTGGCCCGGAGAGAC ATTTACCCACCTGGCCATGTCCCTGGCTGTGTGACACCCCTCTGTGAAGACCCCAACCCCTGCCTCC CCACCCAGCCAGTTTCTAGCAAGGGCAGGAC
ESTD- SSA1	--	--	--	---	---	---	TTACITTTGTGGATTGTTCTTTTGTGTGCGAGCACCTTTTCAACATGATGTATCCCATTTGTCCAAG TTTGCTTTGGCTGCTGTGCTGTGGGATATTTGAAGAGATCTTTGCCAGTCCAATGTCTCTAGAGAG TTTTCCCAATGTTTCTTGTAAATAGTTTCATAGTTGAGGCCCTAGATTAAAGTCTTTAATCCATTTTG ATTTGATTTCTGTA
ESTD-TAT	--	--	--	---	---	---	AAATGGTCAGGACCCCTGATCCACAAGAAGTGTGTACCATTTTCATCAGGGCCATCAGTTTCATTCAGCTC CCATGACTGGGATGCTAAGTCAGCAACTGAGTTTCATTCATCTTAAATGACTTTGTGGGACAGGATCA ATTTCTCTCACCTAGAACGTTTGTTTACAACCTTTCTCCAGTATGGATGGGATTATGATGGGGG GAGAAGCAAAATTTTAAATAGGACCCCATGAGACACATCA
ESTD- THRB	--	--	--	---	---	---	TGCGGCTTTCTCCGGCAGGGTAGACTTCTTACTTGGCTGTGATTTCCAGAGAAAGAGTCCCAAG CACACGAAACAGAAAGTTGCAGATCCCATGAGGCCCGAGTCTCAATCACACAGGATCACTTCATCCA CACTGGATTGGCCCAACAAGTCTGAGTGCCAGCCAGGACTCAACGGTCCCTGTAGATGGG
ESTD- TNFA	--	--	--	---	---	---	TTCTGCATCCTGTCTGGAAGTTAGAAGGAAACAGACCACAGACCTGTGTCCTCCAAAGAAATGGAGG CAATAGGTTTGGGGGCATGAGGACGGGTTTCAAGCTCCAGGGTCTACACACAAATCAGTCAGTG GCCCAGAAAGACCCCTCAGAATCGGAGCAGGGAGATGGGAGTGTGAGGGGTATCCTTGATGCTT GTGTGTCCTCAACTTTCCAAATCCCGCCCGCGGATGG
ESTD-TYR	--	--	--	---	---	---	TAGTGAAGTTTTCATCTCTGTGAGCTTCTGGATTCTTGTCCACCCGCAACAAGAGTCTATGC CAAGGCAGAAAGCTGTGCTTCATGGGCAAAATCAATGTCTCTCCAGATTTCCAGATCCCCCAAGCA GTGCATCCATTGACACATAATAATGCATCCAGACAAAGAGGTCAATAATTGATGTGCGTTAAACAT GGGTGTGATCCATTTTTCATTTGGCCATAGTCCCTATGGGATGACA

[illegible]

EST11458 6	--	--	--	---	---	CCACTTGGTAGTGCCAGTGTGACTCATCCACAATGATTTTCCAGTGCTCATCTTGTCTCGAGTTT CTCTGCCATGTTGCTATTGACGACGGACCTGTCCCAAGCCAGATGATTTACCATTTCCACAGTGGT CCATTAAACAATTCTATGAGCCAGGAGAGAGATTACGTATTCCTGCAAGCCGGCTATGTGTC CGAGGAGGATGAGAAAGTTTATCTGCCCTCTCACAGGACTGTGGCC
EST39852 8	--	--	--	---	---	CGGCTTCCTCCAGGTATTGTCAGAGGCGGAGATGACCTCTATGTCTCAGATGCATTCCATAAG GCATTTCTTGAGGTGAGTACACCTTCCCCACTCTCTACGGTACAGAAAGGAGATGCATGAACAGCA GGAACACGTGGAAAGGCCTGTTTCCAGTGTTAAGGCATGCAAAAGGCCTCCACAGGCTGCTATAAT ACAGCCCT
EST62448 0	--	--	--	---	---	ACCTGGTGTGCTGGTGTGCTGGTGAACCTGGTCTCTTGGCAITGCGGCCCTCTGCGGCCCTGG TCTCTGCTGGTGTGGGTAGTCTGGAGTCAACGTGCTCTAGTGAAGCTGGTGTGATGGCAAC CTGGGAACGATGGTCCCAAGGTGCGATGTTCAACCGGACACAAAGGAGAGCGGGTTACCCCTGG CAATAT
EST36027 2	--	--	--	---	---	AGTGACTTCCAAGGAAATGGCTACCCAACTTGCCTTCATGCGCCTGCTGGCCAACTATGCCTCTCAGA ACATCACCTACCCTGCAAGAACAGCATTCATACATGGATGAGGAGACTGGAAACCTGAAAAAGG CTGTCACTACAGGGCTCTAATGATGTTGAACCTGTTGCTGAGGGCAACAGCAGGTTCACTTACACT GTTCTGTAGATGGTCTCTAAAAGACAAATGAATGGGGAAGACAA
EST12274 0	--	--	--	---	---	CCCCAGTTGACAGCCACTGCTCTAGACTAAGTTTCTTCTCCAATAGAGCCTTACCAAAGTGAT TACATAAAGAAAGTCAAGTGGTTTACTCCTCATGACCAATATTTCTCCCTCTTAGGATGAGGTGA TAGTAAATGACCGATGGGTGAGAACTGTTCTGTCAACCATGGAGGATACTATAACTGTGAAGATAA ATTCAAGCCACAGAGCTTGCCAGATC
EST76807 EST44438 7	--	--	--	---	---	ATGCTAAGGGGATCGGACATGAAAGGACCCCTGTAGCCGATTGTCTATCTCCAGCGGCCCTGTCTATC CAGCTCACTCATCAATGGGCCAGTCAAGCCAGGCACTGGGCTCCGGAGGACTCAACCACTGCCCCCT GCTGCCATGTGGACTGGTCAAGTTGAGGACTTCTTG GCAGCCAGGAGCGCTGCACCATGCCCGCATAGATGCGGAACCTCAAGCTCGACTTCAAGGACGTCCT GCTCCGACCTAAGCGGAGCAGCTCAAGAGCCGAGCGGAGGTGGG
EST12839 3	--	--	--	---	---	TGAAAAACACACAAAATCTTCTCCAGATGCCCTATGGCTGTGGAGAGCAGAAATATGGTCTCTTTGCT CCTAACATCTATGACTGGATTATCTAAATGAACACAGCAGCTTACTCCAGAGATCAAGTCCAAGG CCATTGGCTATCTCAACACTGGTGAGTGATTACTTGAGTAAGGAAACTTGAATGTTATTCAACTGG ATTTCCAGTAGGTTTCAGTTACTTATGAATATTATGATACCTTAGCTTAG
EST54419 8	--	--	--	---	---	CTTCTGCCATTTGAATGATATTGTTGCTGTGGACCTGAGCACTTTTATGGCAAAATGATCACTA TTTTCTTGACCCCTACTACAATCCTGGGAGATGATTTGGGTTAGCGTGGTCTGATGTTGTCTACTA TAGTCCAAAGTGAA

EST10398 2	--	--	--	---	---	---	TGCTGGGGTGGCAAGGCTGCAACAAGGAGGCAACCCAGGAGGCTTTTATGAAGCGGGCCATGGTA AGATGCTGCCACCTCTTATCTACTTGATGATGTTTACATTTGGGGCTTGACITTTCAACACGAGGAAG CATTGTTTCTTCGGGCAAGAAGGTATCTACCAATAGTGTCTATTAGGCATTG
EST36751 7	--	--	--	---	---	---	CCAAAGTGTTCAAATTTAGCTTGCAGGTTTAACTCGATTACTTTTCTATTCAAACTCTCTGTAAAA TTGAAATATGAACCTTAGTTTCTGATCTATGTTTCAAGTTAAACAG
EST40562	--	--	--	---	---	---	CACGTGGAAGGAGCTATTTTGGAGGCTTTAAGAGTAAAGAACTCTGCCCAAACTTGTGGCTGAC TTTATGGCTAAGAAGTTTCACTGGATGCAATTAAACAAATATTTTACCTTTTGAATAAATAATG AAGGATTTGACCTGCTTGGCTCTGGAAGAGATATCCGTACCGTCTGACGTTTGAACAATACAGAT GCCTTCCCTTGTAGCAGTTTTCAGCCTCTCTACCCCTA
EST18288 3	--	--	--	---	---	---	GCTCTATACCCCTGTGGTCTCCACGCTCTCTGGACTTCAACAGAACTGGATGTTGCTGCTGAGAA GATTGACAGGTTTATGACAGGCTGTACAGGATGGAAGACTGGCTGCTCCCTGACGGGAGCCAGTGTGG ACAGCACCTGGCTTTCAACACCTACGTCCACTTCCAAGGTAAAGGCAAACTCTCTGCTGGCTCTGGC CCTAGGACTTAGTATCC
EST70523 3	--	--	--	---	---	---	TTCCGGCAGCCCCCATCTTGGCACCTTGGTCCCTCAGGGGCCACCCCGCGGCACTCACCGCTCT CGCTCTGGTAACATCCGGCGGGCGCTCTTGGACACATAGCTGGACCGTTTCCGTATAGGAGG ACCGTGTAGGCTTCTCTGTCGGGGCTTGCAGGGGCCAGCCCTGCAGAGAGAGGGGTCTCTGCTGGT TGAGCTGAACACAGCTGTGGAGTGTCTCCACGCTG
EST58707 7	--	--	--	---	---	---	CAGTGTATCTGGAAGCCTACAGGACACCAAAATACCTTATCATCAATTTGTTACAGGAGGCTTT AAGTTCAGGATCTTTGGCTACATGAAGGCCAAATTCGAGAGACCTTAGAATACACGAGACCGGA ATGTATCAATGGACATTCAGCAGGAACCTCAACGATACCTGTCTCTGGTAGGCCAGGTTTATAGCA CACTTGTCACTACATTTCTGATTGGTGGACTCTTGTGCTAAGAACCTT
EST74167 6	--	--	--	---	---	---	AGACCATGAAGGAGTTGAAGGCCTACAAATCGAACTGGAGGAACAACCTGACCCCGGTGGCGGAGG AGACGGGGCACGGCTGTCCAAGGAGCTGCAGGCGCGCAGGCGCGGCTGGCGCGGACATGGAGGA CGTGGCGGGCGGCTGTGTCAGTACCGGGGCGAGGTGCAGGCACTCTCGGCAAGCAACCGGAGGC TGCGGGTGGCGCTGGCTCCACCTGCGCAAGCTGGTAAAGCGGCTCTC
EST43211 8	--	--	--	---	---	---	CGCTGTGTCAGTAACCGGGGAGGTGCAGGCCATGCTCGGCCAGACCGAGGAGCTGCGGGTGCG CCTCGCTCCCACTGCGCAAGCTGCGTAAGCGGCTCTCCGCGATGCCGATGAOCTGCAGAAAGCGGC TGGCAGTGTACAGGCGGGGCGGCGAGGGGCGGAGGCGGCTCAGCGGCATCCGCGAGCGGCTG GGGCGCTGTGTTGAACAGGGCGGCTGCGGGGCGGCGGCTGTTGGGCTC
EST36770 4	--	--	--	---	---	---	TGTAGCCAAAGTCACCTGCATCATCATTTTGGCTGTGGCAGGCTTGGCCAGTTTGCAGCTATAATCC ATCGAAATGATTTTTCATTGAGAACACCAATATTACAGTTTGTGCTTTCATTATGATGCCAAAT TCAACCTCCCGATAGGCTGGGCTGACCAAAATATACTGGGTTCTGTTTCTCTTCTGATCAT TCTTACAAGTTATACCTTATTGGAAAGGCCCTAAAGAAGGCTTAG





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## EQUIVALENTS

While this invention has been particularly shown and described with references to preferred embodiments thereof, it will be understood by those skilled in the art that

5 various changes in form and details may be made therein without departing from the spirit and scope of the invention as defined by the appended claims. Those skilled in the art will recognize or be able to ascertain using no more than routine experimentation, many equivalents to the

10 specific embodiments of the invention described specifically herein. Such equivalents are intended to be encompassed in the scope of the claims.

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## CLAIMS

WE CLAIM:

1. A nucleic acid segment shown in column 7 of the Table,  
or a portion thereof which includes a polymorphic site,  
5 or the complement of the segment or portion thereof.
2. The nucleic acid segment of claim 1 that is DNA.
3. The nucleic acid segment of claim 1 that is RNA.
4. The segment of claim 1 that is less than 100 bases.
5. The segment of claim 1 that is less than 50 bases.
- 10 6. The segment of claim 1 that is less than 20 bases.
7. The segment of claim 1, wherein the polymorphic site is  
biallelic.
8. The segment of claim 1, wherein the polymorphic form  
occupying the polymorphic site is the reference base  
15 for the fragment listed in the Table, column 3.
9. The segment of claim 1, wherein the polymorphic form  
occupying the polymorphic site is an alternative form  
for the fragment listed in the Table, column 4.
- 10 20 10. An allele-specific oligonucleotide that hybridizes to a  
segment of a fragment shown in the Table, column 7 or  
its complement.
11. The allele-specific oligonucleotide of claim 10 that is  
a probe.



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12. The allele-specific oligonucleotide of claim 10,  
wherein a central position of the probe aligns with the  
polymorphic site of the fragment.
13. The allele-specific oligonucleotide of claim 10 that is  
5 a primer.
14. The allele-specific oligonucleotide of claim 13,  
wherein the 3' end of the primer aligns with the  
polymorphic site of the fragment.
15. The allele-specific oligonucleotide of Claim 10, which  
10 is selected from the group consisting of the nucleotide  
sequences of the Table, column 5.
16. The allele-specific oligonucleotide of Claim 10, which  
is selected from the group consisting of the nucleotide  
sequences of the Table, column 6.
- 15 17. An isolated nucleic acid comprising a sequence of the  
Table, column 7 or the complement thereof, wherein the  
polymorphic site within the sequence or complement is  
occupied by a base other than the reference base shown  
in the Table, column 3.
- 20 18. A method of analyzing a nucleic acid, comprising  
obtaining the nucleic acid from an individual; and  
determining a base occupying any one of the polymorphic  
sites shown in the Table.
19. The method of claim 18, wherein the determining  
25 comprises determining a set of bases occupying a set of  
the polymorphic sites shown in the Table.

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20. The method of claim 18, wherein the nucleic acid is obtained from a plurality of individuals, and a base occupying one of the polymorphic positions is determined in each of the individuals, and the method
- 5 further comprising testing each individual for the presence of a disease phenotype, and correlating the presence of the disease phenotype with the base.